

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 06:37:00 / Search time 18.6667 Seconds
(without alignments)

77.297 Million cell updates/sec

Title: US-10-676-049-1

Perfect score: 79
Sequence: 1 VDTDSSTGLRWTP 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2522

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	35.4	14	2	PH1768
2	26	32.9	10	2	UN0024
3	25	31.6	13	2	S23372
4	24	30.4	11	2	PT0273
5	24	30.4	12	2	S74144
6	23	29.1	10	2	S39030
7	23	28.1	10	2	S66248
8	22	27.8	10	2	S27178
9	22	27.8	12	2	A42324
10	22	27.8	14	2	PH1758
11	22	27.8	14	2	PH1759
12	22	27.8	14	2	PH1767
13	22	27.8	14	2	A28018
14	22	27.8	15	2	PA0001
15	22	27.8	15	2	PA0114
16	21	26.6	10	1	RHLMGS
17	21	26.6	10	1	HE0787
18	21	26.6	10	2	D60787
19	21	26.6	10	2	B60787
20	21	26.6	10	2	A60788
21	21	26.6	10	2	C60589
22	21	26.6	10	2	D60588
23	21	26.6	13	2	PH1636
24	21	26.6	15	2	PH1612
25	21	26.6	15	2	B59137
26	20	25.3	5	2	A60803
27	20	25.3	5	2	G37196
28	20	25.3	10	1	SP8GNK
29	20	25.3	10	2	TI7075

30	20	25.3	11	2	A34662	Achafina cardio-ex
31	20	25.3	14	2	PH1757	T cell receptor al
32	20	25.3	14	2	PH1766	T cell receptor al
33	20	25.3	14	2	PH1769	T cell receptor al
34	19	24.1	11	1	BOCC	eleodoisin - curled
35	19	24.1	11	1	BOCC	eleodoisin - musky
36	19	24.1	11	2	A34243	H-hyosopborin - Ja
37	19	24.1	12	2	A54315	entractin/nidogen -
38	19	24.1	12	2	PH1308	Ig heavy chain DJ
39	19	24.1	13	2	S57567	T cell receptor V-
40	19	24.1	13	2	C59137	protein P13 - gold
41	19	24.1	15	2	T46625	hypothetical prote
42	19	24.1	15	2	S08209	hypothetical prote
43	19	24.1	15	2	P80450	23k protein 4307 -
44	19	24.1	15	2	PL0109	complement factor
45	18.5	23.4	15	2	A42413	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH1768 T cell receptor alpha chain V region (clone 2V alpha 7.2-3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1768

R:Forcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; UID:93301585; PMID:8391057

A:Accession: PH1768

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-14 <FOR>

Query Match

Best Local Similarity 35.4%; Score 28; DB 2; Length 14;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 ITDSSITGLRW 12

Db 4 VTDSNYQLTW 13

RESULT 2

UN0024 neurokinin A - chicken

C:Species: Gallus gallus (chicken)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Aug-2000

C:Accession: UN0024

R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thin, L.

Regul. Pept. 20, 171-180, 1988

A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A:Reference number: UN0023; UID:88204263; PMID:2452461

A:Accession: UN0024

A:Molecule type: protein

A:Residues: 1-10 <CON>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:10/Modified site: amidated carboxyl end (Met) #status Predicted

Query Match

Best Local Similarity 32.9%; Score 26; DB 2; Length 10;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 TDSSTGL 10

Db 3 TDSFVGL 9

RESULT 3

S23372
T-cell receptor alpha chain J region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S23372
R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman
Eur. J. Immunol. 21, 2749-2754, 1991
A>Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu
A:Reference number: S23364; MUID:92037820; PMID:1657615
A:Accession: S23372
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-13 <PLU>
A:Cross-references: EMBL:X58167
C:Keywords: T-cell receptor

Query Match 31.6%; Score 25; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GSRWT 13
DB 8 GSRWT 12

RESULT 4
PT0273
IG heavy chain CRD3 region (clone 3-109A) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0273
R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0273
A:Molecule type: DNA
A:Residues: 1-11 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.4%; Score 24; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 RWTP 14
DB 3 RWSP 6

RESULT 5
S74144
aggrecan - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S74144
R:Bomassar, L.J.; Stinn, J.L.; Paguio, C.G.; Frank, E.H.; Moore, V.L.; Lark, M.W.; Sandy
Arch. Biochem. Biophys. 333, 359-367, 1996
A>Title: Activation and inhibition of endogenous matrix metalloproteinases in articular
A:Reference number: S74144; MUID:96404934; PMID:8809074
A:Accession: S74144
A:Molecule type: mRNA
A:Residues: 1-12 <BOV>
A:Experimental source: cartilage
C:Keywords: cartilage; glycoprotein

Query Match 30.4%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDIITDSIGL 10
DB 2 VDIPBSFFGV 11

RESULT 6
S39030
lysoyl-bradykinin - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 18-Aug-2000
C:Accession: S39030
R:Conlon, J.M.; Olson, K.R.
FEBS Lett. 334, 75-78, 1993
A>Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pla
A:Reference number: S39030; MUID:94039817; PMID:8224232
A:Accession: S39030
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <CON>
C:Superfamily: unassigned animal peptides

Query Match 29.1%; Score 23; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 WTPPL 15
DB 6 WSPL 9

RESULT 7
S66248
processing enzyme, 33k - black gram (fragment)
C:Species: Vigna mungo (black gram)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66248
R:Okamoto, T.; Minamikawa, T.
Eur. J. Biochem. 231, 300-305, 1995
A>Title: Purification of a processing enzyme (VMP-1) that is involved in post-translati
A:Reference number: S66248; MUID:95361851; PMID:7635141
A:Accession: S66248
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <OKA>

Query Match 29.1%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 GSRWTP 15
DB 3 GTRWAVL 9

RESULT 8
S27178
neurokinin A-related peptide - laughing frog
C:Species: Rana ridibunda (laughing frog)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S27178
R:Wang, Y.; Badgley-Parker, T.; Lovas, S.; Charrel, N.; Vaudry, H.; Burcher, E.; Conlon
Biochem. J. 287, 827-832, 1992
A>Title: Primary structure and receptor-binding properties of a neurokinin A-related pep
A:Reference number: S27178; MUID:93075037; PMID:1332683
A:Accession: S27178
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <WAN>
C:Superfamily: unassigned animal peptides

Query Match 27.8%; Score 22; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DSSIGL 10
DB 1 DSSIGL 10

Db 4 DSFIGL 9

RESULT 9
A42324
Cytochrome P450c27/25 - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Feb-1996
C/Accession: A42324
R/Shayig, R.M.; Avadhanl, N.G.
J. Biol. Chem. 267, 2421-2428, 1992
A/Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat mltoc ap.

A/Reference number: A42324; MUID:92129322; PMID:11733943
A/Accession: A42324
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <SHA>
A/Note: sequence extracted from NCBI backbone (NCBIN:78404, NCBIIP:78410)

Query Match 27.8%; Score 22; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 ITDSSIGLRW 12
: ||: ||
Db 5 SRMRLRW 11

RESULT 10
PH1758
T cell receptor alpha chain V region (clone IV alpha 7.2-2) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1758
R/Portcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057
A/Accession: PH1758
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-14 <FOR>

Query Match 27.8%; Score 22; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 ITDSSIGLRW 12
: ||: ||
Db 4 VLDSNYQLIW 13

RESULT 11
PH1759
T cell receptor alpha chain V region (clone IV alpha 7.2-3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1759
R/Portcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057
A/Accession: PH1759
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-14 <FOR>

Query Match 27.8%; Score 22; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 ITDSSIGLRW 12
: ||: ||
Db 4 VLDSNYQLIW 13

RESULT 12
PH1767
T cell receptor alpha chain V region (clone 2V alpha 7.2-2) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1767
R/Portcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057
A/Accession: PH1767
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-14 <FOR>

Query Match 27.8%; Score 22; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 ITDSSIGLRW 12
: ||: ||
Db 4 VRDSNYQLIW 13

RESULT 13
A28018
Very late antigen-1 alpha chain - human (fragment)
N/Alternate names: VLA-1 alpha chain
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
C/Accession: A28018
R/Takada, Y.; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A/Title: The very late antigen family of heterodimers is part of a superfamily of molec

A/Reference number: A94151; MUID:87204112; PMID:3033641
A/Accession: A28018
A/Molecule type: protein
A/Residues: 1-14 <INX>
C/Keywords: duplication; heterodimer; membrane protein

Query Match 27.8%; Score 22; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDITDS 6
: ||: ||
Db 3 VDVVXDS 8

RESULT 14
PA0001
Photosystem I iron-sulfur center protein - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C/Accession: PA0001
R/Kamo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.
submitted to JIPID, July 1994

A/Description: separation and characterization of Arabidopsis proteins by two-dimension
A/Reference number: PA0001
A/Accession: PA0001
A/Molecule type: protein
A/Residues: 1-15 <KAM>
A/Experimental source: stem
C/Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; photosynthesis; photosystem

Query Match 27.8%; Score 22; DB 2; Length 15;

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Page 4

Best Local Similarity 55.6%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDITDSTIG 9
| | | | |
| | | | |
Db 4 VKIYDTXIG 12

RESULT 15

PA014
Photosystem I, iron-sulfur protein II - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 07-Apr-1995 #sequence__revision 26-May-1995 #text_change 30-Jun-1995
C:Accession: PA014
R:Kamo, M.; Tsugita, A.
submitted to JIPID, March 1995
A:Reference number: PA014
A:Accession: PA014
A:Molecule type: Protein
A:Residues: 1-15 <KAM>

Query Match 27.8%; Score 22; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDITDSTIG 9
| | | | |
| | | | |
Db 4 VKIYDTXIG 12

Search completed: September 21, 2004, 06:46:06
Job time : 20.6667 secs

OM protein - protein search, using sw model

Run on: September 21, 2004, 06:14:13 ; Search time 10.6667 Seconds
(without alignments)
73.224 Million cell updates/sec

Title: US-10-676-049-1

Sequence: 1 VDIRDSSIGLRTPPL 15

Scoring table: BLAST62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 801

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	32.9	10	1	TKNB_CHICK
2	23	29.1	10	1	BRK_ONCMY
3	22	27.8	10	1	TKNB_RANRI
4	21	26.6	10	1	GON1_PETMA
5	20	25.3	5	1	BP77_BOTIN
6	20	25.3	10	1	TKNK_PIG
7	20	25.3	11	1	CEP1_ACHFU
8	20	25.3	11	1	PRC1_CARMO
9	20	25.3	13	1	ET21_LITRU
10	20	25.3	13	1	ET22_LITRU
11	20	25.3	13	1	YENP_PHOLU
12	20	25.3	15	1	CKX_WHEAT
13	20	25.3	15	1	DIDH_PSRSP
14	20	25.3	15	1	RBS_PHYPA
15	20	25.3	15	1	UC14_MAIZE
16	19	24.1	10	1	AKGX_LOCMT
17	19	24.1	11	1	TKN_ELEMO
18	19	24.1	12	1	RFL_CONSP
19	19	24.1	14	1	ALYF_ALYOB
20	18	22.8	7	1	TPFY_PACDA
21	18	22.8	8	1	PBP_BRANA
22	18	22.8	10	1	TKNB_RANCA
23	18	22.8	12	1	OPS3_DROVI
24	18	22.8	12	1	TKN_KASSE
25	18	22.8	14	1	ECDC_LYMDI
26	17	21.5	9	1	COM_CONVE
27	17	21.5	9	1	NEF_HV12B
28	17	21.5	10	1	GON3_ONCKE
29	17	21.5	10	1	GON3_PETMA
30	17	21.5	10	1	GONL_SQDAC
31	17	21.5	11	1	TKN1_PSEBU
32	17	21.5	11	1	TKN2_PSEBU
33	17	21.5	12	1	TKN1_KASMA

34	17	21.5	13	1	TV13_PHYRO	P04096 phyllomedusa
35	17	21.5	15	1	ESTB_SCHGA	P81011 schizaphis
36	17	21.5	15	1	HS11_PINPS	P81083 pinus pinas
37	17	21.5	15	1	PH2_PERAM	P82695 periplaneta
38	16	20.3	5	1	UF01_MOUSE	P38639 mus muscu
39	16	20.3	8	1	AKX_TABAT	P14595 tabanus atr
40	16	20.3	8	1	HTF2_PERAM	P04549 periplaneta
41	16	20.3	9	1	UHA2_HUMAN	P40929 homo sapien
42	16	20.3	10	1	GON2_CHICK	P37043 gallus gall
43	16	20.3	10	1	HTF2_CARMO	P11385 carausius m
44	16	20.3	10	1	HTF TABAT	P14596 tabanus atr
45	16	20.3	10	1	LABA_JATWU	P13270 jatropha mu

ALIGNMENTS

RESULT 1

TKNB_CHICK STANDARD; PRT; 10 AA.

AC P19851, 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurokinin A (Substance K) (Neuromedin I).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine; PubMed=2452461;
RA MEDLINE=88204263; PubMed=2452461;
RA Conlon J.M., Kateoulis S., Schmidt W.E., Thim L.;
RT "Arg3] substance P and neurokinin A from chicken small intestine.",
RL Regul. Pept. 20:171-180(1988).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
CC PIR; JN0024; JN0024.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1134 MW; 5A6B4062C9D5B41 CRC64;

Query Match

Best Local Similarity 71.4%; Pred. No. 1.4e+02; Length 10;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 TDSSTGL 10
|||
Db 3 TDSFVGL 9

RESULT 2

BRK_ONCMY STANDARD; PRT; 10 AA.

AC Q9PR21, 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;

RN [1]
RN SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasocactive peptide related to lysyl-bradykinin from trout plasma.";
RL FEBS Lett. 334:75-78 (1993).
CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: Belongs to the bradykinin family.
DR PIR: S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 29.1%; Score 23; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 12 WTPL 15
DB 6 WSPL 9

RESULT 3
TNB_RANRI STANDARD; PRT; 10 AA.
ID P29135;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurokinin A.
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=93075037; PubMed=1332683;
RA Wang Y., Badger-Parker T., Lovas S., Chatterel N., Vaudy H., Burcher E., Conlon J.M.;
RT "Primary structure and receptor-binding properties of a neurokinin A-related peptide from frog gut.";
RL Biochem. J. 287:827-832 (1992).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretagogues, and contract (directly or indirectly) many smooth muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR: S27178; S27178.
DR InterPro: IPR002040; Tachy_Neurokinin.
DR Pfam: PF02202; TACHYKININ; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1160 MW; 526B40705955BA7 CRC64;

Query Match 27.8%; Score 22; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 DSSIGL 10
DB 4 DSSIGL 9

RESULT 4
CON1_PETWA STANDARD; PRT; 10 AA

DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (Luliberin I).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86168192; PubMed=3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT "Primary structure of gonadotropin-releasing hormone from lamprey brain.";
RL J. Biol. Chem. 261:4812-4819 (1986).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the GnRH family.
DR PIR: A01412; RLHMS.
DR InterPro: IPR02012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.
FT MOD RES 1 1
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1244 MW; 1E4B36237B1735AB CRC64;

Query Match 26.6%; Score 21; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 10 LKWP 14
DB 5 LKWP 9

RESULT 5
BPP7_BOTIN STANDARD; PRT; 5 AA.
ID P30435;
DT 01-APR-1993 (Rel. 25, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Quelana jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintria A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227 (1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: G37196; G37196.
KW Hypotensive agent; Pyroglutamate carboxylic acid.
FT MOD RES 1 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B0000 CRC64;

Query Match 25.3%; Score 20; DB 1; Length 5;
CON1_PETWA STANDARD; PRT; 10 AA

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 RWRP 14
Db 2 KMAP 5

RESULT 6
TKNK_PIG
ID TKNK_PIG STANDARD; PRT; 10 AA.
AC P01292;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin B (NKB) (Neuromedin K).
GN TAC3 OR NKB.
OS Sus scrofa (Pig), and
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 8406;
RN [1]
RP SEQUENCE.
RC SPECIES=Pig; TISSUE=Spinal cord;
RX MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
spinal cord.";
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).
RN [2]
RP SEQUENCE.
RC SPECIES=R. ridibunda; TISSUE=Brain;
RX MEDLINE=204543; PubMed=1658233;
RA O'Hare F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secreteagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR: A01560; SPPGNK.
DR InterPro: IPR002040; Tachy Neurokinin.
DR PROSITE: PS00267; TACHYKININ: 1.
KM Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CA1 CRC64;

Query Match 25.3%; Score 20; DB 1; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DITDSIGL 10
Db 1 DMHDFVGL 9

RESULT 7
CEP1_ACHFU
ID CEP1_ACHFU STANDARD; PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.

RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -1- FUNCTION: Potentiates the beat of the ventricle, and has also
CC excitatory actions on the penis retractor muscle, the buccal
CC muscle and the identified neurons controlling the buccal muscle
CC movement of achatina.
CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR: A34662; A34662.
KM Hormone; Amidation.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1305 MW; 82D65B9C7741365 CRC64;

Query Match 25.3%; Score 20; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 GWRWP 14
Db 2 GQSWRP 7

RESULT 8
PKC1_CARMO
ID PKC1_CARMO STANDARD; PRT; 11 AA.
AC P82684;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Cam-PK-1) (FXPR1-Amide).
OS Carausius morosus (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatoidea; Euphasmida; Phasmatoidea;
OC Heteronemiidae; Carausius.
OX NCBI_TaxID=7022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca.
RA Predel R., Kellner R., Gaede G.;
RT "Myotropic neuropeptides from the retrocerebral complex of the stick
RT insect, Carausius morosus (Phasmatoidea: Lonchodidae).";
RL Eur. J. Entomol. 96:275-278(1999).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
CC CC -1- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; FALSE NEG.
KM Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225B846C1A8 CRC64;

Query Match 25.3%; Score 20; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GWRWP 14
Db 4 GYVTP 9

RESULT 9
E121_LITRU
ID E121_LITRU STANDARD; PRT; 13 AA.
AC P82057;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 2.1.
OS Litorea rubella (Desert tree frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wambitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella."  
RL Aust. J. Chem. 52:639-645(1999).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES 13  
SQ SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;  
  
Query Match 25.3%; Score 20; DB 1; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;  
Matches 2; Conservative 2; Mismatches 1;  
  
OY 10 LRWTP 14  
DB 6 VKMWP 10  
  
RESULT 10  
E122_LITRU STANDARD; PRT; 13 AA.  
AC P82098;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Electrin 2.2.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wambitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella."  
RL Aust. J. Chem. 52:639-645(1999).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES 13  
SQ SEQUENCE 13 AA; 1598 MW; C1808EF33B57322 CRC64;  
  
Query Match 25.3%; Score 20; DB 1; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;  
Matches 2; Conservative 2; Mismatches 1;  
  
OY 10 LRWTP 14  
DB 6 VKMWP 10  
  
RESULT 11  
YPNP_PHOLU STANDARD; PRT; 13 AA.  
AC P41123;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Photochemical protein in pmp 3' region (ORF3) (Fragment).  
OS Photobacterium luminescens (Xenorhabdus luminescens)
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OC Enterobacteriaceae; Photobacterium.  
OX NCBI_TaxID=29488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K122;  
RX MEDLINE=9426731; PubMed=8206856;  
RA Clarke D.J., Downs B.C.A.;  
RT "The gene coding for polynucleotide phosphorylase in Photobacterium sp.  
RT strain K122 is induced at low temperatures."  
RL J. Bacteriol. 176:3775-3784(1994).  
CC -----  
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CC -----  
DR EMBL; X76069; CAA53672.1; -.  
KW Hypothetical protein.  
FT NON TER 13  
SQ SEQUENCE 13 AA; 1634 MW; 6477A4F6267A364 CRC64;  
  
Query Match 25.3%; Score 20; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;  
  
OY 10 LRW 12  
DB 5 LRW 7  
  
RESULT 12  
CXK_WHEAT STANDARD; PRT; 15 AA.  
AC P58763;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Cytokinin dehydrogenase (EC 1.5.99.12) (CXK) (CXK) (Fragment).  
OS Triticum aestivum (wheat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
OC Triticeae; Triticum.  
OX NCBI_TaxID=4565;  
RN [1]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC STRAIN=cv. Samantha.  
RX MEDLINE=2109312; PubMed=11168382;  
RA Galuszka P., Fireport I., Sebeles M., Sauer P., Jacobsen S., Pec P.;  
RT "Cytokinin oxidase or dehydrogenase? Mechanism of cytokinin  
RT degradation in cereals."  
RL Eur. J. Biochem. 268:450-461(2001).  
CC -1- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-  
CC substituted adenine derivatives that are plant hormones, where the  
CC substituent is an isopentenyl group. Substrate preference is 2-(2-  
CC Hydroxyethylamino)-9-methyl-N(6)-isopentenyladenine >>  
CC isopentenyladenine > cis-zeatin = isopentenyladenosine = zeatin >>  
CC zeatin riboside.  
CC -1- CATALYTIC ACTIVITY: N(6)-dimethylallyl-adenine + electron acceptor  
CC = adenine + 3-methylbut-2-enal + reduced electron acceptor +  
CC H(2)O.  
CC -1- COFACTOR: FAD.  
CC -1- SUBUNIT: Monomer.  
CC -1- SUBCELLULAR LOCATION: Might be located on membranes.  
CC -1- MISCELLANEOUS: Optimal pH is 6.5.  
KM Oxidoreductase; Flavoprotein; FAD.  
FT UNSURE 1  
FT UNSURE 1  
FT UNSURE 1  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1709 MW; 85B589BD53FCEDDEF CRC64;
```

Query Match 25.3%; Score 20; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 ITDSI 8
 DB 10 VITKSL 15

RESULT 13
 ID DICH_PSESP STANDARD; PRT; 15 AA.
 AC P80701; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 3-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.50) (3-alpha-HSD)
 OS (Hydroxyprostaglandin dehydrogenase) (HSD29) (Fragment).
 DE Pseudomonas sp.
 CC Bacteria; Proteobacteria.
 CC NCB1_taxid=306;
 RN NCB1
 RP SEQUENCE.
 RX MEDLINE=97100200; PubMed=8944761;
 RA Oppermann U.C.T., Maser E.;
 RT "Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl
 reductase from the Gram-negative bacterium Comamonas testosteroni";
 RL Eur. J. Biochem. 241:744-749(1996).
 CC -1- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND
 3-OXO-REDUCTASE ACTIVITIES TOWARDS A VARIETY OF CIS OR TRANS FUSED
 A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL
 COMPOUNDS, INCLUDING A METYRAPONE-BASED CLASS OF INSECTICIDES, TO
 THEIR RESPECTIVE ALCOHOL METABOLITES.
 CC -1- CATALYTIC ACTIVITY: Androstereone + NAD(P) (+) = 5-alpha-androstane-
 3,17-dione + NAD(P)H.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 (SDR) family.
 DR InterPro: IPR002198; ADH short.
 DR PROSITE: PS00061; ADH_SHORT; PARTIAL.
 KM Oxidoreductase; NAD.
 FT DOMAIN 6 >15 INVOLVED IN COFACTOR BINDING
 (BY SIMILARITY).
 FT NON_TER 15
 FT SEQUENCE 15 AA; 1315 MW; 9506860D070A7790 CRC64;

Query Match 25.3%; Score 20; DB 1; Length 15;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VDIITDSIGL 10
 DB 3 IAITGSASGI 12

RESULT 14
 ID RBS_PHYPA STANDARD; PRT; 15 AA.
 AC P80657; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO
 small subunit) (Fragment).
 OS RBCS.
 GN Physcomitrella patens (Woss).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 CC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 CC NCB1_taxid=3218;
 RN NCB1
 RP SEQUENCE.
 RC TISSUE=Protonema;
 RX MEDLINE=97275459; PubMed=9129336;

RA Kastren B., Buck F., Nuahe J., Reski R.;
 RT "Cytochrome affects nuclear- and plasmome-encoded energy-converting
 plastid enzymes";
 RL Planta 201:261-272(1997).
 CC -1- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 ribulose 1,5-bisphosphate, the primary event in photosynthetic
 carbon dioxide fixation, as well as the oxidative fragmentation of
 the pentose substrate in the photorespiration process. Both
 reactions occur simultaneously and in competition at the same
 active site.
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
 2 3-phospho-D-glycerate.
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) =
 3-phospho-D-glycerate + 2-phosphoglycolate.
 CC -1- SUBUNIT: 8 large chains + 8 small chains.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- SIMILARITY: Belongs to the RuBisCO small chain family.
 KM Photosynthesis; Carbon dioxide fixation; Photorespiration;
 KM Lyase; Oxidoreductase; Monooxygenase; Chloroplast.
 FT NON_TER 15
 FT SEQUENCE 15 AA; 1801 MW; 28B9E7AC4AED6CE0 CRC64;

Query Match 25.3%; Score 20; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 WTPL 15
 DB 4 WNP1 7

RESULT 15
 ID UC14_MAIZE STANDARD; PRT; 15 AA.
 AC P80620; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 258)
 DE (Fragment).
 OS Zea mays (Maize).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 CC NCB1_taxid=4577;
 RN NCB1
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.9, its MW is: 34.6 kDa.
 DR Maize-2DPAGE; P80620; COLEOPTILE.
 DR MaizeDB; 123944; -.
 FT NON_TER 15
 FT SEQUENCE 15 AA; 1564 MW; CFOBBA0B7DE6658 CRC64;

Query Match 25.3%; Score 20; DB 1; Length 15;
 Best Local Similarity 30.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 5 DSSIGLRWTP 14
 DB 5 DGAAYEWSP 14

Search completed: September 21, 2004, 06:41:16
 Job time : 12.6667 secs

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OM protein - protein search, using sw model

Run on: September 21, 2004, 06:30:41 ; Search time 58.3333 Seconds
(without alignments)
81.133 Million cell updates/sec

Title: US-10-676-049-1

Perfect score: 79
Sequence: 1 VDIRSSIGLRWTP.L 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3954

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SPTREMBL.25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	35.4	13	5 Q9USJ2	Q9USJ2 trypanosoma
2	24	30.4	10	10 Q8GZC8	Q8GZC8 hordium vul
3	23	29.1	10	8 Q8SHR1	Q8SHR1 thampoleon
4	23	29.1	12	2 Q80959	Q80959 neisseria g
5	23	29.1	12	4 Q9UBJ5	Q9UBJ5 homo sapien
6	23	29.1	14	2 Q9RSP6	Q9RSP6 leionella
7	22	27.8	9	9 Q83366	Q83366 bacterioph
8	21.5	27.2	15	2 Q9RAY0	Q9RAY0 pseudomonas
9	21	26.6	10	13 Q9PRU9	Q9PRU9 sparus aura
10	21	26.6	11	12 Q80CP0	Q80CP0 tomato leaf
11	21	26.6	12	11 Q9EYV3	Q9EYV3 mus musculu
12	21	26.6	13	8 Q8MEJ9	Q8MEJ9 ginkgo bilo
13	21	26.6	14	4 Q7ZSS0	Q7ZSS0 homo sapien
14	20	25.3	9	8 Q8SHF0	Q8SHF0 chamealeo n
15	20	25.3	10	8 Q8SHI3	Q8SHI3 chamealeo c
16	20	25.3	10	8 Q8SH88	Q8SH88 brookesia t

18	20	25.3	10	8 Q8SH19	Q8SH19 chamealeo c
19	20	25.3	10	8 Q8SH90	Q8SH90 brookesia s
20	20	25.3	10	8 Q8G697	Q8G697 chamealeo d
21	20	25.3	10	8 Q8SH93	Q8SH93 brookesia p
22	20	25.3	10	8 Q8SH16	Q8SH16 chamealeo c
23	20	25.3	10	8 Q8SH85	Q8SH85 brookesia t
24	20	25.3	10	8 Q8SHAS	Q8SHAS brookesia a
25	20	25.3	10	8 Q8SHU5	Q8SHU5 calumma par
26	20	25.3	10	8 Q8SHG2	Q8SHG2 chamealeo j
27	20	25.3	10	8 Q8SHH4	Q8SHH4 chamealeo f
28	20	25.3	10	8 Q79912	Q79912 chamealeo f
29	20	25.3	10	8 Q8SHR7	Q8SHR7 chamealeo p
30	20	25.3	10	8 Q8SHD8	Q8SHD8 chamealeo r
31	20	25.3	10	8 Q8SH22	Q8SH22 brookesia b
32	20	25.3	10	8 Q8SHK7	Q8SHK7 calumma glo
33	20	25.3	10	8 Q8SHF3	Q8SHF3 chamealeo m
34	20	25.3	10	8 Q8SHI0	Q8SHI0 chamealeo d
35	20	25.3	10	8 Q8SHD2	Q8SHD2 chamealeo w
36	20	25.3	10	8 Q8SHC9	Q8SHC9 fucifer ba
37	20	25.3	10	8 Q8SHG5	Q8SHG5 chamealeo h
38	20	25.3	10	8 Q8SHH7	Q8SHH7 chamealeo e
39	20	25.3	10	8 Q8SH96	Q8SH96 brookesia e
40	20	25.3	10	8 Q8SH84	Q8SH84 chamealeo q
41	20	25.3	10	8 Q8SHR1	Q8SHR1 chamealeo q
42	20	25.3	10	8 Q8SHU8	Q8SHU8 calumma osh
43	20	25.3	10	8 Q8SHI2	Q8SHI2 chamealeo a
44	20	25.3	10	8 Q8SH83	Q8SH83 brookesia t
45	20	25.3	10	8 Q8SHF9	Q8SHF9 chamealeo j

ALIGNMENTS

RESULT 1
Q9USJ2 PRELIMINARY; PRT; 13 AA.

AC Q9USJ2; 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE GPI-phospholipase C (Fragment).
GN GPI-PLC.
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

OX NCBI_TaxID=5691;
RN [1]
RC SEQUENCE FROM N.A.
RA Web H.D., Gaud A.F., Carrington M.;
RT "The trypanosoma brucei GPI-PLC gene is not linked to functionally
RT related genes or to genes showing the same developmentally regulated
RT expression";
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL; AJ250727; CAB60093.1; --
DR GO; GO:0004629; F:phospholipase C activity; IEA.
DR InterPro; IPR003633; VarsurfGlyc_PPLC.
DR Pfam; PF03490; Varsurf_PPLC; 1.
DR NON TER 13 13
SQ SEQUENCE 13 AA; 1541 MW; 535AA96B464CA373 CRC64;

Query Match 35.4%; Score 28; DB 5; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 GLRWTP 14
|:::|
Db 4 GYKMS 9

RESULT 2
Q8GZC8 PRELIMINARY; PRT; 10 AA.

AC Q8GZC8;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE MIA330ORF 2a.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Halderman D.A., Wei P., Wise R.P.;
RT "Powdery mildew-induced MIA mRNAs are alternatively spliced and
RL contain multiple upstream open reading frames.";
DR EMBL; AF523679; AAO16003.1;
SQ SEQUENCE 10 AA; 1350 MW; 5A473E2440573B53 CRC64;

Query Match 30.4%; Score 24; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 IGLRW 12
DB 6 INLRW 10

RESULT 3
ID Q8SHB1 PRELIMINARY; PRT; 10 AA.
AC Q8SHB1;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Rhampholeon breviceaudatus (Bearded pygmy chameleon).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Iguania; Acrotodonta; Chamaeleonidae;
OC Chamaeleon.
OX NCBI_TaxID=91912;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata)."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448771; AAL90595.1;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON-TER
SQ SEQUENCE 10 AA; 1291 MW; 86218E2733641771 CRC64;

Query Match 29.1%; Score 23; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 WTP 14
DB 2 WTP 4

RESULT 4
ID Q50959 PRELIMINARY; PRT; 12 AA.
AC Q50959

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11A;
RX MEDLINE=89210824; PubMed=2854063;
RA Taha M.K., So M., Selfert H.S., Bilyard E., Marchal C.;
RT "Pilin expression in Neisseria gonorrhoeae is under both positive and
RT negative transcriptional control.";
RL EMBL; J74367-4378(1988).
DR EMBL; X13965; CAB37342.1;
DR PIR; S04380; S04380.
FT NON-TER
SQ SEQUENCE 12 AA; 1436 MW; 9684516C16C87735 CRC64;

Query Match 29.1%; Score 23; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 3.1e+03;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 5 DSSIGLRW 12
DB 3 BASLGVRV 10

RESULT 5
ID Q9UBJ5 PRELIMINARY; PRT; 12 AA.
AC Q9UBJ5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE ALI-1 protein (Fragment).
GN ALI-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=99342982; PubMed=10416593;
RA Reichel M., Hensel J.P., Giller E., Breitenlohner I., Repp R.,
RA Grell J., Beck J.D., Fey G.H., Marschalek R.;
RT "Rapid isolation of chromosomal breakpoints from patients with t(4;11)
RT acute lymphoblastic leukemia: implications for basic and clinical
RT research.";
RL Cancer Res. 59:3357-3362(1999).
DR EMBL; Y18927; CAB56461.1;
DR EMBL; Y18926; CAB56460.1;
FT NON-TER
SQ SEQUENCE 12 AA; 1396 MW; 9D7FC6E450B861B5 CRC64;

Query Match 29.1%; Score 23; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 SIGLRWT 13
DB 5 STGSEWT 11

RESULT 6
ID Q9R5P6 PRELIMINARY; PRT; 14 AA.
AC Q9R5P6

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OC NCBI_TaxID=446;
RN [1]
RP SEQUENCE.
RX MEDLINE=92121130; PubMed=1310095;
RA Hoffman P.S., Seyer J.H., Butler C.A.;
RT "Molecular characterization of the 28- and 31-kilodalton subunits of
RL the Legionella pneumophila major outer membrane protein.";
FT J. Bacteriol. 174:908-913(1992).
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1490 MW; 3541B0FBLAF55F48 CRC64;

Query Match
Best Local Similarity 29.1%; Score 23; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 WTP 14
Db 4 WTP 6

RESULT 7
Q8366 PRELIMINARY; PRT; 9 AA.
ID Q8366
AC Q8366.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E gene product (Fragment).
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
CX NCBI_TaxID=10847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88118956; PubMed=2963134;
RA Buckley K.J., Hayashi M.;
RT "Role of premature translational termination in the regulation of
RL U. Mol. Biol. 198:599-607(1987).
DR EMBL; X07809; CAA30668.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1207 MW; C093B37731B36412 CRC64;

Query Match
Best Local Similarity 27.8%; Score 22; DB 9; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LRMT 13
Db 2 VRMT 5

RESULT 8
Q9R4Y0 PRELIMINARY; PRT; 15 AA.
ID Q9R4Y0
AC Q9R4Y0.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE NAD+-dependent MORPHINONE reductase (Fragment).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID=303;
RN [1]
RP SEQUENCE.
RX MEDLINE=94311862; PubMed=8037698;
RA French C.E., Bruce N.C.;
RT "Purification and characterization of morphinone reductase from
RL Pseudomonas putida M10.";
DR Biochem. J. 301:97-103(1994).

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SQ SEQUENCE 15 AA; 1621 MW; 2A67BEE936973977 CRC64;

Query Match
Best Local Similarity 27.2%; Score 21.5; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 7; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 2 DITDSIGLRWTP 15
Db 2 DITFSNPGL-TRPL 14

RESULT 9
Q9PRU9 PRELIMINARY; PRT; 10 AA.
ID Q9PRU9
AC Q9PRU9.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Gonadotropin-releasing hormone, SRGNH-1.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
CX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE.
RX MEDLINE=95083645; PubMed=7991588;
RA Powell J.F., Zohar Y., Elizur A., Park M., Fischer W.H., Craig A.G.,
RA Rivier J.E., Lovejoy D.A., Sherwood N.M.;
RT "Three forms of gonadotropin-releasing hormone characterized from
RL brains of one species.";
DR Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085(1994).
SQ SEQUENCE 10 AA; 1132 MW; 8156685AB587735 CRC64;

Query Match
Best Local Similarity 26.6%; Score 21; DB 13; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 SIGLRW 12
Db 3 SLGYSW 8

RESULT 10
Q80GPO PRELIMINARY; PRT; 11 AA.
ID Q80GPO
AC Q80GPO.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE VI oit (Fragment).
OS Tomato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
CX NCBI_TaxID=28350;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93174952; PubMed=8438578;
RA Mullineaux P.M., Rigden J.E., Dry I.B., Krake L.R., Rezaian M.A.;
RT "Mapping of the polycistronic RNAs of tomato leaf curl geminivirus.";
RL Virology 193:414-423(1993).
DR EMBL; S55329; AAP13894.1; -.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1400 MW; 3F10FDP211F2C737 CRC64;

Query Match
Best Local Similarity 26.6%; Score 21; DB 13; Length 11;
Best Local Similarity 75.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 WTP 15
Db 2 WDPL 5

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RESULT 11

Q9E0V3 PRELIMINARY; PRT; 12 AA.
 AC Q9E0V3
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Alpha-sarcoglycan (Fragment).
 GN SGCA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=2109368; PubMed=11179961,
 RA Wakabayashi-Takai E., Noguchi S., Ozawa E.;
 RT "Identification of myogenesis-dependent transcriptional enhancers in
 RT promoter region of mouse gamma-sarcoglycan gene."
 RL Eur. J. Biochem. 268:948-957(2001).
 DR EMBL; AB044625; BAB18770.1;
 FT NON_TER
 SQ SEQUENCE 12 AA; 1257 MW; D382726D594361B2 CRC64;

Query Match

Best Local Similarity 26.6%; Score 21; DB 11; Length 12;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 WTPL 15
 DB 7 WTPL 10

RESULT 12

Q8WEJ9 PRELIMINARY; PRT; 13 AA.
 AC Q8WEJ9
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase (Fragment).
 GN NAD1.
 OS Ginkgo biloba (Ginkgo).
 OC Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
 OX NCBI_TaxID=3311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21555473; PubMed=11697913;
 RA Gugerli F., Speisen C., Buchler U., Brunner I., Brodbeck S.,
 RA Palmer J.D., Qiu Y.L.;
 RT "The evolutionary split of pinaceae from other conifers: evidence from
 RT an intron loss and a multigene phylogeny."
 RL Mol. Phylogenet. Evol. 21:167-175(2001).
 DR EMBL; AF227466; AAL38910.1;
 DR GO; GO:0005739; C:Mitochondrion; IEA.
 KM Mitochondrion.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 13 AA; 1419 MW; C00F6805F94945BD CRC64;

Query Match

Best Local Similarity 26.6%; Score 21; DB 8; Length 13;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DSSIGL 10
 DB 5 BASIGL 10

RESULT 13

Q7Z5S0 PRELIMINARY; PRT; 14 AA.
 ID Q7Z5S0
 AC Q7Z5S0
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Utsch T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullanb S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Small D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Strausberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC054509; AAH54509.1;
 KM Hypothetical protein.
 SQ SEQUENCE 14 AA; 1893 MW; 5A6DE30E6465257 CRC64;

Query Match 26.6%; Score 21; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RWT 13
 DB 12 RWT 14

RESULT 14

Q8SHF0 PRELIMINARY; PRT; 9 AA.
 ID Q8SHF0
 AC Q8SHF0
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Chamaeleo namaquensis (Namaqua chameleon).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
 OX NCBI_TaxID=179917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 RT Chamaeleonidae (Reptilia, Squamata).";

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF448757; AAI90553.1; -
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1205 MW; 358CB72733640733 CRC64;

Query March 25.3%; Score 20; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 10 LRW 12
 |||
 Db 3 LRW 5

RESULT 15

Q8SH13 PRELIMINARY; PRT; 10 AA.
 AC Q8SH13;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Chamaeleo cristatus (Crested chameleon).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
 OX NCBL_TaxID=179905;
 RN [1]
 RP TOWNSEND T.M., LARSON A.L.;
 RA "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 RT Chamaeleonidae (Reptilia, Squamata)."
 RI Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF448746; AAI90520.1; -
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 10 AA; 1353 MW; 5E2180C733640727 CRC64;

Query Match 25.3%; Score 20; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 10 LRW 12
 |||
 Db 4 LRW 6

Search completed: September 21, 2004, 06:45:05
 Job time : 60.3333 secs

Blank

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:57:18 / Search time 72.3333 Seconds

(without alignments)
58.593 Million cell updates/sec

Title: US-10-676-049-1

Perfect score: 79

Sequence: 1 VDIRSSIGRWTPPL 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 447529

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29JAN04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003as:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	5	AA017875 EDB fibro
2	50	63.3	9	5	ABG98139 Anti-neov
3	50	63.3	9	6	ABP74400 Human ED-
4	50	63.3	9	7	ADC09259 Epitope w
5	46	58.2	8	5	ABG98138 Anti-neov
6	46	58.2	8	6	ABP74399 Human ED-
7	46	58.2	8	7	ADC09258 Epitope w
8	34	43.0	13	5	AAE27396 Human gra
9	34	43.0	13	6	AAE30616 Human gra
10	32	40.5	7	4	AA46943 H11 bindi
11	31.5	39.9	14	4	AA998173 Human SNP
12	31	39.2	10	4	AA999351 Neurokin
13	30	38.0	7	4	AA447019 H11 bindi
14	30	38.0	7	4	AA447014 H11 bindi
15	30	38.0	14	4	AA497558 Human pep
16	29	36.7	8	5	ABP67158 Human CD6
17	29	36.7	9	5	ABP67152 Human CD6
18	29	36.7	9	5	ABP67151 Human CD6
19	29	36.7	10	5	ABP67145 Human CD6
20	29	36.7	10	5	ABP67147 Human CD6
21	29	36.7	10	5	ABP67146 Human CD6
22	29	36.7	11	5	ABP67142 Human CD6
23	29	36.7	11	5	ABP67143 Human CD6
24	29	36.7	11	5	ABP67141 Human CD6
25	29	36.7	12	5	ABP67139 Human CD6

26	29	36.7	12	5	ABP67138 Human CD6
27	29	36.7	12	5	ABP67140 Human CD6
28	29	36.7	13	5	ABP67136 Human CD6
29	29	36.7	13	5	ABP67137 Human CD6
30	29	36.7	13	7	ADP15546 Melanoma
31	29	36.7	14	4	ABP67130 Human CD6
32	29	36.7	14	5	ABP67137 Human CD6
33	29	36.7	14	6	AAE33653 Human BCA
34	28	35.4	10	2	AAE37028 Peptide c
35	28	35.4	11	2	AAW13931 CDR-3 fra
36	28	35.4	13	2	AAE63408 Peptide f
37	28	35.4	13	2	AAE63306 Peptide f
38	28	35.4	13	2	ABU03202 Human 1mm
39	28	35.4	13	6	ABU03151 Human 1mm
40	28	35.4	13	6	ABU03186 Human 1mm
41	28	35.4	13	6	ABR55642 Peptide d
42	28	35.4	13	7	ABR42749 Pyranoson
43	28	35.4	14	4	AAW97449 Human pep
44	28	35.4	14	4	AAW98067 Human pep
45	28	35.4	14	4	AAW98276 Human pep

ALIGNMENTS

RESULT 1
AA017875 standard; peptide, 15 AA.
XX
AC AA017875;
XX
DT 20-AUG-2002 (first entry)
XX
DE EDB fibronectin domain binding peptide #1.
XX
KM EDB fibronectin domain; EDBFD; angiogenesis; gene therapy; transplant;
KW implant; receptor molecule interaction.
XX
OS Unidentified.
XX
PN WO200220563-A2.
XX
PD 14-MAR-2002.
XX
PF 30-AUG-2001; 2001WO-EP010016.
XX
PR 07-SEP-2000; 2000DE-01045803.
PR 02-MAY-2001; 2001DE-01023133.
XX
PA (SCHD) SCHERING AG.
PA (REDL/) REDLITZ A.
PA (KOPP/) KOPITZ M.
PA (EGNE/) EGNER U.
PA (BAHR/) BAHR I.
PA (MENR/) MENRAD A.
XX
PI Menrad A;
XX
DR WPI; 2002-479458/51.
XX
PT New proteins binding specifically to the ED-b-fibronectin domain. are
PT cell adhesion and proliferation mediators useful e.g. in screening tests.
XX
PS Claim 2; Page 40; 66pp; German.
XX
CC The present invention relates to a new protein which binds specifically
CC to the EDB fibronectin domain (EDbFD), is specifically expressed or
CC activated in endothelial cells, stromal cells of a tumour and tumour
CC cells, and has an apparent molecular weight of 120-130 kDa for the light
CC chain and 150-160 kDa for the heavy chain. The protein can be used to
CC screen compounds which bind to EDBFD or its receptor, for coating
CC surfaces to which endothelial cells bind, in cell cultures, in
CC combination with transplants or in combination with implants

ADC09259
 ID ADC09259 standard; peptide; 9 AA.
 XX
 AC ADC09259;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Epitope with high affinity for MHC class I #SEQ ID 284.
 XX
 KM Epitope; immunological; vaccine;
 KM major histocompatibility complex class I; MHC class I; cancer;
 KM immunisation.
 XX
 OS Unidentified.
 XX
 PN WO2003008537-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 29-MAR-2002; 2002WO-US010189.
 XX
 PR 06-APR-2001; 2001US-0282211P.
 PR 07-NOV-2001; 2001US-0337017P.
 PR 07-MAR-2002; 2002US-0363210P.
 XX
 PA (CTL-I-) CTL IMMUNOTHERAPIES CORP.
 PI Simard JTL, Diamond DC, Liu L, Xie Z;
 XX
 DR WPI; 2003-248010/24.
 XX
 PT Epitope having high affinity for major histocompatibility complex class I
 PT useful for treating an animal, evaluating immunogenicity of a vaccine or
 PT therapeutic composition and for diagnosing a disease.
 XX
 PS Claim 1; SEQ ID NO 284; 239pp; English.
 XX
 CC The invention relates to an isolated epitope polypeptide that has high
 CC affinity for major histocompatibility complex (MHC) class I, and an
 CC epitope cluster comprising the polypeptide. Also disclosed is a vaccine
 CC or immunotherapeutic composition containing an epitope of the invention.
 CC Compositions of the invention may be used in the treatment of cancer. The
 CC method can be combined with a radiation therapy, chemotherapy,
 CC biochemotherapy or surgery. The composition is also useful for evaluating
 CC immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
 CC-peptide complexes of the invention are useful for determining specific T
 CC cell frequency. This method is useful for evaluating immunological
 CC response, by performing the method prior to and subsequent to an
 CC immunisation step. Compositions of the invention are useful for
 CC diagnosing a disease. The current sequence represents an epitope of the
 CC invention with high affinity for MHC class I.
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 63.3%; Score 50; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred.No.1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 SIGLRWTPPL 15
 DB 1 SIGLRWTPPL 9
 XX
 RESULT 5
 ABG98138
 ID ABG98138 standard; peptide; 8 AA.
 XX
 AC ABG98138;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Anti-neovascular preparation associated epitope #92.
 XX

KM Cell-mediated immunity; cellular immune response; CTL response;
 KM tumour neovascularity; anti-angiogenesis.
 XX
 OS Homo sapiens.
 XX
 PN WO200269907-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 07-MAR-2002; 2002WO-US007204.
 XX
 PR 07-MAR-2001; 2001US-0274063P.
 XX
 PA (CTL-I-) CTL IMMUNOTHERAPIES CORP.
 PI Simard JTL, Diamond DC;
 XX
 DR WPI; 2002-750433/81.
 XX
 PT Evaluating cell-mediated immunity, in particular cytotoxic T lymphocyte
 PT responses, by implanting vascular cells, useful for treatment and
 PT research models for directly targeting tumor neovascularity.
 XX
 PS Example 5; Page 25; 73pp; English.
 XX
 CC The invention describes a method of evaluating cell-mediated immunity
 CC comprising implanting vascular cells into an immunodeficient mammal,
 CC establishing an immune response in the mammal, and assaying a
 CC characteristic to determine cell-mediated immunity in the mammal. The
 CC methods and compositions of the present invention are useful for the
 CC generation of a cellular immune response, in particular a CTL response,
 CC for treatment directly against a tumour neovascularity. They can also be
 CC used for making research models targeting tumour neovascularity. The
 CC present invention using the anti-angiogenesis approach takes advantage of
 CC the need of tumours to recruit a blood supply to support their continued
 CC growth. This approach aims to disrupt a tumour's supply of nutrients to
 CC cause it to die or at least limit its growth. This is the amino acid
 CC sequence of a peptide associated with the neo-vasculature preparation
 CC for treatment of cancer described in the invention
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 58.2%; Score 46; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred.No.1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 IGLRWTPPL 15
 DB 1 IGLRWTPPL 8
 XX
 RESULT 6
 ABP74399
 ID ABP74399 standard; peptide; 8 AA.
 XX
 AC ABP74399;
 XX
 DT 03-FEB-2003 (first entry)
 XX
 DE Human ED-B epitope SEQ ID NO:283.
 XX
 KM Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
 KM T cell.
 XX
 OS Homo sapiens.
 XX
 PN WO200281646-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 04-APR-2002; 2002WO-US011101.
 XX
 PR 06-APR-2001; 2001US-0282211P.
 XX

PR 07-NOV-2001; 2001US-0337017P.
PR 07-MAR-2002; 2002US-0363210P.
XX
XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
PI Simard JTL, Diamond DC, Liu L, Xie Z;
XX
XX WPI; 2003-067518/06.
XX
XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid
PT encoding the peptides, that are useful epitopes of target-associated
PT antigens.
XX
PS Claim 1; Page 20; 352pp; English.

CC The present invention describes an isolated epitope (I) and an epitope
CC cluster. Also described is a vaccine or immunotherapeutic composition
CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
CC treating an animal, by administering to an animal the vaccine or
CC immunotherapeutic composition. VC is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic composition, by
CC administering VC to an HLA-transgenic animal and evaluating
CC immunogenicity based on a characteristic of the animal, or by in vitro
CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
CC useful for determining specific T cell frequency, by contacting T cells
CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
CC ABP74173 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 8 AA;

Query Match 58.2%; Score 46; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 IGLRWTP 15
| | | | |
DB 1 IGLRWTP 8

RESULT 7
ADC09258
ID ADC09258 standard; peptide; 8 AA.
XX
XX ADC09258;
XX
XX 18-DEC-2003 (first entry)
XX

DE Epitope with high affinity for MHC class I #SEQ ID 283.
XX

KM Epitope; immunological; vaccine;
KM major histocompatibility complex class I; MHC class I; cancer;
KM immunisation.
XX

OS Unidentified.
XX

FN WO2003008537-A2.
XX

PD 30-JAN-2003.
XX

PF 29-MAR-2002; 2002WO-US010189.
XX

PR 06-APR-2001; 2001US-0282211P.
PR 07-NOV-2001; 2001US-0337017P.
PR 07-MAR-2002; 2002US-0363210P.
XX

PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX

PI Simard JTL, Diamond DC, Liu L, Xie Z;
XX

DR WPI; 2003-248010/24.
XX

XX Epitope having high affinity for major histocompatibility complex class I
PT useful for treating an animal, evaluating immunogenicity of a vaccine or
PT therapeutic composition and for diagnosing a disease.
XX
XX Claim 1; SEQ ID NO 283; 239pp; English.

CC The invention relates to an isolated epitope polypeptide that has high
CC affinity for major histocompatibility complex (MHC) class I, and an
CC epitope cluster comprising the polypeptide. Also disclosed is a vaccine
CC or immunotherapeutic composition containing an epitope of the invention.
CC Compositions of the invention may be used in the treatment of cancer. The
CC method can be combined with a radiation therapy, chemotherapy,
CC biomedotherapy or surgery. The composition is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
CC-peptide complexes of the invention are useful for determining specific T
CC cell frequency. This method is useful for evaluating immunological
CC response by performing the method prior to and subsequent to an
CC immunisation step. Compositions of the invention are useful for
CC diagnosing a disease. The current sequence represents an epitope of the
CC invention with high affinity for MHC class I.
XX

SQ Sequence 8 AA;

Query Match 58.2%; Score 46; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 IGLRWTP 15
| | | | |
DB 1 IGLRWTP 8

RESULT 8
AAE27396
ID AAE27396 standard; peptide; 13 AA.
XX

AC AAE27396;
XX

DT 13-DEC-2002 (first entry)
XX

DE Human granulocyte colony stimulating factor (G-CSF) peptide #18.
XX

KM Human; fusion protein; immunological; major histocompatibility complex;
KM MHC; nausea; gastric upset; granulocyte colony stimulating factor; G-CSF.
XX

OS Homo sapiens.
XX

PN WO20026514-A2.
XX

PD 29-AUG-2002.
XX

PF 18-FEB-2002; 2002WO-EP001690.
XX

PR 19-FEB-2001; 2001EP-00103955.
PR 05-APR-2001; 2001EP-00108291.
XX

PA (MERE) MERCK PATENT GMBH.
XX

PI Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
PI Hanton M, Watkins J, Baker M, Way JC;
XX

DR WPI; 2002-667054/71.
XX

PT New modified fusion protein with reduced immunogenicity, useful for
PT combining favorable properties of a composition, comprises an
PT immunoglobulin molecule linked to a non-immunoglobulin target
PT polypeptide.
XX

PS Example 6; Page 54; 92pp; English.
XX

CC The invention relates to an immunogenically modified fusion protein
CC derived from a parent fusion protein, comprising first and second

CC proteins/polypeptides, where the first protein is an immunoglobulin
 CC molecule or its fragment and the second protein is non-immunoglobulin
 CC target polypeptide each linked to the other directly or by a linker
 CC molecule. The immunogenically modified fusion protein is useful in
 CC combining known favourable properties of a composition or in creating new
 CC properties of a composition which elicits biological or pharmacological
 CC efficacy without having undesirable physiological effects such as nausea
 CC or gastric upset. The present sequence is human granulocyte colony
 CC stimulating factor (G-CSF) peptide with potential major
 CC histocompatibility complex (MHC) class II binding activity. This peptide
 CC is used in the exemplification of the invention

XX Sequence 13 AA;

Query Match 43.0%; Score 34; DB 5; Length 13;
 Best Local Similarity 55.6%; Pred. No. 35;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 SIGLRWPL 15
 Db 2 SLGIWAPL 10

RESULT 9

AAE30616
 ID AAE30616 standard; peptide; 13 AA.

AC AAE30616;

DT 24-FEB-2003 (first entry)

XX Human granulocyte colony-stimulating factor (G-CSF) peptide #18.

KW Human granulocyte colony-stimulating factor; G-CSF; immune response;

KM T-cell epitope; gene therapy.

OS Homo sapiens.

PN WO200277034-A2.

PD 03-OCT-2002.

XX 05-FEB-2002; 2002WO-EP001171.

XX 06-FEB-2001; 2001EP-00102617.

PR 19-FEB-2001; 2001EP-00103954.

XX (MERE) MERCK PATENT GMEH.

XX Carr FJ, Carter G, Jones T, Williams S;

XX WPI; 2003-018891/01.

XX New modified granulocyte colony-stimulating factor with reduced
 PT immunogenicity, useful for treating diseases requiring minimal immune
 PT stimulation.

XX Disclosure; Page 12; 33pp; English.

XX The invention relates to modified granulocyte colony-stimulating factor
 CC (G-CSF) with reduced immunogenicity. The modified G-CSF is useful in
 CC treating diseases where a drug that elicits minimal immune response when
 CC administered to the human subject is required. The 13-mer T-cell epitope
 CC peptide and peptide sequences of the invention are useful in the
 CC manufacture of G-CSF having substantially no or less immunogenicity than
 CC any non-modified molecule with the same biological activity when used in
 CC vivo. The invention is also used in gene therapy. The present sequence is
 CC human G-CSF peptide of the invention

XX Sequence 13 AA;

Query Match 43.0%; Score 34; DB 6; Length 13;
 Best Local Similarity 55.6%; Pred. No. 35;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 SIGLRWPL 15
 Db 2 SLGIWAPL 10

RESULT 10

AA46943
 ID AA46943 standard; peptide; 7 AA.

AC AA46943;

DT 25-OCT-2001 (first entry)

XX H11 binding site consensus conforming peptide (CCP) #3214.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPSC;

KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

KM cytostatic; vaccine; tumour-specific immunogenic response inducer;

KW astrocytoma; fibrosarcoma; myosarcoma; liposarcoma; oligodendroglioma;

KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.

OS Synthetic.

PN CA2290722-A1.

PD 08-JUN-2001.

XX 08-DEC-1999; 99CA-02290722.

XX 08-DEC-1999; 99CA-02290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

XX Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated antigen-
 PT binding fragments of an antibody that binds specifically to the complex.

XX Example 4; Page 112; 154pp; English.

XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumors that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPSCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPSCs
 CC or a population of different SPSCs consisting of immunogenic cancer cell
 CC surface-associated SPSC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AA43707 to AA47109 represent peptides
 CC which are used in the exemplification of the present invention

XX Sequence 7 AA;

Query Match 40.5%; Score 32; DB 4; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 LRWTPPL 15
 Db 1 IRWTPPI 6


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RESULT 13
AA47019
ID AA47019 standard; peptide; 7 AA.
XX
AC AA47019;
XX
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #3290.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-02290722.
XX
PR 08-DEC-1999; 99CA-02290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, Macdonald GC;
XX
DR WPI; 2001-425937/46.
XX
PT Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated antigen-
PT binding fragments of an antibody that binds specifically to the complex.
XX
PS Example 4; Page 112; 154pp; English.
XX
CC The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AA43707 to AA47109 represent peptides
CC which are used in the exemplification of the present invention
XX
SQ Sequence 7 AA;
XX
Query Match 38.0%; Score 30; DB 4; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 10 LRWTP 14
DB 1 MRWTP 5

```

```

XX
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #3285.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-02290722.
XX
PR 08-DEC-1999; 99CA-02290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, Macdonald GC;
XX
DR WPI; 2001-425937/46.
XX
PT Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated antigen-
PT binding fragments of an antibody that binds specifically to the complex.
XX
PS Example 4; Page 112; 154pp; English.
XX
CC The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AA43707 to AA47109 represent peptides
CC which are used in the exemplification of the present invention
XX
SQ Sequence 7 AA;
XX
Query Match 38.0%; Score 30; DB 4; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 10 LRWTP 14
DB 1 MRWTP 5

```

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RESULT 14
AA47014
ID AA47014 standard; peptide; 7 AA.
XX
AC AA47014;
XX

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```

RESULT 15
AA97558
ID AA97558 standard; peptide; 14 AA.
XX
AC AA97558;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #833 encoded by a SNP oligonucleotide.
XX

```

KM Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KM neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KM complement related protein; cytochrome; kinesin; cytokine; interferon;
 KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KM multifactorial disease; autoimmune disease; infection;
 KM nervous system disease.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

XX 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.

XX Disclosure; Page 3850; 4143pp; English.

CC The present invention relates to oligonucleotides (see AAU26793-AAU34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms

XX Sequence 14 AA;

Query March 38.0%; Score 30; DB 4; Length 14;

Best Local Similarity 66.7%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 9 GLRWP 14

DB 8 GLRWVP 13

Search completed: September 21, 2004, 06:40:39

Job time : 75.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 06:42:10 ; Search time 70.6667 Seconds

(without alignments)
68.165 Million cell updates/sec

Title: US-10-676-049-1

Perfect score: 1 VDTDSIGLRWTP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1342398 segs, 321133274 residues

Total number of hits satisfying chosen parameters: 221706

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubppa/PCTUS_PUBCOMB.pep:*
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9: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep:*
12: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
13: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
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17: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	9	US-09-942-117-1
2	69	87.3	13	9	US-09-942-117-9
3	54	68.4	15	9	US-09-942-117-10
4	50	63.3	9	14	US-10-094-699-97
5	47	59.5	15	9	US-10-117-937-284
6	46	58.2	15	9	US-09-942-117-8
7	45	58.2	8	14	US-10-094-699-96
8	45	58.2	15	9	US-10-117-937-283
9	34	43.0	13	12	US-10-467-396-19
10	34	43.0	13	16	US-10-468-370-229
11	32	40.5	15	9	US-09-942-117-11
12	29	36.7	13	14	US-10-220-033-39
13	29	36.7	15	9	US-09-942-117-16
14	28	35.4	13	10	US-09-899-046-87
15	28	35.4	13	10	US-09-899-046-241

16	28	35.4	13	10	US-09-878-281-87	Sequence 87, Appl
17	28	35.4	13	10	US-09-878-281-241	Sequence 241, Appl
18	28	35.4	13	12	US-09-873-224-87	Sequence 87, Appl
19	28	35.4	13	12	US-09-873-224-241	Sequence 241, Appl
20	28	35.4	13	14	US-10-104-943-13	Sequence 13, Appl
21	28	35.4	13	14	US-10-104-943-58	Sequence 58, Appl
22	28	35.4	13	14	US-10-104-943-74	Sequence 74, Appl
23	28	35.4	13	15	US-10-283-940-12	Sequence 12, Appl
24	28	35.4	13	15	US-10-283-963-14	Sequence 14, Appl
25	28	35.4	14	14	US-10-104-943-24	Sequence 24, Appl
26	28	35.4	14	14	US-10-104-943-48	Sequence 48, Appl
27	28	35.4	14	14	US-10-104-943-68	Sequence 68, Appl
28	28	35.4	14	14	US-10-271-078-37	Sequence 37, Appl
29	28	35.4	15	11	US-09-833-245-630	Sequence 630, Appl
30	28	35.4	15	11	US-10-354-240-49	Sequence 49, Appl
31	28	35.4	15	14	US-10-354-240-50	Sequence 50, Appl
32	27.5	34.8	12	10	US-09-932-613-128	Sequence 128, Appl
33	27.5	34.8	12	10	US-09-932-122-128	Sequence 128, Appl
34	27.5	34.8	14	10	US-09-932-613-455	Sequence 455, Appl
35	27.5	34.8	14	10	US-09-932-122-455	Sequence 455, Appl
36	27	34.2	9	16	US-10-415-014-211	Sequence 211, Appl
37	27	34.2	9	16	US-10-415-014-444	Sequence 444, Appl
38	27	34.2	9	16	US-10-415-014-616	Sequence 616, Appl
39	27	34.2	12	16	US-10-254-446A-191	Sequence 191, Appl
40	27	34.2	12	16	US-10-706-391-38	Sequence 38, Appl
41	27	34.2	13	9	US-09-986-632-15	Sequence 15, Appl
42	27	34.2	13	14	US-10-167-831-73	Sequence 73, Appl
43	27	34.2	13	14	US-10-167-831-91	Sequence 91, Appl
44	27	34.2	14	12	US-10-016-349A-171	Sequence 171, Appl
45	27	34.2	15	9	US-09-894-018-273	Sequence 273, Appl

ALIGNMENTS

RESULT 1
US-09-942-117-1
Sequence 1, Application US/099422117
Publication No. US2002019700A1
GENERAL INFORMATION:
APPLICANT: MENRAD, ANDREAS
APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPPLITZ, MARCUS
APPLICANT: EGNER, URSULA
APPLICANT: BÄHR, INKE
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBROBLAST DOMAINS
FILE REFERENCE: SCH-1832
CURRENT APPLICATION NUMBER: US/09/942,117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-1
Query Match 100.0%; Score 79; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDTDSIGLRWTP 15
DB 1 VDTDSIGLRWTP 15

RESULT 2

US-09-942-117-9
; Sequence 9, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAHR, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942,117
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-9

Query Match 87.3%; Score 69; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITDSSIGLRWTP 15
DB 1 ITDSSIGLRWTP 13

RESULT 3

US-09-942-117-10
; Sequence 10, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAHR, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942,117
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-10

Query Match 68.4%; Score 54; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SSIGLRWTP 15
DB 1 SSIGLRWTP 15

DB 1 SSIGLRWTP 10

RESULT 4
US-10-094-699-97
; Sequence 97, Application US/10094699
; Publication No. US20030046714A1
; GENERAL INFORMATION:
; APPLICANT: SIEMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: CTILIM, 015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-699-97

Query Match 63.3%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SIGLRWTP 15
DB 1 SIGLRWTP 9

RESULT 5
US-10-117-937-284
; Sequence 284, Application US/10117937
; Publication No. US2003020239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIEMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTILIM, 027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-284

Query Match 63.3%; Score 50; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SIGLRWTP 15
DB 1 SIGLRWTP 9

RESULT 6
US-09-942-117-8


```

; Sequence 8, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAHN, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942.117
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-942-117-8

Query Match          59.5%; Score 47; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDIITSSIGL 10
        |||||
Db      6 VDIITSSIGL 15

RESULT 7
US-10-094-699-96
; Sequence 96, Application US/10094699
; Publication No. US20030046714A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J. L.
; APPLICANT: DIAMOND, David, C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: CTILIM.015A
; CURRENT APPLICATION NUMBER: US/10/094.699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-699-96

Query Match          58.2%; Score 46; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 IGLRWTPPL 15
        |||||
Db      1 IGLRWTPPL 8

RESULT 8
US-10-117-937-283
; Sequence 283, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.

```

```

; APPLICANT: SIMARD, John, J. L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTILIM.027A
; CURRENT APPLICATION NUMBER: US/10/117.937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-283

Query Match          58.2%; Score 46; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 IGLRWTPPL 15
        |||||
Db      1 IGLRWTPPL 8

RESULT 9
US-10-467-396-19
; Sequence 19, Application US/10467396
; Publication No. US20040062749A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED GRANULOCYTE COLONY STIMULATING
; FILE REFERENCE: MER.113
; CURRENT APPLICATION NUMBER: US/10/467.396
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102617.6
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP/02/01171
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-467-396-19

Query Match          43.0%; Score 34; DB 12; Length 13;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      7 SIGRWTPPL 15
        |||||
Db      2 SIGRWTPPL 10

RESULT 10
US-10-468-370-229
; Sequence 229, Application US/10468370

```

```
Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Carr, Francis J.
APPLICANT: Jones, Tim
APPLICANT: Carter, Graham
APPLICANT: Hamilton, Anita
APPLICANT: Williams, Stephen
APPLICANT: Hanlon, Marian
APPLICANT: Watkins, John
APPLICANT: Baker, Matthew
APPLICANT: May, Jeffrey
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
FILE REFERENCE: MBR-118
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: EP 01103955.9
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: PCT/EP02/01690
PRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 229
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-229

Query Match      43.0%; Score 34; DB 16; Length 13;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      7 SIGLRWTP 15
Db      2 SLGIPWAPL 10

RESULT 11
US-09-942-117-11
Sequence 11, Application US/09942117
GENERAL INFORMATION:
APPLICANT: MENRAD, ANDREAS
APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPPLITZ, MARCUS
APPLICANT: EGNER, URSULA
APPLICANT: BAHR, INKE
FILE REFERENCE: SCH-1832
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
CURRENT APPLICATION NUMBER: US/09/942,117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-942-117-11
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 RWTP 15
Db      1 RWTP 5

RESULT 12
US-10-220-033-39
Sequence 39, Application US/10220033
Publication No. US20030186906A1
GENERAL INFORMATION:
APPLICANT: Schlengersiepen, Karl-Hermann
APPLICANT: Schlengersiepen, Reimar
TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
FILE REFERENCE: gene
TITLE OF INVENTION: and a molecule binding to an expression product of that
FILE REFERENCE: P6813US0
CURRENT APPLICATION NUMBER: US/10/220,033
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: PCT/EP01/02694
PRIOR FILING DATE: 2001-03-10
PRIOR APPLICATION NUMBER: EP00105190.3
PRIOR FILING DATE: 2000-03-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide
OTHER INFORMATION: obtained by screening randomly synthesized
OTHER INFORMATION: peptides
US-10-220-033-39

Query Match      36.7%; Score 29; DB 14; Length 13;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      5 DSSIGLRWTP 14
Db      1 ETVIVITWTP 10

RESULT 13
US-09-942-117-16
Sequence 16, Application US/09942117
GENERAL INFORMATION:
APPLICANT: MENRAD, ANDREAS
APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPPLITZ, MARCUS
APPLICANT: EGNER, URSULA
APPLICANT: BAHR, INKE
FILE REFERENCE: SCH-1832
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
CURRENT APPLICATION NUMBER: US/09/942,117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
```

Query Match 36.7%; Score 29; DB 9; Length 15;
Best Local Similarity 62.5%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITDSSIGLRWTPV 15
DB 4 DVVDSVWG 11

RESULT 14
US-09-899-046-87
Sequence 87, Application US/09899046
Publication No. US20030008274A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: New sequences of hepatitis C virus
TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,046
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
FILING DATE:
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
POSITION IN GENOME:
MAP POSITION: positions 230 to 242 of the V3 region of HCV type 3
US-09-899-046-87

Query Match 35.4%; Score 28; DB 10; Length 13;
Best Local Similarity 30.8%; Pred. No. 9.6e+02;
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 ITDSSIGLRWTPV 15
DB 1 VQDNTSTCWTPTV 13

RESULT 15
US-09-899-046-241
Sequence 241, Application US/09899046
Publication No. US20030008274A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: New sequences of hepatitis C virus
TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
NUMBER OF SEQUENCES: 270
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,046
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
FILING DATE:
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-899-046-241

Query Match 35.4%; Score 28; DB 10; Length 13;
Best Local Similarity 30.8%; Pred. No. 9.6e+02;
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 ITDSSIGLRWTPV 15
DB 1 VQDNTSTCWTPTV 13

Search completed: September 21, 2004, 07:03:17
Job time : 70.6667 secs

This Page Blank (uspto)

OM protein - protein search, using sw model

Run on: September 21, 2004, 06:15:34 ; Search time 13.6657 Seconds
(without alignments)
56.663 Million cell updates/sec

Title: US-10-676-049-1

Perfect score: 79
Sequence: 1 VDTTSSIGLRWTPL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 146418

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/aa/5A COMB pep:*
2: /cgn2_6/prodata/2/aa/5A COMB pep:*
3: /cgn2_6/prodata/2/aa/6A COMB pep:*
4: /cgn2_6/prodata/2/aa/6A COMB pep:*
5: /cgn2_6/prodata/2/aa/PCTUS COMB pep:*
6: /cgn2_6/prodata/2/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	34.2	13	3	US-09-188-579-53	Sequence 53, Appl
2	27	34.2	13	3	US-09-315-444-53	Sequence 53, Appl
3	27	34.2	13	4	US-09-721-362-53	Sequence 53, Appl
4	27	34.2	13	4	US-09-752-165-73	Sequence 73, Appl
5	27	34.2	13	4	US-09-752-165-91	Sequence 91, Appl
6	27	34.2	14	4	US-09-555-352-11	Sequence 11, Appl
7	27	34.2	15	2	US-08-553-257A-60	Sequence 60, Appl
8	27	34.2	15	4	US-09-009-953-18	Sequence 18, Appl
9	27	34.2	15	4	US-09-009-953-26	Sequence 26, Appl
10	27	34.2	15	4	US-09-009-953-31	Sequence 31, Appl
11	27	34.2	15	4	US-09-009-953-59	Sequence 59, Appl
12	27	34.2	15	4	US-09-009-953-77	Sequence 77, Appl
13	27	34.2	15	4	US-09-009-953-78	Sequence 78, Appl
14	27	34.2	15	4	US-09-311-784A-420	Sequence 420, Appl
15	27	34.2	15	4	US-09-441-992-60	Sequence 60, Appl
16	27	34.2	7	4	US-09-638-202A-32	Sequence 32, Appl
17	27	34.2	7	4	US-09-096-749A-32	Sequence 32, Appl
18	26	32.9	8	1	US-08-191-571-20	Sequence 20, Appl
19	26	32.9	8	5	PCT-US95-00296-20	Sequence 20, Appl
20	26	32.9	10	1	US-07-899-205-2	Sequence 2, Appl
21	26	32.9	10	1	US-08-193-393-1	Sequence 1, Appl
22	26	32.9	10	1	US-08-184-935-9	Sequence 9, Appl
23	26	32.9	10	1	US-08-269-288-3	Sequence 3, Appl
24	26	32.9	10	1	US-08-338-484-2	Sequence 2, Appl
25	26	32.9	10	1	US-08-175-432-2	Sequence 2, Appl
26	26	32.9	10	1	US-08-462-413-3	Sequence 3, Appl
27	26	32.9	10	1	US-08-391-910-3	Sequence 3, Appl

28	26	32.9	10	1	US-08-418-994-3	Sequence 3, Appl
29	26	32.9	10	1	US-08-462-949-32	Sequence 32, Appl
30	26	32.9	10	1	US-08-391-814-3	Sequence 3, Appl
31	26	32.9	10	1	US-08-167-870-2	Sequence 2, Appl
32	26	32.9	10	1	US-08-462-415-3	Sequence 3, Appl
33	26	32.9	10	1	US-08-023-764B-32	Sequence 32, Appl
34	26	32.9	10	1	US-08-463-874-3	Sequence 3, Appl
35	26	32.9	10	1	US-08-318-391-3	Sequence 3, Appl
36	26	32.9	10	2	US-08-496-118-2	Sequence 2, Appl
37	26	32.9	10	2	US-07-737-371E-75	Sequence 75, Appl
38	26	32.9	10	3	US-08-257-966-3	Sequence 3, Appl
39	26	32.9	10	3	US-08-636-407-1	Sequence 1, Appl
40	26	32.9	10	4	US-09-311-626B-26	Sequence 26, Appl
41	26	32.9	10	4	US-09-311-626B-43	Sequence 43, Appl
42	26	32.9	10	4	US-08-153-847-3	Sequence 3, Appl
43	26	32.9	11	2	US-08-762-106-31	Sequence 31, Appl
44	26	32.9	11	3	US-09-320-774-31	Sequence 31, Appl
45	26	32.9	12	1	US-08-492-599-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-188-579-53
; Sequence 53, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 53
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Crithidia fasciculata
; FEATURE:
; OTHER INFORMATION: Motif V of RNA guanylyltransferase.
US-09-188-579-53

Query Match 34.2%; Score 27; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 LRWTPL 15
DB 2 LKWKPL 7
RESULT 2
US-09-315-444-53
; Sequence 53, Application US/09315444A
; Patent No. 6232070
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP
; CURRENT APPLICATION NUMBER: US/09/315,444A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/188,579
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 53
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Crithidia fasciculata
; FEATURE:
; OTHER INFORMATION: Motif V of RNA guanylyltransferase.
US-09-315-444-53

Query Match 34.2%; Score 27; DB 3; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 10 LRWTP1 15
Db 2 LKWKPL 7

RESULT 3
US-09-721-362-53
; Sequence 53, Application US/09721362
; Patent No. 6420163
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP/D
; CURRENT APPLICATION NUMBER: US/09/721,362
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/315,444
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 53
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Crithidia fasciculata
; FEATURE:
; OTHER INFORMATION: Motif V of RNA guanylyltransferase.
US-09-721-362-53

Query Match 34.2%; Score 27; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 LRWTP1 15
Db 2 LKWKPL 7

RESULT 4
US-09-752-165-73
; Sequence 73, Application US/09752165
; Patent No. 6451583
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6388
; CURRENT APPLICATION NUMBER: US/09/752,165
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 73
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Crithidia fasciculata
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Motif V of RNA guanylyltransferase from Crithidia fasciculata
US-09-752-165-73

Query Match 34.2%; Score 27; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 LRWTP1 15
Db 2 LKWKPL 7

RESULT 5
US-09-752-165-91
; Sequence 91, Application US/09752165

; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; APPLICANT: Ho, C. Kiong
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; TITLE OF INVENTION: For Treatment of Parasitic Infections
; FILE REFERENCE: D6388
; CURRENT APPLICATION NUMBER: US/09/752,165
; CURRENT FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 91
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Motif V of RNA guanylyltransferase from Plasmodium falciparum
US-09-752-165-91

Query Match 34.2%; Score 27; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 10 LRWTP1 15
Db 2 LKWKPL 7

RESULT 6
US-09-555-352-11
; Sequence 11, Application US/09555352
; Patent No. 6544779
; GENERAL INFORMATION:
; APPLICANT: Cichutek, Klaus
; APPLICANT: Merges-Mullitzer, Heike
; TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
; FILE REFERENCE: 11692-005001
; CURRENT APPLICATION NUMBER: US/09/555,352
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/DE98/03542
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: DE 197 52 855.4
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Murine leukemia virus
US-09-555-352-11

Query Match 34.2%; Score 27; DB 4; Length 14;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SIGLRWT 13
Db 3 TLGVRWS 9

RESULT 7
US-08-553-257A-60
; Sequence 60, Application US/08553257A
; Patent No. 5994083
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; APPLICANT: MOLECOLARE P. ANGELETTI S.p.A.
; APPLICANT: FELICI, Franco
; APPLICANT: LUZZAGO, Alessandra
; APPLICANT: NICOSIA, Alfredo
; APPLICANT: MONACI, Paolo
; APPLICANT: CORTESE, Riccardo

TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
TITLE OF INVENTION: DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,257A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT94/00054
FILING DATE: 05-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: RM83A000301
FILING DATE: 11-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-257A-60
Query Match 34.2%; Score 27; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 WTPL 15
Db 4 WTPL 7
RESULT 8
US-09-009-953-18
Sequence 18, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953

FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-009-953-18
Query Match 34.2%; Score 27; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 DITDSIGL 10
Db 5 NVNNSIGL 13
RESULT 9
US-09-009-953-26
Sequence 26, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-009-953-26

Query Match 34.2%; Score 27; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 DITDSIGL 10
Db 2 NVNSSIGL 10

RESULT 10
US-09-009-953-31
Sequence 31, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-Jan-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-009-953-31

Query Match 34.2%; Score 27; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 2 DITDSIGL 10
Db 2 NVNSSIGL 10

RESULT 11
US-09-009-953-59
Sequence 59, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-Jan-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-009-953-59

Query Match 34.2%; Score 27; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 DITDSIGL 10
Db 2 NVNSSIGL 10

RESULT 12
US-09-009-953-77
Sequence 77, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-Jan-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-009-953-77
Query Match 34.2%; Score 27; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 DITDSSIGL 10
DB 5 NVNWSIGL 13
RESULT 13
US-09-009-953-78
Sequence 78, Application US/0900953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-Jan-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-009-953-78
Query Match 34.2%; Score 27; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 DITDSSIGL 10
DB 3 NVNWSIGL 11
RESULT 14
US-09-311-784A-420
Sequence 420, Application US/09311784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
Immune Response and Methods of Using the Same
FILE REFERENCE: 39863-20022.01/09/311,784A
CURRENT APPLICATION NUMBER: US/09/311,784A
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 420
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PF CSP 410 (peptide 27.0392)
US-09-311-784A-420
Query Match 34.2%; Score 27; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 DITDSSIGL 10
DB 5 NVNWSIGL 13
RESULT 15
US-09-441-992-60
Sequence 60, Application US/09441992
Patent No. 6541210
GENERAL INFORMATION:
APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
MOLECOLARE P. ANGELIETTI S.P.A.
FELICI, Franco

Tue Sep 21 07:03:57 2004

us-10-676-049-1.closed.rat

Page 6

LUZZAGO, Alessandra
NICOSIA, Alfredo
MONACI, Paolo
CORTESE, Riccardo
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible,
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/441,992
FILING DATE: 18-No. 6541210-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,257
FILING DATE: <Unknown>
APPLICATION NUMBER: RM93A000301
FILING DATE: 11-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELIC1=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-441-992-60

Query Match 34.2%; Score 27; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 WTPL 15
|||
Db 4 WTPL 7

Search completed: September 21, 2004, 06:42:04
Job time : 15.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 06:37:00 / Search time 18.6667 Seconds

(Without alignments)
77.297 Million cell updates/sec

Title: US-10-676-049-2

Perfect score: 85
Sequence: 1 GYTVTGLEPGLDYP 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2522

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.78:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	38.8	14	2	PH1305	Ig heavy chain DJ
2	27	31.8	10	2	S62880	polygalacturonase
3	26	30.6	13	2	A61514	glutathione transf
4	25	29.4	10	1	RHAQ1	gonadolibertin I -
5	25	29.4	15	2	B56046	urinary tract ston
6	24	28.2	10	2	PT0243	Ig heavy chain CRD
7	24	28.2	15	2	A56970	GUWAI - soybean
8	23.5	27.6	14	2	PH1306	Ig heavy chain DJ
9	23	27.1	10	1	RHPSG	gonadolibertin - pi
10	23	27.1	10	1	RHPSG	gonadolibertin - pi
11	22	25.9	9	2	S70345	amine oxidase (cop
12	22	25.9	10	2	S71868	glutathione transf
13	22	25.9	11	2	G61497	seed protein ws-23
14	22	25.9	14	2	A61002	photosystem II oxy
15	22	25.9	14	2	PT0252	Ig heavy chain CRD
16	22	25.9	15	2	PA0097	starch phosphoryla
17	22	25.9	15	2	A08416	lombroline kinase
18	22	25.9	15	2	B26501	lipoprotein lipase
19	21	24.7	10	2	PH1592	Ig H chain V-D-J r
20	21	24.7	11	2	S19775	wound-induced prot
21	21	24.7	11	2	PH1632	Ig H chain V-D-J r
22	21	24.7	11	2	PH1583	Ig H chain V-D-J r
23	21	24.7	12	2	FN0170	alcohol dehydrogen
24	21	24.7	12	2	PC4377	telomeric and tetr
25	20	23.5	9	2	J00914	MHC class I histoc
26	20	23.5	11	2	PH0929	T-cell receptor be
27	20	23.5	12	2	PN0162	malate dehydrogena
28	20	23.5	13	2	PN0176	acidic ribosomal p
29	20	23.5	13	2	PT0304	Ig heavy chain CRD

30	20	23.5	13	2	PH1596	Ig H chain V-D-J r
31	20	23.5	14	2	PA0109	portin por 1B - Ara
32	20	23.5	14	2	PA0045	portin por 1 - Arabi
33	20	23.5	14	2	PH1597	Ig H chain V-D-J r
34	20	23.5	14	2	PH1598	Ig H chain V-D-J r
35	20	23.5	15	2	PH1319	Ig heavy chain DJ
36	20	23.5	15	2	PA0079	malate dehydrogena
37	20	23.5	15	2	PA0071	superoxide dismuta
38	20	23.5	15	2	S79987	cytochrome-c oxida
39	20	23.5	15	2	S67975	apolipoprotein CB2
40	20	23.5	15	2	PH1366	Ig heavy chain DJ
41	19	22.4	9	2	E41978	calliFERamide 5 -
42	19	22.4	10	2	S33844	alpha-2-macroglobu
43	19	22.4	10	2	S62208	polyferredoxin - M
44	19	22.4	10	2	A61007	hemennin (EC 3.4.
45	19	22.4	11	2	PH1600	Ig H chain V-D-J r

ALIGNMENTS

RESULT 1
PH1305
Ig heavy chain DJ region (clone C85-1B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1305
R/Maserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Royera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1305
A/Molecule type: DNA
A/Residues: 1-14 <WAS>
A/Keywords: heterodimer; immunoglobulin

Query Match 38.8%; Score 33; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYTVTGLEP 10
DB 5 GYTVTGAREP 14

RESULT 2
S62880
polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
C/Species: Aspergillus sp.
C/Date: 28-Oct-1986 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C/Accession: S62880
R/Stratillova, E.; Dzufova, M.; Markovic, O.; Joernvall, H.
FEBS Lett. 382, 164-166, 1996
A/Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A/Reference number: S62880; MUID:96196586; PMID:8612742
A/Accession: S62880
A/Molecule type: protein
A/Residues: 1-10 <STR>
C/Keywords: glycosidase; hydrolase
F/4/Active site: Tyr #status predicted

Query Match 31.8%; Score 27; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 YTVTGLEP 10
DB 2 YATVTKEP 9

RESULT 3
A61514
glutathione transferase (EC 2.5.1.18), 26k - fluke (Schistosoma japonicum) (fragment)

C:Species: Schistosoma japonicum
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 07-May-1999
C:Accession: A61514
R: Mitchell, G.F.
Mol. Biochem. Parasitol. 27, 249-256, 1988
A:Title: Expression of an enzymatically active parasite molecule in Escherichia coli: SC
A:Reference number: A61514; PMID:88142994; PMID:3278228
A:Accession: A61514
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <MIT>
C:Keywords: transferase

Query Match 30.4%; Score 26; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYVTGGL 8
|||:|
Db 5 GYWKIKGL 12

RESULT 4

RHA01

gonadoliberin I - American alligator

N:Alternate names: gonadotropin-releasing hormone I

C:Species: Alligator mississippiensis (American alligator)

C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997

C:Accession: A60066

R: Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson

Regul. Pept. 33, 105-116, 1991

A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of

A:Reference number: A60066; PMID:91352338; PMID:1882082

A:Accession: A60066

A:Molecule type: protein

A:Residues: 1-10 <LOV>

C:Superfamily: gonadoliberin

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.4%; Score 25; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GLERGL 11
|||:|
Db 6 GLQPG 10

RESULT 5

B56046 urinary tract stone matrix protein 2, 21K - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995

C:Accession: B56046

R: Biette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995

A:Description: Isolation, characterization and sequence of stone proteins.

A:Reference number: A56046

A:Accession: B56046

A:Molecule type: protein

A:Status: preliminary

A:Residues: 1-15 <BIN>

Query Match 29.4%; Score 25; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YTVTGLERGL 11
|||:|
Db 1 YLVLGQVAPG 10

RESULT 6
PT0243 Ig heavy chain CRD3 region (clone 2-103A) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0243

R: Yamada, M.; Waserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

U. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A:Reference number: PT0222; PMID:9108337; PMID:1899102

A:Accession: PT0243

A:Molecule type: DNA

A:Residues: 1-10 <YAW>

A:Experimental source: B lymphocyte

C:Keywords: heterotrimer; immunoglobulin

Query Match 28.2%; Score 24; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 8.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYVTGGL 7
|||:|
Db 2 GYDSSG 8

RESULT 7

A56970 GLYMA1 - soybean (fragment)

C:Species: Glycine max (soybean)

C:Date: 02-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 08-Sep-1995

C:Accession: A56970

R: Codina, M.R.

submitted to the Protein Sequence Database, September 1995

A:Reference number: A56970

A:Accession: A56970

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <COD>

Query Match 28.2%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGL 8
|||:|
Db 1 YTTNGL 6

RESULT 8

PH1306 Ig heavy chain DJ region (clone C56-100) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1306

R: Waserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

U. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DH joining in young children with B precursor lymph

A:Reference number: PH1302; PMID:93094761; PMID:1460419

A:Accession: PH1306

A:Molecule type: DNA

A:Residues: 1-14 <WAS>

A:Keywords: heterotrimer; immunoglobulin

Query Match 27.6%; Score 23.5; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 YTVTGL-EP 10
|||:|
Db 6 YTTGARP 14

RESULT 9
RHRCG
gonadoliberin - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997
C/Accession: A01411
R/Baba, Y.; Matsuo, H.; Schally, A.V.
Biochem. Biophys. Res. Commun. 44: 459-463, 1971
A/Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of the
A/Reference number: A90172; MUID:72114303; PMID:4946067
A/Accession: A01411
A/Molecule type: protein
A/Residues: 1-10 <BAB>
R/Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45: 822-827, 1971
A/Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase method
A/Reference number: A90176; MUID:72065376; PMID:4942726
A/Contents: annotation; synthesis
A/Note: the synthetic and natural hormones have the same physicochemical and biological
R/Baba, Y.; Arimura, A.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45: 483-487, 1971
A/Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.
A/Reference number: A90175; MUID:72117544; PMID:4946275
A/Contents: annotation
A/Note: Trp-3 appears to be essential for biological activity
C/Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and follicle
C/Superfamily: gonadoliberin
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 27.1%; Score 23; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GLEPG 11
DB 6 GLRPG 10

RESULT 10
RHSHG
gonadoliberin - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Mar-1997
C/Accession: A93780; A01411
R/Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Monahan, M.; Rivier, J.; Fellows, R.; Bl
Proc. Natl. Acad. Sci. U.S.A. 69: 278-282, 1972
A/Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing factor
A/Reference number: A93780; MUID:72094314; PMID:4550508
A/Accession: A93780
A/Molecule type: protein
A/Residues: 1-10 <BUR>
A/Note: the natural and synthetic hormones have the same biological activity
C/Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and follicle
C/Superfamily: gonadoliberin
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 27.1%; Score 23; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GLEPG 11
DB 6 GLRPG 10

RESULT 11
S70345
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (Fragments)
C/Species: Aspergillus niger

C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C/Accession: S70345
R/Frederott, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T
Biochim. Biophys. Acta 1295: 59-72, 1996
A/Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the
A/Reference number: S70344; MUID:96283794; PMID:8679675
A/Accession: S70345
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-516-9 <PRE>
C/Keywords: oxidoreductase

Query Match 25.9%; Score 22; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 LEPGIDY 14
DB 3 IEPNXY 9

RESULT 12
S71868
glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment)
M/Alternate names: glutathione S-transferase class mu 4
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 07-May-1999
C/Accession: S71868
R/Rouini, P.; Anglade, P.; Debrunwer, L.; Tulliez, J.
Biochem. J. 317: 879-884, 1996
A/Title: Characterization of pig liver glutathione S-transferases using HPLC-electrosp
A/Reference number: S71864; MUID:96332484; PMID:8760377
A/Accession: S71868
A/Molecule type: protein
A/Residues: 1-10 <ROU>
C/Comment: At least five species-independent classes of cytosolic glutathion transferas
s mitochondrial form are known.
C/Complex: dimer
C/Function:
A/Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
A/Pathway: detoxification; xenobiotics metabolism
A/Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
es of damage
C/Superfamily: glutathione transferase
C/Keywords: dimer; transferase

Query Match 25.9%; Score 22; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYTVTG 7
DB 4 GYWDING 10

RESULT 13
G61497
seed protein wa-23 - winged bean (fragment)
C/Species: Psophocarpus tetragonolobus (winged bean)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C/Accession: G61497
R/Hizano, H.
U/Protein: Chem. 8: 115-130, 1989
A/Title: Microsequence analysis of winged bean seed proteins electrophoretically
A/Accession: G61497
A/Reference number: A61491; MUID:89351606; PMID:2765119
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-11 <HIR>
C/Keywords: glycoprotein; seed

Query Match 25.9%; Score 22; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LEFG 11
 ||||
 Db 8 LEFG 11

RESULT 14

A61002
 photosystem II oxygen-evolving complex protein 1 - common tobacco (fragment)
 N;Alternate names: thylakoid membrane protein
 C;Species: Nicotiana tabacum (common tobacco)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C;Accession: A61002
 R;Bauw, G.; Rasmussen, H.H.; Van Den Bultke, M.; Van Damme, J.; Puype, M.; Gesser, B.; C
 Electrophoresis 11, 528-536, 1990
 A;Title: Two-dimensional gel electrophoresis, protein electrophototyping and microsequencin
 A;Reference number: A61002; MUID:91031404; PMID:1699755
 A;Accession: A61002
 A;Molecule type: protein
 A;Residues: 1-14 <BAU>
 C;Keywords: chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 25.9%; Score 22; DB 2; Length 14;
 Best Local Similarity 33.3%; Pred. No. 2.4e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GLERGDYD 15
 |:-:-:-|
 Db 2 GVPPXLRPD 10

RESULT 15

PT0252
 Ig heavy chain CDR3 region (clone 2-109D) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0252
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.U.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A;Reference number: PT0222; MUID:9108337; PMID:1699102
 A;Accession: PT0252
 A;Molecule type: DNA
 A;Residues: 1-14 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotrimer; immunoglobulin

Query Match 25.9%; Score 22; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTV 5
 ||||
 Db 10 GYTV 14

Search completed: September 21, 2004, 06:46:06
 Job time : 18.6667 secs

OM protein - protein search, using sw model

Run on: September 21, 2004, 06:14:13 ; Search time 10.6667 Seconds
(without alignments)
73.224 Million cell updates/sec

Title: US-10-676-049-2

Perfect score: 85
Sequence: 1 GYTVTGLEPDIYD 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 801

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	30.6	10	1 AMPN_HELAM	P81731 helicoverpa
2	25	29.4	10	1 GONL_ALIMI	P37041 alligator m
3	24	28.2	13	1 UN12_CLOPA	P81553 clostridium
4	24	28.2	15	1 SODM_STRGR	P80733 streptomyce
5	23	27.1	10	1 GONM_CUOPA	P81749 clupea pall
6	23	27.1	15	1 UC19_MAIZE	P80625 zea mays (m
7	22	25.9	15	1 KLOM_LUMTE	P11918 lumbricus t
8	21	24.7	10	1 UHA3_HUMAN	P40930 homo sapien
9	20.5	24.1	10	1 PAR1_PARMA	P81863 pardachirus
10	20	23.5	10	1 LABA_JATMU	P13270 jatropha mu
11	20	23.5	13	1 SODM_CANFA	P54712 canis famli
12	20	23.5	13	1 YPE2_LACTC	P42021 lactococcus
13	20	23.5	14	1 COCO_LIMPO	P35586 limulus pol
14	20	23.5	15	1 COXI_THUOB	P80978 thunnus cbe
15	20	23.5	15	1 DIDE_PERSP	P80701 pseudomons
16	19	22.4	8	1 UF06_MOUSE	P38644 mus muscula
17	19	22.4	9	1 FAR5_CALVO	P41860 calliphora
18	19	22.4	10	1 VEG6_BACSU	P80699 bacillus su
19	19	22.4	13	1 CD71_LITEM	P82051 littoria ewl
20	19	22.4	13	1 FIBB_PABIT	P14478 oryctolagus
21	19	22.4	14	1 DHS1_ANACY	P17874 anabaena cy
22	19	22.4	14	1 GIGS_SPTOL	P55235 spiracia ol
23	19	22.4	15	1 UC16_MAIZE	P80622 zea mays (m
24	18	21.2	9	1 TKL1_LOCOM	P16223 locusta mig
25	18	21.2	10	1 PNEU_HUMAN	P22103 homo sapien
26	18	21.2	10	1 FNEU_PAP	P21996 ratius norv
27	18	21.2	10	1 TKL2_LOCOM	P16224 locusta mig
28	18	21.2	10	1 TKL3_LOCOM	P30249 locusta mig
29	18	21.2	12	1 PORD_MERTM	P80903 methanobact
30	18	21.2	13	1 CHEP_PABIT	P42718 parapolidia
31	18	21.2	13	1 FR12_PEA	P83445 pisum sativ
32	18	21.2	14	1 IF2G_PAP	P81795 ratius norv
33	18	21.2	15	1 NXSO_PSETE	P59073 pseudonaja

34	18	21.2	15	1 PH2_PERAM	P82695 periplaneta
35	17.5	20.6	13	1 IDH4_CANFA	P54836 canis famli
36	17	20.0	5	1 RE32_TITRU	P82073 littoria rub
37	17	20.0	9	1 UPAG_HUMAN	P30092 homo sapien
38	17	20.0	10	1 FARP_LOCOM	P38553 locusta mig
39	17	20.0	13	1 MPI_MICOC	P1532 micropylitis
40	17	20.0	14	1 FIBB_MANDL	P14474 mandrillius
41	17	20.0	15	1 AVP2_CAVPO	P83508 cavia porce
42	17	20.0	15	1 GR78_HORSE	P16392 equus cabal
43	17	20.0	15	1 PGTS_PELAC	P80564 pelodactyl
44	17	20.0	15	1 UC29_MAIZE	P80635 zea mays (m
45	17	20.0	15	1 UP02_MAIZE	P83439 metarhizium

ALIGNMENTS

RESULT 1	AMPN_HELAM	STANDARD;	PRT;	10 AA.
ID	P81731;			
AC	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 43, Last sequence update)			
DE	15-MAR-2004 (Rel. 43, Last annotation update)			
OS	Helicoverpa armigera (cotton bollworm)			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelegrina;			
NC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuidae;			
OX	Noctuidae; Heliothinae; Helicoverpa.			
RN	[1]			
RP	SEQUENCE:			
RC	TISSUE=Midgut;			
RA	Ingle S.S., Trivedi N., Prasad R., Rao K.K., Chappar H.S.,			
RT	"Aminopeptidase-N as a receptor for Bacillus thuringiensis CryIAC			
RT	toxin from Helicoverpa armigera."			
RL	Submitted (MAR-1999) to Swiss-Prot.			
CC	-I- FUNCTION: ACTS AS A RECEPTOR FOR B.THURINGIENSIS TOXIN CRYIAC.			
CC	-I- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-I-			
CC	Xbb- from a peptide, amide or arylamide. Xaa is preferably Ala,			
CC	but may be most amino acids including Pro (slow action). When a			
CC	terminal hydrophobic residue is followed by a prolyl residue, the			
CC	two may be released as an intact Xaa-Pro dipeptide.			
CC	-I- COFACTOR: Binds 1 zinc ion per subunit (by similarity).			
CC	-I- SIMILARITY: Belongs to peptidase family M1.			
DR	InterPro: IPR006025; Pept_M_Zn_BS.			
DR	PROSITE: PS00142; ZINC_PROTEASE; PARTIAL.			
KW	Hydrolase; Metalloprotease; Aminopeptidase; Zinc.			
FT	NON TER			
SQ	SEQUENCE 10 AA; 1093 MW; 05042E8B7B11F1B8 CRC64;			
Query Match	30.6%; Score 26; DB 1; Length 10;			
Best Local Similarity	50.0%; Pred. No. 2.4e+02;			
Matches	5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;			
CY	1 GYTVTGLEP 10			
DB	1 GYTVTGLEP 10			
RESULT 2	GONL_ALIMI	STANDARD;	PRT;	10 AA.
ID	P37041; P20407;			
AC	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DE	28-FEB-2003 (Rel. 41, Last annotation update)			
OS	Gonadolibetin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)			
OC	Alligator mississippiensis (American alligator).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauia; Crocodylia; Alligatorinae; Alligator.			
OX	NCBI_TaxID=8496;			

RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1892082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
from brains of the American alligator (*Alligator mississippiensis*).";
RL Regul. Pept. 33:105-116(1991).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the GnRH family.
DR PIR: A60066; RHA01.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KM Hormone; Amiation; Hypothalamus; Pyroglutamate carboxylic acid.
FT MOD_RES 1
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1172 MW; 284B3D7286B45A3 CRC64;

Query Match 29.4%; Score 25; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GLEPG 11
Db 6 GLEPG 10

RESULT 3
UN12_CLOPA STANDARD; PRT; 13 AA.
ID UN12_CLOPA
AC P81353;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 12 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=MS;
RX MEDLINE=88291870; PubMed=9629918;
RA Flengserud R., Skjeldestad L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5";
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.8, ITS MW IS: 42.7 KDa.
FT VARIANT 4
FT VARIANT 5
FT NON_TER 13
SQ SEQUENCE 13 AA; 1465 MW; 70AA9B98455D405B CRC64;

Query Match 28.2%; Score 24; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 3 YVTGLGPGI 12
Db 2 YVLCGEPGI 11

RESULT 4
SODM_STRGR STANDARD; PRT; 15 AA.
ID SODM_STRGR
AC P80733;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).
GN SOD2.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE.
RC STRAIN=KCTC 9006;
RX MEDLINE=97056064; PubMed=8906409;
RA Young H.-D., Young H., Lee J.-W., Yim Y.-I., Lee J.K., Han Y.C.,
Kang S.-O.;
RT "Unique isozymes of superoxide dismutase in Streptomyces griseus";
RL Arch. Biochem. Biophys. 334:341-348(1996).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 iron or zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Tetramer.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodefe; 1.
DR PROSITE: PS00089; SOD MN; PARTIAL.
KM Oxidoreductase; Metal-binding; Iron; Zinc.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;

Query Match 28.2%; Score 24; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. No. 7.6e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 TVTGLGPGIDY 14
Db 2 TVTLPPEPPDY 12

RESULT 5
GON1_CLUPA STANDARD; PRT; 10 AA.
ID GON1_CLUPA
AC P81749;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberrin I (Gonadotropin-releasing hormone I) (GnRH-I) (4H-RH)
DE (Laliberrin I).
GN GNRH1.
OS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
OC Clupea.
OX NCBI_TaxID=30724;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Brain; and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carolsfeld J., Powell J.F.F., Craig M., Fischer W.H., Craig A.G.,
Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring";
RL Endocrinology 141:505-512(2000).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the GnRH family.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KM Hormone; Amiation; Hypothalamus; Pyroglutamate carboxylic acid.
FT MOD_RES 1
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1105 MW; 284B20B72871F5A3 CRC64;

Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GLSPG 11
DB 6 GLSPG 10

RESULT 6

UC19_MAIZE STANDARD; PRT; 15 AA.
AC P80625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (spot 406) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBI_Taxid=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzel P., Riccardi F., Morin C., Damerwal C., Huet J.-C.,
RA Pennolet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.6, its MW is: 18.4 KDa.
DR Maize-2DPAGE; P80625; COLEOPTILE.
DR MaizeDB; 123951; -.
FT NON_TER 1 1
FT TER 15 15
SQ SEQUENCE 15 AA; 1672 MW; 1CF69DAD8737F9D CRC64;

Query Match 27.1%; Score 23; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YTVTGLSPGI 12
DB 5 YTVTGCSPPV 14

RESULT 7

KLOM_LUMTE STANDARD; PRT; 15 AA.
ID P11918;
AC P11918;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Lumbiricine kinase (EC 2.7.3.5) (LK) (Fragment).
OS Lumbiricine terrestris (Common earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbiricina; Lumbiricidae; Lumbiricus.
NCBI_Taxid=6398;
RN [1]
RP SEQUENCE.
RX MEDLINE=72066544; Pubmed=5128744;
RA der Terrossian E., Desvages G., Pradel L.A., Kassab R., van Thoi N.;
RT "Comparative structural studies of the active site of ATP: guanidine
RT phosphotransferases. The essential cysteine tryptic peptide of
RT lumbiricine kinase from Lumbiricus terrestris muscle.";
RL Eur. J. Biochem. 22:585-592(1972).
CC -I- CATALYTIC ACTIVITY: ATP + lumbiricine = ADP + N-phospholumbiricine.
CC -I- SUBUNIT: Homodimer.
CC -I- SIMILARITY: Belongs to the ATP:guanido phosphotransferase family.
DR PIR; A08416; A08416.
DR InterPro; IPR000745; ATP-gua_Ptrans.
DR PROSITE; PS00112; GUANIDO_KINASE; 1.

KW Kinase: Transferase. 1
FT NON_TER 1
FT ACT_SITE 6
FT NON_TER 15
SQ SEQUENCE 15 AA; 1565 MW; 2A45FEF6140E90C4 CRC64;

Query Match 25.9%; Score 22; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GYTVTGLSPG 11
DB 2 GYTVCPGSMNG 12

RESULT 8

UHA3_HUMAN STANDARD; PRT; 10 AA.
ID UHA3_HUMAN
AC P40930;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; Pubmed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.8, its MW is: 47.3 KDa.
FT NON_TER 10 10
FT TER 10 10
SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;

Query Match 24.7%; Score 21; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 LEPTIDY 14
DB 2 VEPTITY 8

RESULT 9

PAP1_PAPMA STANDARD; PRT; 10 AA.
ID P81863;
AC P81863;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Paradoxin I (PXI) (Fragment).
OS Paradoxin marmoratus (Red sea moose sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Solariidae; Solariidae; Paradoxini.
NCBI_Taxid=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; Pubmed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moose sole (Paradoxin
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -I- FUNCTION: Exhibits unusual shark repellent and surfactant

CC	properties. Forms voltage-dependent, ion-permeable channels in	
CC	membranes. At high concentration causes cell membrane lysis. Shown	
CC	to be 5-10 times more toxic, cytolytic and active in membrane pore	
CC	formation than pardaxin II.	
CC	-1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.	
CC	-1- SUBCELLULAR LOCATION: Secreted.	
CC	-1- SIMILARITY: Belongs to the pardaxin family.	
KM	Toxin.	
FT	NON TER	10
SQ	SEQUENCE	10 AA; 1063 MW; D399C36760572DD9 CRC64;

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Query Match      24.1%;   SCORE 20.5; DB 1;   Length 10;
Best Local Similarity 38.5%;
Matches          5; Conservative      3; Mismatches      2; Indels      3; Gaps      1
QY              1 GYTVTGTGEPGD 13
                |::|::|::|
Db              1 GPF--ALPPIGIF 10

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RESULT 10
LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA

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JT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Labaditin.
 OS Jatropha multifida (Physic nut).
 OC Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid 1; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaceae;
 OC Jatropha.
 OX NCBI_TaxID=3996;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=latex;
 RA Kosari S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.
 RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha
 RT multifida L. (Euphorbiaceae). Isolation and sequence determination
 RT by means of two-dimensional NMR.",
 RL FEBS Lett. 256:91-96(1989).
 CC -!- FUNCTION: Labaditin is an active peptide which inhibits the
 CC classical pathway of complement activation in vitro. Activity
 CC seems to be based on an interaction with C1.
 CC -!- PTM: This is a cyclic peptide.
 CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine
 CC for treatment of infected wounds, skin infections and scabies.
 SQ SEQUENCE 10 AA; 1089 MW; D98AADS36ZDIB362 CRC64;

Query March	23.5%	Score 20	DB 1	Length 10
Best Local	Similarity 57.1%	Pred. No. 2.2e+03		
Matches	4	Conservative	1	Mismatches 2
				Indels 0
				Gaps 0
QY	1 GYTTTG 7			
	:			
Db	2 GYTTTG 8			

RESULT 11		
SODM_CANFA		
ID	SODM_CANFA	STANDARD; PRT; 13 AA.
AC	P54712;	
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment)	
GN	SOD2.	
OS	Canis familiaris (Dog).	
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
OX	NCBI_TaxID=9615;	

RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Mann M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins";
RL Electrophoresis 15:2795-2802(1997).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (by similarity).
CC -1- SUBUNIT: Homotrimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR HSC-2DPAGE; P54712; DOG.
DR Interpro; IPR001189; SODismutase.
DR Pfam; PF00081; sodef; 1.
DR PROSITE; PS00088; SOD_MN, PARTIAL.
FT Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1476 MW; 9C9561D9BBE0672A CRC64;

Query Match	23.5%	Score 20;	DB 1;	Length 13;
Best Local Similarity	50.0%	Pred. No. 2.8e+03;		
Matches	3;	Conservative	1;	Mismatches 2;
				Indels 0;
				Gaps 0;
QY	10	PCIDPD	15	
		:		
Db	5	PDPDPD	10	

RESULT 12	TYPE2 LACLC	STANDARD;	PRT;	13 AA.
ID	_TYPE2 LACLC			
AC	P42021;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DS	Hypochemical Protein in pBET 5'-region (ORF2) (Fragment).			
OS	Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus			
NCBI_TaxID=1359;				

RP SEQUENCE FROM N.A.
RX MEDLINE=94245610; Pubmed=8186586;
RA Mierau I., Haandrikman A.J., Veltrop O., Tan P.S.T., Leenhouts K.L.,
RA Konings W.N., Venema G., Kok J.
RT "Tripeptidase gene (pept) of *Lactococcus lactis*: molecular cloning
RT and nucleotide sequencing of pept and construction of a chromosomal
RT deletion mutant.";
RL J. Bacteriol. 176:2854-2861(1994).
CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL; L27596; AAA20625.1; -.
KW Hypothetical protein.
FT NON TER 1 1
SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64

Query Match	23.5%;	Score 20;	DB 1;	Length 13;
Best Local Similarity	57.1%;	Pred. No. 2.8e+03;		
Matches	4;	Conservative	1;	Mismatches 2;
			Indels	0;
			Gaps	0

6 TELEPGI 12
| : | |
MAY 9

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RESULT 13
ID COCO_LIMPO STANDARD; PRT; 14 AA.
AC P35586;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
OC Cocomase (EC 3.4.21.-) (Fragment).
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE.
RX MEDLINE=78037243; PubMed=335821;
RA Law J.H., Dunn P.E., Kramer K.J.;
RT "Insect proteases and peptidases."
RL Adv. Enzymol. Relat. Areas Mol. Biol. 45:389-425(1977).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage Arg-, Lys-.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR MEROPS; S01.112; -.
DR InterPro; IPR001254; Peptidase_S1.
DR PROSITE; PS50240; TRYPSIN_DOM; PARTIAL.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolyase; Serine protease.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1452 MW; 1615FB1D73747570 CRC64;

Query Match 23.5%; Score 20; DB 1; Length 14;
Best Local Similarity 55.6%; Pred. No. 3.1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 VTGLEPGID 13
Db 2 VGGFTIGID 10

RESULT 14
COCI_THUOB
ID COCI_THUOB STANDARD; PRT; 15 AA.
AC P80978;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c oxidase polypeptide Vic-2 (EC 1.9.3.1) (Fragments).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RX TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver."
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
DR PIR; S77987; S77987.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1696 MW; 4C4C966C73A40294 CRC64;

Query Match 23.5%; Score 20; DB 1; Length 15;
Best Local Similarity 36.4%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 VTGLEPGIDYD 15
Db 5 VVAKKPMSDYE 15

RESULT 15
DIDH_PSESP
ID DIDH_PSESP STANDARD; PRT; 15 AA.
AC P80701;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 3-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.50) (3-alpha-HSD)
DE (Hydroxysteroidglanidin dehydrogenase) (HSD29) (Fragment).
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE.
RX MEDLINE=97100200; PubMed=8944761;
RA Oppermann U.C.T., Maser E.;
RT "Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl
RT reductase from the Gram-negative bacterium Comamonas testosteroni."
RL Eur. J. Biochem. 241:744-749(1996)
CC -1- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND
CC 3-OXO-REDUCTASE ACTIVITIES TOWARDS A VARIETY OF CIS OR TRANS FUSED
CC A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL
CC COMPOUNDS, INCLUDING A METYRAPONE-BASED CLASS OF INSECTICIDES, TO
CC THE RESPECTIVE ALCOHOL METABOLITES.
CC -1- CATALYTIC ACTIVITY: Androstereone + NAD(P)(+) = 5-alpha-androstane-
CC 3,17-dione + NAD(P)H.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
DR InterPro; IPR002198; ADH_short.
DR PROSITE; PS00061; ADH_SHORT; PARTIAL.
KW Oxidoreductase; NAD.
FT DOMAIN 6
FT NON_TER 15
SQ SEQUENCE 15 AA; 1315 MW; 950686D070A7790 CRC64;

Query Match 23.5%; Score 20; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 VTGLEPGI 12
Db 5 ITGSASGI 12

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Search completed: September 21, 2004, 06:41:17
cdd time : 11.667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 06:30:41 : Search time 58.333 Seconds
(without alignments)
81.133 Million cell updates/sec

Title: US-10-676-049-2

Perfect score: 85
Sequence: 1 GYTVTGLPGLDID 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3954

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL.25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_rhbc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriaph: *
17: sp_archaeop: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	32.9	15	11	Q9QUT7
2	26	30.6	15	11	Q9QW89
3	23	27.1	11	7	Q7876
4	23	27.1	15	4	Q9UC0
5	23	27.1	15	10	Q98V7
6	22.5	26.5	15	4	Q9UC4
7	22	25.9	11	11	P97755
8	22	25.9	14	10	P82340
9	21	24.7	9	5	P82208
10	21	24.7	9	11	Q80V06
11	21	24.7	9	16	Q935G0
12	21	24.7	11	10	Q04131
13	21	24.7	13	2	P94878
14	20.5	24.1	15	6	Q9TR9
15	20.5	24.1	15	6	Q9TR9
16	20	23.5	6	5	P83569

17	20	23.5	9	7	Q31415	Q31415 gallus gall
18	20	23.5	10	6	Q9TR48	Q9TR48 bos taurus
19	20	23.5	10	11	Q9QV8	Q9QV8 mus sp. pro
20	20	23.5	11	6	Q9TRX0	Q9TRX0 sus scrofa
21	20	23.5	11	7	Q19718	Q19718 homo sapien
22	20	23.5	13	3	Q93824	Q93824 candida tro
23	20	23.5	14	12	Q85578	Q85578 sigma virus
24	20	23.5	15	4	Q9UJ51	Q9UJ51 homo sapien
25	20	23.5	15	4	Q9UCB9	Q9UCB9 homo sapien
26	20	23.5	15	10	Q98V6	Q98V6 tritium ae
27	19	22.4	7	5	Q721C0	Q721C0 caenorhabdi
28	19	22.4	11	2	P66319	P66319 desulfovibr
29	19	22.4	12	6	Q46664	Q46664 macropus ro
30	19	22.4	12	8	Q9T2U3	Q9T2U3 bos taurus
31	19	22.4	13	5	Q86NG6	Q86NG6 caenorhabdi
32	19	22.4	13	6	Q855C9	Q855C9 sus scrofa
33	19	22.4	14	4	Q9P2A2	Q9P2A2 homo sapien
34	19	22.4	15	8	Q78794	Q78794 pyralella 1
35	18.5	21.8	12	2	Q9R7P1	Q9R7P1 staphylococ
36	18	21.2	8	7	Q95213	Q95213 oryctolagus
37	18	21.2	10	11	Q9QVE9	Q9QVE9 mus sp. pro
38	18	21.2	12	4	Q16452	Q16452 homo sapien
39	18	21.2	13	5	Q9TRR4	Q9TRR4 titius serr
40	18	21.2	13	13	Q9S556	Q9S556 carassius a
41	18	21.2	13	13	Q722N7	Q722N7 xenopus lae
42	18	21.2	14	8	Q98696	Q98696 hordeum vul
43	18	21.2	14	10	Q94IT6	Q94IT6 fragaria nu
44	18	21.2	15	4	Q9UC90	Q9UC90 homo sapien
45	18	21.2	15	5	P82211	P82211 bombyx mori

ALIGNMENTS

RESULT 1	Q9QUT7	PRELIMINARY;	PRT;	15 AA.
ID	Q9QUT7	PRELIMINARY;	PRT;	15 AA.
AC	Q9QUT7	PRELIMINARY;	PRT;	15 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	Glutathione S-transferase (Fragment).			
OS	Mus sp.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10095;			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=92329477; PubMed=1627586;			
RX	Singhal S.S., Saxena M., Ahmad H., Awasthi Y.C.;			
RA	"Glutathione S-transferase of mouse liver: sex-related differences in			
RT	the expression of various isozymes."			
RL	Biochim. Biophys. Acta 1117:105-105(1992).			
DR	HSP; P04905; 2CST.			
SQ	SEQUENCE 15 AA; 1754 MW; 0284DB620E166ED4 CRC64;			
Query Match	Score 28; DB 11; Length 15;			
Best Local Similarity	62.5%; Pred. No. 8.6e+02;			
Matches	5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
Cy	1 GYTVTGL 8			
Db	5 GYTVVRL 12			
RESULT 2	Q9QW89	PRELIMINARY;	PRT;	15 AA.
ID	Q9QW89	PRELIMINARY;	PRT;	15 AA.
AC	Q9QW89	PRELIMINARY;	PRT;	15 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Glutathione S-transferase subunit D (EC 2.5.1.18) (Fragment).			

OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96036981; PubMed=7495987;
 RA Roulim P., Debrauer U., Tulliez J.;
 RT "Electrosensory ionization-mass spectrometry as a tool for
 RT characterization of glutathione S-transferase isozymes.";
 RL Anal. Biochem. 229:304-312(1995).
 DR GO: GO:0004364; F:glutathione transferase activity; IEA.
 SQ SEQUENCE 15 AA; 1701 MW; 9A54C712143F7C4A CRC64;

Query Match 30.6%; Score 26; DB 11; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYVTGTGL 8
 ||| : |||
 DB 5 GYWDIRGL 12

RESULT 3
 ID 077876 PRELIMINARY; PRT; 11 AA.
 AC 077876;
 DT 01-NOV-1998 (TRENBLREL. 08, Created)
 DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE MHC class II B locus 1 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Tillio E., Zaleska-Ruczynska Z., McAndrew B., Vinsek V.,
 RA Figueira F., Sultman H., Klein U.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF049985; AAC41324.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1178 MW; 9AC131FAB2D2DB45 CRC64;

Query Match 27.1%; Score 23; DB 7; Length 11;
 Best Local Similarity 57.1%; Pred. No. 4.1e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YTVTGLE 9
 ||| : |||
 DB 5 YVVTGCD 11

RESULT 4
 ID 09UCC0 PRELIMINARY; PRT; 15 AA.
 AC 09UCC0;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
 DE Insulin-like growth factor receptor alpha subunit (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=94079685; PubMed=8257688;
 RA Kasuya T., Paz I.B., Maddux B.A., Goldfine I.D., Hefta S.A.,
 RA Kaibita-Yamaguchi Y.;
 RT "Characterization of human placental insulin-like growth factor-
 RT I/insulin hybrid receptors by protein microsequencing and
 RT purification.";
 RL Biochemistry 32:13531-13536(1993).
 SQ SEQUENCE 15 AA; 1721 MW; 98BC151D6D81784B CRC64;

Query Match 27.1%; Score 23; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PGID 13
 ||| : |||
 DB 5 PGID 8

RESULT 5
 ID 09S8V7 PRELIMINARY; PRT; 15 AA.
 AC 09S8V7;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
 DE High-molecular-weight glutenin subunit (Fragment).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93003354; PubMed=1390908;
 RA Tao H.P., Adalstein A.E., Kasarda D.D.;
 RT "Intermolecular disulfide bonds link specific high-molecular-weight
 RT glutenin subunits in wheat endosperm.";
 RL Biochim. Biophys. Acta 1159:13-21(1992).
 SQ SEQUENCE 15 AA; 1559 MW; CD1A6F573C945AFD CRC64;

Query Match 27.1%; Score 23; DB 10; Length 15;
 Best Local Similarity 50.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYVTGT 6
 ||| : |||
 DB 9 GYVPS 14

RESULT 6

ID 09UCC4 PRELIMINARY; PRT; 15 AA.
 AC 09UCC4;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
 DE 33 kDa heparin-RELEASABLE protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=94059921; PubMed=8241100;
 RA Novotny M.F., Maffei T., Mehta R.L., Milner P.G.;
 RT "Identification of novel heparin-releasable proteins, as well as the
 RT cytokines midkine and pleiotrophin, in human postheparin plasma.";
 RL Arterioscler. Thromb. 13:1798-1805(1993).
 SQ SEQUENCE 15 AA; 1823 MW; D54F35684E7085D7 CRC64;

Query Match 26.5%; Score 22.5; DB 4; Length 15;
 Best Local Similarity 41.7%; Pred. No. 7.1e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 3 YTVGLPGIDY 14
| : | | |
Db 4 YVIFQADPG-DY 14

RESULT 7
ID P97755 PRELIMINARY; PRT; 11 AA.
AC P97755;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE Secretogranin II (SGII) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96343805; PubMed=8756552;
RA Jones L.C., Day R.N., Pittler S.J., Valentine D.L., Scammell J.G.;
RT "Cell-specific expression of the rat secretogranin II promoter.";
RL Endocrinology 137:1815-1822(1996).
DR EMBL; AF107301; -; NOT_ANNOTATED_CDS.
FT NON TER 1
SQ SEQUENCE 11 AA; 1298 MW; 384E8DA446C1B5A7 CRC64;

Query Match 25.9%; Score 22; DB 11; Length 11;
Best Local Similarity 57.1%; Pred. No. 6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 LEPGIDY 14
| : | | |
Db 2 LEPSTOY 8

RESULT 8
ID P82340 PRELIMINARY; PRT; 14 AA.
AC P82340;
DT 01-JUN-2000 (TREMBlrel. 14, Created)
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT204) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009579; C:thylakoid; IEA.
KM Chloroplast; Thylakoid.
FT NON TER 14
SQ SEQUENCE 14 AA; 1505 MW; 2EABFAF980FD3D77 CRC64;

Query Match 25.9%; Score 22; DB 10; Length 14;
Best Local Similarity 37.5%; Pred. No. 8e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 TGLEPGID 13
| : | | |
Db 1

Db 3 SGQFPVVD 10

RESULT 9
ID P82208 PRELIMINARY; PRT; 9 AA.
AC P82208;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrgota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN=XINSHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
RT silkworm.";
RL I Chuan Hsueh Pao 28:217-224(2001).
FT NON TER 9
SQ SEQUENCE 9 AA; 1009 MW; 377C3AB845B042D7 CRC64;

Query Match 24.7%; Score 21; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 PGIDYD 15
| : | | |
Db 2 PVISYD 7

RESULT 10
ID Q80YU6 PRELIMINARY; PRT; 9 AA.
AC Q80YU6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CAMP-responsive element modulator (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94073967; PubMed=8252624;
RA Molina C.A., Foulkes N.S., Talli E., Sassone-Corsi P.;
RT "Inducibility and negative autoregulation of CREM: an alternative
RT promoter directs the expression of ICBF, an early response
RT repressor.";
RL Cell 75:875-886(1993).
DR EMBL; S67785; AAP14017.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 880 MW; C258AB1A861B2CD CRC64;

Query Match 24.7%; Score 21; DB 11; Length 9;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 VTGLEPG 11
| : | | |
Db 3 VTGDETG 9

RESULT 11
ID Q935G0 PRELIMINARY; PRT; 9 AA.
AC Q935G0;

DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Hypothetical protein HCM2.0001c (Fragment).
 GN HCM2.0001C.
 OS Salmonella typhi.
 OG Plasmid pHC2.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmomella.
 OX NCBI_Taxid=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Compston P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 RA Krogli M., Larsen T.S., Leather S., Moulé S., O'Gaora P., Parry C.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmomella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR EMBL; AL51384; CAD09688.1; -;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 XM Hypothetical protein; Plasmid; Complete proteome.
 FT NON TER
 SQ SEQUENCE 9 AA; 904 MW; C12E287DD731B2CD CRC64;

Query Match 24.7%; Score 21; DB 16; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 TVTGLE 9
 ID 004131 PRELIMINARY; PRT; 11 AA.
 AC 004131;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Wound induced protein (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_Taxid=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=pik-red; TISSUE=Pericarp;
 RX MEDLINE=91355936; PubMed=715787;
 RA Parsons B.L., Mattoo A.K.;
 RT "Wound regulated accumulation of specific transcripts in tomato fruit:
 RT interactions with fruit development, ethylene and light.";
 RL Plant Mol. Biol. 17:463-464(1991).
 DR EMBL; X59884; CAA42539.1; -;
 DR PIR; S19775; S19775.
 FT NON TER
 SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

Query Match 24.7%; Score 21; DB 10; Length 11;
 Best Local Similarity 75.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 GIDY 14

RESULT 13
 ID 09S8L4 PRELIMINARY; PRT; 15 AA.
 AC 09S8L4;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Beta-D-glucoside glucosyltransferase (EC 3.2.1.21) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_Taxid=4577;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94347094; PubMed=8068000;
 RA Feldausch J., Vente A., Zetl R., Bako L., Campos N., Palme K.;
 RT "Characterization of two membrane-associated beta-glucosidases from
 RT maize (Zea mays L.) coleoptiles.";
 RL Biochem. J. 302:15-21(1994).
 DR GO; GO:0008422; F:beta-glucosidase activity; IEA.
 SQ SEQUENCE 15 AA; 1667 MW; 46C40370DC8C730B CRC64;

Query Match 24.7%; Score 21; DB 10; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 14
 ID P94878 PRELIMINARY; PRT; 13 AA.
 AC P94878;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Lin protein (Fragment).
 GN LIN.
 OS Lactococcus lactis.
 OC Bacteria; Firmicutes; Lactobacilliales; Streptococcaceae; Lactococcus.
 OX NCBI_Taxid=1358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCO 763;
 RX MEDLINE=97352670; PubMed=9209029;
 RA Nardi M., Renault P., Monnet V.;
 RT "Duplication of the pepf gene and shuffling of DNA fragments on the
 RT lactose plasmid of Lactococcus lactis.";
 RL J. Bacteriol. 179:4164-4171(1997).
 DR EMBL; X97978; CAA68131.1; -;
 DR GO; GO:0000150; F:recombinase activity; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR006118; Recombinase.
 DR PROSITE; PS00397; RECOMBINASES_1; 1.
 FT NON TER
 SQ SEQUENCE 13 AA; 1410 MW; CDFDE9101C9BD40D CRC64;

Query Match 24.1%; Score 20.5; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.3e+04;
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 GYTV-TGLE 9
 ID 4 GYARVSTGLQ 13

RESULT 15

ID O9TRR9 PRELIMINARY; PRT; 15 AA.

AC O9TRR9:

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Calcyclin-associated protein, CAP50=Ca2+/phospholipid-binding protein 1-8 fragment (Fragment).

DE OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OC NCBI_taxid=9986;

OX [1]

RP MEDLINE=92250478; PubMed=1533622;

RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;

RT "A calyculin-associated protein is a newly identified member of the Ca2+/phospholipid-binding proteins, annexin family."

RL U. Biol. Chem. 267:8919-8924(1992).

FT NON_TER 1 15

PT 15 15

SQ SEQUENCE 15 AA; 1686 MW; 299E23A743829077 CRC64;

QY 2 YVTVTGLEPGIDY 14
|:|:|
3 YHDISGDTSG-DY 14

Db 3 YHDISGDTSG-DY 14

Search completed: September 21, 2004, 06:45:08

Job time : 61.333 secs

Blank

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:57:18 / Search time 72.3333 Seconds

(without alignments)
58.593 Million cell updates/sec

Title: US-10-676-049-2

Perfect score: 85

Sequence: 1 GYTYVTGLEPGIDYD 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 447529

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	AAO17876	AAO17876 EDB fibro
2	72	84.7	15	AAO4093	AAO4093 Anti-genic
3	72	84.7	15	AAO8821	AAO8821 ED-B anti
4	56	65.9	15	AAO17877	AAO17877 EDB fibro
5	40	47.1	15	AAO19571	AAO19571 Fibrinoge
6	40	47.1	15	AAO19567	AAO19567 Fibrinoge
7	40	47.1	15	AAO19570	AAO19570 Fibrinoge
8	40	47.1	15	AAO19573	AAO19573 Fibrinoge
9	40	47.1	15	AAO19569	AAO19569 Fibrinoge
10	40	47.1	15	AAO19574	AAO19574 Fibrinoge
11	40	47.1	15	AAO19575	AAO19575 Fibrinoge
12	37	43.5	15	AAO19576	AAO19576 Fibrinoge
13	34	40.0	11	AAO195726	AAO195726 Liver res
14	34	40.0	13	AAO195726	AAO195726 Liver res
15	34	40.0	13	AAO195726	AAO195726 Liver res
16	33	38.8	15	AAO19568	AAO19568 Peptide h
17	33	38.8	15	AAO19568	AAO19568 Peptide h
18	33	38.8	15	AAO19568	AAO19568 Peptide h
19	33	38.8	15	AAO19568	AAO19568 Peptide h
20	33	38.8	15	AAO19568	AAO19568 Peptide h
21	33	38.8	15	AAO19568	AAO19568 Peptide h
22	33	38.8	15	AAO19568	AAO19568 Peptide h
23	32.5	38.2	12	AAO19568	AAO19568 Peptide h
24	32	37.6	14	AAO19568	AAO19568 Peptide h
25	32	37.6	15	AAO19568	AAO19568 Peptide h

26	32	37.6	15	AAO19568	AAO19568 Peptide h
27	31	36.5	10	AAO19568	AAO19568 Peptide h
28	31	36.5	10	AAO19568	AAO19568 Peptide h
29	31	36.5	10	AAO19568	AAO19568 Peptide h
30	31	36.5	10	AAO19568	AAO19568 Peptide h
31	31	36.5	11	AAO19568	AAO19568 Peptide h
32	31	36.5	11	AAO19568	AAO19568 Peptide h
33	31	36.5	15	AAO19568	AAO19568 Peptide h
34	31	36.5	15	AAO19568	AAO19568 Peptide h
35	31	36.5	15	AAO19568	AAO19568 Peptide h
36	31	36.5	15	AAO19568	AAO19568 Peptide h
37	31	36.5	15	AAO19568	AAO19568 Peptide h
38	31	36.5	15	AAO19568	AAO19568 Peptide h
39	31	36.5	15	AAO19568	AAO19568 Peptide h
40	31	36.5	15	AAO19568	AAO19568 Peptide h
41	30.5	35.9	15	AAO19568	AAO19568 Peptide h
42	30	35.3	12	AAO19568	AAO19568 Peptide h
43	30	35.3	15	AAO19568	AAO19568 Peptide h
44	30	35.3	15	AAO19568	AAO19568 Peptide h
45	30	35.3	15	AAO19568	AAO19568 Peptide h

ALIGNMENTS

RESULT 1	AAO17876	standard; peptide, 15 AA.
ID	AAO17876	
XX	AAO17876	
AC	AAO17876	
DT	20-AUG-2002	(first entry)
XX		
DE	EDB fibronectin domain binding peptide #2.	
XX		
KW	EDB fibronectin domain; EDBFD; angiogenesis; gene therapy; transplant;	
XX	implant; receptor molecule interaction.	
OS	Unidentified.	
XX		
PN	WO200220563-A2.	
XX		
PD	14-MAR-2002.	
XX		
PF	30-AUG-2001; 2001WO-EP010016.	
XX		
PR	07-SEP-2000; 2000DE-01045803.	
XX		
PR	02-MAY-2001; 2001DE-01023133.	
XX		
PA	(SCHD) SCHERING AG.	
XX		
PA	(REPL) REPLITZ A.	
XX		
PA	(KOPP) KOPF M.	
XX		
PA	(EGNE) EGNER U.	
XX		
PA	(BAHR) BAHR I.	
XX		
PI	(MENR) MENRAD A.	
XX		
DR	Menrad A;	
XX		
PT	WPI; 2002-479458/51.	
XX		
PT	New proteins binding specifically to the ED-b fibronectin domain, are	
XX	cell adhesion and proliferation mediators useful e.g. in screening tests.	
PS	Claim 2; Page 41; 66pp; German.	
XX		
CC	The present invention relates to a new protein which binds specifically	
XX	to the EDB fibronectin domain (EDBFD), is specifically expressed or	
CC	activated in endothelial cells, stromal cells of a tumour and tumour	
XX	cells, and has an apparent molecular weight of 120-130 kDa for the light	
CC	chain and 150-160 kDa for the heavy chain. The protein can be used to	
XX	screen compounds which bind to EDBFD or its receptor, for coating	
CC	surfaces to which endothelial cells bind, in cell cultures, in	
XX	combination with transplants or in combination with implants	


```

XX 14-MAR-2002.
PD
XX
XX 30-AUG-2001; 2001MO-EP010016.
PE
XX 07-SEP-2000; 2000DE-01045803.
PR 02-MAY-2001; 2001DE-01023133.
XX
XX (SCHD ) SCHERING AG.
PA (REDL/) REDLITZ A.
PA (KOPF/) KOPFITZ M.
PA (EGNE/) EGNER U.
PA (BAHR/) BAHR I.
PA (MENR/) MENRAD A.
XX
XX Menrad A;
PI
XX WPI; 2002-479458/51.
DR
XX
XX New proteins binding specifically to the ED-b fibronectin domain, are
PT cell adhesion and proliferation mediators useful e.g. in screening tests.
XX
XX Claim 2; Page 41; 66pp; German.
PS
XX
CC The present invention relates to a new protein which binds specifically
CC to the ED-b fibronectin domain (EDbFD), is specifically expressed or
CC activated in endothelial cells, stromal cells of a tumour and tumour
CC cells, and has an apparent molecular weight of 120-130 kDa for the light
CC chain and 150-160 kDa for the heavy chain. The protein can be used to
CC screen compounds which bind to EDbFD or its receptor, for coating
CC surfaces to which endothelial cells bind, in cell cultures, in
CC combination with transplants or in combination with implants
CC (specifically lung implants, artificial heart pacemakers or valves,
CC vascular implants, endoprotheses, screws, bars, plates, wires, nails,
CC rods, artificial joints, breast implants, artificial cranial plates,
CC false teeth, tooth fillings or tooth bridges, as it improves the
CC integration of transplants or implants in the body. The protein is also
CC useful in clarifying EDB-specific adhesion mechanisms and receptor
CC molecule interactions involved in angiogenesis. The present sequence is a
CC protein of the invention
XX
XX
SQ Sequence 15 AA;
XX
XX
XX Query Match 65.9%; Score 56; DB 5; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.016; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0;
XX
XX QY 6 TGLEPGIDYD 15
XX |||||
XX 1 TGLEPGIDYD 10
XX
XX
XX RESULT 5
XX AAB19571
XX ID AAB19571 standard; peptide; 15 AA.
XX
XX AC AAB19571;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Fibrinogen-derived peptide with anti-cell adhesion activity.
XX
XX KW Cell adhesion; inhibitor; antimetastatic; metastasis; cancer; antitumour;
XX antiinflammatory; antirheumatic; antiallergic;
XX antithrombotic; antifibrotic; immunostimulant; vulnerary; therapy;
XX fibronectin; human; mutant; mutein.
XX
XX OS Homo sapiens.
XX Synthetic.
XX
XX PN EPI036798-A1.
XX
XX PD 20-SEP-2000.

```

```

XX
XX 16-MAR-2000; 2000EP-00105572.
PF
XX
XX 16-MAR-1999; 99JP-00070127.
PR
XX (HISM ) HISAMITSU PHARM CO LTD.
XX
XX PI Akiyama K, Goto T, Fukai F, Ueki M;
XX WPI; 2000-588967/56.
DR
XX
XX Novel peptides having cell adhesion inhibiting properties are useful for
PT treating cancer metastasis, inflammation and fibrosis.
XX
XX Claim 3; Page 8; 25pp; English.
PS
XX
XX The present sequence represents a peptide derived from amino acid
XX residues 1567-1581 of human fibronectin, but having the residue
XX equivalent to Val-1581 substituted by alanine. Native and Ala-substituted
XX fibronogen-derived peptides of the invention (see AAB19566-71) are
XX physiologically active, possessing cell adhesion inhibitory activity
XX against human chronic myelocytic leukaemia K562 cells, human histiocytic
XX lymphoma U937 cells and the Ramos cell line derived from human Burkitt's
XX lymphoma, but not against human melanoma A375SW or fibrosarcoma HT1080
XX cells. The peptides are used as antimetastatic agents that inhibit
XX metastasis of cancers based on cell adhesion. They are also useful for
XX investigating and treating diseases in which adhesion between cells or
XX between cells and extracellular matrices are implicated, such as cancer,
XX rheumatism, asthma, allergy, thrombosis, organ transplant rejection,
XX wound healing such as fibrosis, inflammation, immuno-inflammatory
XX conditions including enteritis such as ulcerative colitis, and autoimmune
XX diseases. The peptides are prepared by chemical synthesis and are
XX modified with biotin
XX
XX
SQ Sequence 15 AA;
XX
XX
XX Query Match 47.1%; Score 40; DB 3; Length 15;
XX Best Local Similarity 75.0%; Pred. No. 8.1;
XX Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 GLEPGVDY 14
XX |||||
XX 1 GLKPGVDY 8
XX
XX
XX RESULT 6
XX AAB19567
XX ID AAB19567 standard; peptide; 15 AA.
XX
XX AC AAB19567;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Fibrinogen-derived peptide with anti-cell adhesion activity.
XX
XX KW Cell adhesion; inhibitor; antimetastatic; metastasis; cancer; antitumour;
XX antiinflammatory; antirheumatic; antiallergic;
XX antithrombotic; antifibrotic; immunostimulant; vulnerary; therapy;
XX fibronectin; human.
XX
XX OS Homo sapiens.
XX
XX PN EPI036798-A1.
XX
XX PD 20-SEP-2000.
XX
XX PF 16-MAR-2000; 2000EP-00105572.
XX
XX PR 16-MAR-1999; 99JP-00070127.
XX
XX (HISM ) HISAMITSU PHARM CO LTD.
XX
XX PI Akiyama K, Goto T, Fukai F, Ueki M;

```

XX WPI; 2000-588967/56.
XX Novel peptides having cell adhesion inhibiting properties are useful for
PT treating cancer metastasis, inflammation and fibrosis.
XX
PS Claim 2; Page 8; 25pp; English.
XX
CC The present sequence represents a peptide corresponding to amino acid
CC residues 1567-1581 of human fibronectin. The peptide is physiologically
CC active, possessing cell adhesion inhibitory activity against human
CC chronic myelocytic leukaemia K562 cells, human histiocytic lymphoma U937
CC cells and the Ramos cell line derived from human Burkitt's lymphoma, but
CC not against human melanoma A375SM or fibrosarcoma HT1080 cells. The
CC peptide, and its claimed alanine-substituted derivatives (see AAB19568-
CC 71), are used as antimetastatic agents that inhibit metastasis of cancers
CC based on cell adhesion. They are also useful for investigating and
CC treating diseases in which adhesion between cells or between cells and
CC extracellular matrices are implicated, such as cancer, rheumatism,
CC asthma, allergy, thrombosis, organ transplant rejection, wound healing
CC such as fibrosis, inflammation, immuno-inflammatory conditions including
CC enteritis such as ulcerative colitis, and autoimmune diseases. The
CC peptides are prepared by chemical synthesis and are modified with biotin
SQ Sequence 15 AA;
OY
Query Match 47.1%; Score 40; DB 3; Length 15;
Best Local Similarity 75.0%; Pred. No. 8.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 7 GLEPGIDY 14
1 GLKPGVDY 8
RESULT 7
AAB19570
ID AAB19570 standard; peptide; 15 AA.
XX
AC AAB19570;
XX
DT 22-JAN-2001 (first entry)
XX
DE Fibrinogen-derived peptide with anti-cell adhesion activity.
XX
KW Cell adhesion; inhibitor; antimetastatic; metastasis; cancer; antitumour;
KW anti-inflammatory; antirheumatic; antiallergic;
KW antithrombotic; antifibrotic; immunostimulant; vulnerary; therapy;
KW fibronectin; human; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN EPI036798-A1.
XX
PD 20-SEP-2000.
XX
PF 16-MAR-2000; 2000EP-00105572.
XX
PR 16-MAR-1999; 99JP-00070127.
XX
PA (HISM) HISAMITSU PHARM CO LTD.
XX
PI Akiyama K, Goto T, Fukai F, Ueki M;
XX
DR WPI; 2000-588967/56.
XX
PT Novel peptides having cell adhesion inhibiting properties are useful for
PT treating cancer metastasis, inflammation and fibrosis.
XX
PS Claim 3; Page 8; 25pp; English.
XX
CC The present sequence represents a peptide derived from amino acid

CC residues 1567-1581 of human fibronectin, but having the residue
CC equivalent to Tyr-1579 substituted by alanine. Native and Ala-substituted
CC fibrinogen-derived peptides of the invention (see AAB19566-71) are
CC physiologically active, possessing cell adhesion inhibitory activity
CC against human chronic myelocytic leukaemia K562 cells, human histiocytic
CC lymphoma U937 cells and the Ramos cell line derived from human Burkitt's
CC lymphoma, but not against human melanoma A375SM or fibrosarcoma HT1080
CC cells. The peptides are used as antimetastatic agents that inhibit
CC metastasis of cancers based on cell adhesion. They are also useful for
CC investigating and treating diseases in which adhesion between cells or
CC between cells and extracellular matrices are implicated, such as cancer,
CC rheumatism, asthma, allergy, thrombosis, organ transplant rejection,
CC wound healing such as fibrosis, inflammation, immuno-inflammatory
CC conditions including enteritis such as ulcerative colitis, and autoimmune
CC diseases. The peptides are prepared by chemical synthesis and are
CC modified with biotin
SQ Sequence 15 AA;
OY
Query Match 47.1%; Score 40; DB 3; Length 15;
Best Local Similarity 75.0%; Pred. No. 8.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 7 GLEPGIDY 14
1 GLKPGVDY 8
RESULT 8
AAB19573
ID AAB19573 standard; peptide; 15 AA.
XX
AC AAB19573;
XX
DT 22-JAN-2001 (first entry)
XX
DE Fibrinogen-derived peptide.
XX
KW Fibrinogen; cell adhesion; inhibitor; human; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN EPI036798-A1.
XX
PD 20-SEP-2000.
XX
PF 16-MAR-2000; 2000EP-00105572.
XX
PR 16-MAR-1999; 99JP-00070127.
XX
PA (HISM) HISAMITSU PHARM CO LTD.
XX
PI Akiyama K, Goto T, Fukai F, Ueki M;
XX
DR WPI; 2000-588967/56.
XX
PT Novel peptides having cell adhesion inhibiting properties are useful for
PT treating cancer metastasis, inflammation and fibrosis.
XX
PS Example 4; Page 8; 25pp; English.
XX
CC The present sequence represents a peptide derived from amino acid
CC residues 1567-1581 of human fibronectin, but having the residue
CC equivalent to Thr-1575 substituted by alanine. Unlike other, claimed
CC fibrinogen-derived peptides of the invention (see AAB19566-71), the
CC present does not have cell adhesion inhibitory activity. The claimed
CC peptides are useful as antimetastatic agents
SQ Sequence 15 AA;
OY
Query Match 47.1%; Score 40; DB 3; Length 15;
Best Local Similarity 75.0%; Pred. No. 8.1;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 GLEPGIDY 14
 ||:|:|
 DB 1 GLKPGVDY 8

RESULT 9
 AAB19569
 ID AAB19569 standard; peptide; 15 AA.
 XX
 AC AAB19569;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Fibrinogen-derived peptide with anti-cell adhesion activity.
 XX
 KM Cell adhesion; inhibitor; antimetastatic; metastasis; cancer; antitumour;
 KM antiinflammatory; antirheumatic; antiallergic;
 KM antifibrotic; antifibrotic; immunostimulant; vulnery; therapy;
 KM fibronectin; human; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN EPI036798-A1.
 XX
 PD 20-SEP-2000.
 XX
 PF 16-MAR-2000; 2000EP-00105572.
 XX
 PR 16-MAR-1999; 99JP-00070127.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Akiyama K, Goto T, Fukai F, Ueki M;
 XX
 DR WPI; 2000-588967/56.
 XX
 PT Novel peptides having cell adhesion inhibiting properties are useful for
 PT treating cancer metastasis, inflammation and fibrosis.
 XX
 PS Claim 3; Page 8; 25pp; English.
 XX
 CC The present sequence represents a peptide derived from amino acid
 CC residues 1567-1581 of human fibronectin, but having the residue
 CC equivalent to Val-1578 substituted by alanine. Native and Ala-substituted
 CC fibrinogen-derived peptides of the invention (see AAB19566-71) are
 CC physiologically active, possessing cell adhesion inhibitory activity
 CC against human chronic myelocytic leukaemia K562 cells, human histiocytic
 CC lymphoma U937 cells and the Ramos cell line derived from human Burkitt's
 CC lymphoma, but not against human melanoma A375SM or fibrosarcoma HT1080
 CC cells. The peptides are used as antimetastatic agents that inhibit
 CC metastasis of cancers based on cell adhesion. They are also useful for
 CC investigating and treating diseases in which adhesion between cells or
 CC between cells and extracellular matrices are implicated, such as cancer,
 CC rheumatism, asthma, allergy, thrombosis, organ transplant rejection,
 CC wound healing such as fibrosis, inflammation, immuno-inflammatory
 CC conditions including enteritis such as ulcerative colitis, and autoimmune
 CC diseases. The peptides are prepared by chemical synthesis and are
 CC modified with biotin
 XX
 SQ Sequence 15 AA;

Query Match 47.1%; Score 40; DB 3; Length 15;
 Best Local Similarity 75.0%; Pred. No. 8.1;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 GLEPGIDY 14
 ||:|:|
 DB 1 GLKPGVDY 8

RESULT 10
 AAB19574
 ID AAB19574 standard; peptide; 15 AA.
 XX
 AC AAB19574;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Fibrinogen-derived peptide.
 XX
 KM Fibrinogen; cell adhesion; inhibitor; human; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN EPI036798-A1.
 XX
 PD 20-SEP-2000.
 XX
 PF 16-MAR-2000; 2000EP-00105572.
 XX
 PR 16-MAR-1999; 99JP-00070127.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Akiyama K, Goto T, Fukai F, Ueki M;
 XX
 DR WPI; 2000-588967/56.
 XX
 PT Novel peptides having cell adhesion inhibiting properties are useful for
 PT treating cancer metastasis, inflammation and fibrosis.
 XX
 PS Example 4; Page 8; 25pp; English.
 XX
 CC The present sequence represents a peptide derived from amino acid
 CC residues 1567-1581 of human fibronectin, but having the residue
 CC equivalent to Ile-1576 substituted by alanine. Unlike other, claimed
 CC fibrinogen-derived peptides of the invention (see AAB19566-71), the
 CC present does not have cell adhesion inhibitory activity. The claimed
 CC peptides are useful as antimetastatic agents
 XX
 SQ Sequence 15 AA;

Query Match 47.1%; Score 40; DB 3; Length 15;
 Best Local Similarity 75.0%; Pred. No. 8.1;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 GLEPGIDY 14
 ||:|:|
 DB 1 GLKPGVDY 8

RESULT 11
 AAB19575
 ID AAB19575 standard; peptide; 15 AA.
 XX
 AC AAB19575;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Fibrinogen-derived peptide.
 XX
 KM Fibrinogen; cell adhesion; inhibitor; human; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN EPI036798-A1.
 XX
 PD 20-SEP-2000.
 XX
 PF 16-MAR-2000; 2000EP-00105572.
 XX

PR 16-MAR-1999; 99JP-00070127.
XX (HISM) HISAMITSU PHARM CO LTD.
XX
PI Akiyama K, Goto T, Fukai F, Ueki M;
XX WPI: 2000-588967/56.
XX
XX Novel peptides having cell adhesion inhibiting properties are useful for
PT treating cancer metastasis, inflammation and fibrosis.
XX
XX Example 4; Page 8; 25pp; English.
XX
XX The present sequence represents a peptide derived from amino acid
CC residues 1567-1581 of human fibronectin, but having the residue
CC equivalent to Thr-1577 substituted by alanine. Unlike other, claimed
CC fibrinogen-derived peptides of the invention (see AAB19566-71), the
CC present does not have cell adhesion inhibitory activity. The claimed
CC peptides are useful as antimetastatic agents
XX
SQ Sequence 15 AA;

Query Match 47.1%; Score 40; DB 3; Length 15;
Best Local Similarity 75.0%; Pred. No. 8.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 GLEPGITV 14
DB 1 GLKPGVDY 8

RESULT 12
AA13276
ID AA13276 standard; peptide; 15 AA.
XX
XX AA13276;
XX
XX 21-JUN-1999 (first entry)
XX
XX Naturally occurring variant of the glutenin epitope Y13221.
XX
XX Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; vaccine;
XX gluten tolerance; gluten-sensitivity; celiac disease; CD; celiac sprue;
XX tropical sprue; childhood food allergy; dermatitis herpetiformis; DH.
XX
XX Synthetic.
XX
XX EP90518-A1.
XX
XX 31-MAR-1999.
XX
XX 23-SEP-1997; 97EP-00202909.
XX
XX 23-SEP-1997; 97EP-00202909.
XX
XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
XX (UYLE-) RIJDSUNIV LEIDEN.
XX
XX Konig F, Van De Wal Y, Drijfhout JW, Kooy-Winkelaar EMC;
XX WPI: 1998-19792/17.
XX
XX New anticeliac peptides of gluten and methods for isolating them, useful
PT as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac
PT disease (CD).
XX
XX Disclosure; Page 28; 58pp; English.
XX
XX Peptides AA13220-13343 represents gluten derived peptides, and their
CC variants. The specification describes a method to find and characterize
CC peptides that are recognized by an intestinal derived gluten-sensitive
CC T-cells. The method comprises establishing and contacting at least one
CC gluten-sensitive T-cell clone with a mixture of gluten-derived peptides,

CC and fractionating the mixture to select peptides that stimulate the
CC clonal cells from bioactive fractions. Peptides AA13220 (gliadin derived
CC peptide) and AA13221 (glutenin derived peptide) were identified using
CC these methods, and can be used in pharmaceutical/medicines (vaccines)
CC for inducing tolerance to gluten, or to treat gluten-sensitivity, i.e.
CC celiac disease (CD) or celiac sprue, tropical sprue, childhood food
CC allergies and dermatitis herpetiformis (DH). The peptides are also useful
CC for elimination of a group of gluten-sensitive T-cells, and for
CC generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by
CC immunization of a mammal with the peptide
XX
SQ Sequence 15 AA;

Query Match 43.5%; Score 37; DB 2; Length 15;
Best Local Similarity 54.5%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYVTWGLEPG 11
DB 4 GYPTSPDQPG 14

RESULT 13
ABR75726
ID ABR75726 standard; peptide; 11 AA.
XX
XX ABR75726;
XX
XX 28-AUG-2003 (first entry)
XX
XX Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:5.
XX Biomarker; liver response; liver response-associated protein isoform;
XX LRPI; liver response-associated feature; LRF.
XX
XX Synthetic.
XX
XX WO2003038444-A2.
XX
XX 08-MAY-2003.
XX
XX 31-OCT-2002; 2002WC-US034847.
XX
XX 31-OCT-2001; 2001US-0335964P.
XX
XX (PF12-) PFIZER PROD INC.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Amacher DE, Pasulo LM, Herath HMC, Holt GD, Stieger TR;
XX WPI: 2003-430566/40.
XX
XX Screening, diagnosing, staging or identifying subject at risk of
PT developing, liver response, or monitoring effect of therapy on liver
PT response, by detecting Liver Response-Associated Protein Isoforms in
PT subject sample.
XX
XX Claim 1; Page 84; 256pp; English.
XX
XX The present invention describes a method (M1) for screening or diagnosing
CC a liver response in a subject, determining the stage or severity of a
CC liver response in a subject, identifying a subject at risk of developing
CC liver response, or monitoring the effect of therapy administered to a
CC subject having liver response, involving detecting liver response
CC associated protein isoforms (LRPIs) (see the peptides given in ABR75395
CC to ABR75806) in a test biological sample from the subject. Alternatively,
CC screening or diagnosing a liver response in a subject, or monitoring the
CC effect of a drug or therapy administered to a subject, involves
CC contacting at least one oligonucleotide probe comprising 10 or more
CC consecutive nucleotides complementary to a nucleotide sequence encoding
CC an LRPI with RNA obtained from a biological sample from the subject or
CC with cDNA copied from the RNA, where the contacting occurs under
CC conditions that permit hybridisation of the probe to the nucleotide

Blank

OM protein - protein search, using sw model

Run on: September 21, 2004, 06:42:10 / Search time 70.6667 Seconds
(without alignments)
68.165 Million cell updates/sec

Title: US-10-676-049-2
Perfect score: 85
Sequence: 1 GYTVTGLEPGIDVD 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1342398 seqs, 321133274 residues

Total number of hits satisfying chosen parameters: 221706

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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2: /cgnt_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
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13: /cgnt_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
14: /cgnt_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
15: /cgnt_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
16: /cgnt_6/prodata/2/pubppa/US10_NEW_PUB.pep:*
17: /cgnt_6/prodata/2/pubppa/US60_NEW_PUB.pep:*
18: /cgnt_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	9	US-09-942-117-2
2	72	84.7	15	10	US-09-300-425B-23
3	72	84.7	15	14	US-10-321-558-2
4	56	65.9	15	9	US-09-942-117-3
5	56	65.9	15	9	US-09-942-117-18
6	34	40.0	13	9	US-10-285-394-5
7	34	40.0	13	9	US-09-813-333-17
8	34	40.0	13	12	US-10-239-103-17
9	34	40.0	13	13	US-10-044-703-17
10	33	38.8	15	10	US-09-880-748-2782
11	33	38.8	15	12	US-10-293-418-2782
12	32.5	38.2	12	14	US-10-071-962-17
13	31	36.5	10	10	US-09-573-822C-163
14	31	36.5	10	10	US-09-573-822C-164
15	31	36.5	10	10	US-09-573-822C-761

16	31	36.5	10	10	US-09-573-822C-762	Sequence 762, App
17	31	36.5	15	10	US-09-880-748-2905	Sequence 2906, Ap
18	31	36.5	15	12	US-10-293-418-2906	Sequence 1206, Ap
19	31	36.5	15	14	US-10-001-938-11	Sequence 11, Appl
20	30	35.3	12	10	US-09-929-266-13	Sequence 13, Appl
21	30	35.3	15	14	US-10-079-167-83	Sequence 83, Appl
22	30	35.3	15	15	US-10-345-000-5	Sequence 5, Appl
23	29.5	34.7	13	16	US-10-663-244-53	Sequence 53, Appl
24	29.5	34.7	13	16	US-10-663-244-101	Sequence 101, App
25	29.5	34.7	15	10	US-09-880-748-2886	Sequence 2886, Ap
26	29.5	34.7	15	12	US-10-293-418-2886	Sequence 2886, Ap
27	29	34.1	10	10	US-09-977-406A-3	Sequence 3, Appl
28	29	34.1	10	14	US-10-291-360-3	Sequence 3, Appl
29	29	34.1	12	14	US-10-165-815-87	Sequence 87, Appl
30	29	34.1	13	14	US-10-086-156-34	Sequence 34, Appl
31	29	34.1	15	9	US-09-942-117-19	Sequence 19, Appl
32	29	34.1	15	9	US-09-942-117-19	Sequence 19, Appl
33	29	34.1	15	10	US-09-880-748-2958	Sequence 2958, Ap
34	29	34.1	15	12	US-10-293-418-2958	Sequence 2958, Ap
35	28	32.9	9	9	US-09-780-053-440	Sequence 440, App
36	28	32.9	10	9	US-09-780-053-110	Sequence 110, App
37	28	32.9	10	9	US-09-780-053-308	Sequence 308, App
38	28	32.9	10	16	US-10-766-283-4	Sequence 4, Appl
39	28	32.9	15	10	US-09-880-748-2164	Sequence 2164, Ap
40	28	32.9	15	10	US-09-880-748-2883	Sequence 2883, Ap
41	28	32.9	15	12	US-10-293-418-2164	Sequence 2164, Ap
42	28	32.9	15	12	US-10-293-418-2883	Sequence 2883, Ap
43	27.5	32.4	10	14	US-10-228-806-50	Sequence 50, Appl
44	27.5	32.4	10	14	US-10-228-806-51	Sequence 51, Appl
45	27.5	32.4	10	15	US-10-100-303A-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-942-117-2
Sequence 2, Application US/09942117
Publication No. US20020197700A1
GENERAL INFORMATION:
APPLICANT: MENRAD, ANDREAS
APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPPLITZ, MARCUS
APPLICANT: EGNER, URSULA
APPLICANT: BARR, INKE
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
FILE REFERENCE: SCH-1832
CURRENT APPLICATION NUMBER: US/09/942,117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-2

Query Match 100.0%; Score 85; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Indels 0; Gaps 0;
CY 1 GYTVTGLEPGIDVD 15
DB 1 GYTVTGLEPGIDVD 15

RESULT 2

US-09-300-425B-23
; Sequence 23, Application US/09300425B
; Publication No. US20030045681A1
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TARLI, Lorenzo
; APPLICANT: VITI, Francesca
; APPLICANT: BIRCHER, Manfred
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
; TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: SCH-17391
; CURRENT APPLICATION NUMBER: US/09/300,425B
; CURRENT FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/075,338
; PRIOR FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: peptide formula
US-09-300-425B-23

Query Match 84.7%; Score 72; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YTVGLEPGIDYD 15
Db 1 YTVGLEPGIDYD 13

RESULT 3

US-10-321-558-2
; Sequence 2, Application US/10321558
; Publication No. US2003017663A1
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TARLI, Lorenzo
; APPLICANT: VITI, Francesca
; APPLICANT: BIRCHER, Manfred
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
; FILE REFERENCE: NOTAR-1 C1
; CURRENT APPLICATION NUMBER: US/10/321,558
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 09/512,082
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 09/300,425
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/075,338
; PRIOR FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-321-558-2

Query Match 84.7%; Score 72; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YTVGLEPGIDYD 15
Db 1 YTVGLEPGIDYD 13

RESULT 4

US-09-942-117-3
; Sequence 3, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942,117
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-942-117-3

Query Match 65.9%; Score 56; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TGLEPGIDYD 15
Db 1 TGLEPGIDYD 10

RESULT 5

US-09-942-117-18
; Sequence 18, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942,117
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-942-117-18

Query Match 65.9%; Score 56; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTGTGLEP 10
DB 6 GYVTGTGLEP 15

RESULT 6
US-10-285-394-5
; Sequence 5, Application US/10285394
; Publication No. US20030228583A1
; GENERAL INFORMATION:
; APPLICANT: AMACHER, DAVID E.
; APPLICANT: PASULO, LISA M.
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
; APPLICANT: HOLT, GORDON DUANE
; APPLICANT: STIGER, THOMAS R.
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
; FILE REFERENCE: POA-003.01
; CURRENT APPLICATION NUMBER: US/10/285,394
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,964
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-394-5

Query Match 40.0%; Score 34; DB 15; Length 11;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 EPGIDY 14
DB 3 EPGVDY 8

RESULT 7
US-09-813-333-17
; Sequence 17, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-17

Query Match 40.0%; Score 34; DB 9; Length 13;
Best Local Similarity 41.7%; Pred. No. 82;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YVTGTGLEPGID 13
DB 2 HYKITGTATGVD 13

RESULT 8
US-10-239-103-17
; Sequence 17, Application US/10239103
; Publication No. US20040057961A1
; GENERAL INFORMATION:
; APPLICANT: Brown University Research Foundation

; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004-061
; CURRENT APPLICATION NUMBER: US/10/239,103
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 09/813,333
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-17

Query Match 40.0%; Score 34; DB 12; Length 13;
Best Local Similarity 41.7%; Pred. No. 82;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YVTGTGLEPGID 13
DB 2 HYKITGTATGVD 13

RESULT 9
US-10-044-703-17
; Sequence 17, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-17

Query Match 40.0%; Score 34; DB 13; Length 13;
Best Local Similarity 41.7%; Pred. No. 82;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YVTGTGLEPGID 13
DB 2 HYKITGTATGVD 13

RESULT 10
US-09-880-748-2782
; Sequence 2782, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2782
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2782

Query Match 38.8%; Score 33; DB 10; Length 15;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 YVTVTGLEPGIDY 14
|:|:|:|:|:
Db 3 YDILTGYGQVDY 15

RESULT 11
US-10-293-418-2782
Sequence 2782, Application US/10293418
Publication No. US2003022396A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2782
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2782

Query Match 38.8%; Score 33; DB 12; Length 15;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 YVTVTGLEPGIDY 14
|:|:|:|:|:
Db 3 YDILTGYGQVDY 15

RESULT 12
US-10-071-962-17
Sequence 17, Application US/10071962
Publication No. US20030170237A1
GENERAL INFORMATION:
APPLICANT: Bauli N.C. Sun
APPLICANT: Ceally R.Y. Sun
TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and
FILE REFERENCE: 98-3
CURRENT APPLICATION NUMBER: US/10/071,962

CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/303,155A
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,575
PRIOR FILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 12
TYPE: PRT
ORGANISM: mouse
US-10-071-962-17

Query Match 38.2%; Score 32.5; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 GYVTVTGLEPGIDY 14
|:|:|:|:|:
Db 2 GFY---GGHPPGFDY 12

RESULT 13
US-09-573-822C-163
Sequence 163, Application US/09573822C
Publication No. US20030199011A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
FILE REFERENCE: Microbe patent
CURRENT APPLICATION NUMBER: US/09/573,822C
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 804
SOFTWARE: ProPatent version 1.0
SEQ ID NO 163
LENGTH: 10
TYPE: PRT
ORGANISM: mycoplasma genitalium
FEATURES:
OTHER INFORMATION: Sequence located in MG271 at 243-252 and may interact with Sequen
US-09-573-822C-163

Query Match 36.5%; Score 31; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YVTVTGLE 9
|:|:|:|:|:
Db 2 FYTVNGVE 9

RESULT 14
US-09-573-822C-164
Sequence 164, Application US/09573822C
Publication No. US20030199011A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
FILE REFERENCE: Microbe patent
CURRENT APPLICATION NUMBER: US/09/573,822C
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 804
SOFTWARE: ProPatent version 1.0
SEQ ID NO 164
LENGTH: 10
TYPE: PRT
ORGANISM: mycoplasma genitalium
FEATURES:
OTHER INFORMATION: Sequence located in MG271 at 243-252 and may interact with Sequen
US-09-573-822C-164

Query Match 36.5%; Score 31; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YYYTGTG 9
:|||||:
Db 2 FYTVNGVE 9

RESULT 15

US-09-573-822C-761
; Sequence 761, Application US/09573822C
; Publication No. US2003019901A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 761
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG271 at 243-252 and may interact with Sequen
; OTHER INFORMATION: this patent.
US-09-573-822C-761

Query Match 36.5%; Score 31; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YYYTGTG 9
:|||||:
Db 2 FYTVNGVE 9

Search completed: September 21, 2004, 07:03:18
Job time : 71.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53 ; Search time 7.5 seconds
(without alignments)
192.383 Million cell updates/sec

Title: US-10-676-049-1
Perfect score: 79
Sequence: 1 VDIITDSSIGLRWTP 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 78: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	79	100.0	90	2	146162	fibronectin ED-B -
2	79	100.0	147	2	S00848	fibronectin, trans
3	79	100.0	1020	2	A29385	fibronectin - chic
4	79	100.0	2477	2	S14428	fibronectin precur
5	64	81.0	2481	2	A43908	fibronectin - Afri
6	58	73.4	3124	2	A40020	collagen alpha 1(X
7	47	59.5	273	2	A28512	fibronectin - chic
8	47	59.5	929	2	TS1027	type XII collagen
9	47	59.5	4135	2	T42629	type XII collagen
10	46	58.2	2265	1	FNEU	tenascin-X - bovin
11	46	58.2	2386	1	FNEU	fibronectin - bovin
12	46	58.2	3566	1	A40701	fibronectin precur
13	45	57.0	26926	1	I38344	tenascin-X precursor
14	44	55.7	357	2	T00764	titin, cardiac muscle
15	44	55.7	554	1	FOHUMP	hypochelical proteol
16	44	55.7	621	2	B57431	macrophage colony-
17	44	55.7	1274	2	S55050	myosin-binding C-pe
18	44	55.7	4006	2	T09070	cardiac myosin-binding
19	43.5	55.1	392	2	B91101	probable tenascin
20	43.5	55.1	392	2	F85946	2-oxoacetyl-1,6-met
21	43	54.4	320	2	S74773	hypochelical prote
22	43	54.4	529	2	T46130	GDP-D-mannose dehyd
23	43	54.4	1118	1	A49724	RNA polymerase III
24	43	54.4	1241	2	T37190	protein-tyrosine-ph
25	42.5	53.8	261	2	S64595	nephrit - human
26	42	53.2	369	1	A23595	probable membrane
27	42	53.2	1142	2	S36845	dihydroorotate oxid
28	42	53.2	1810	1	A32230	myosin-binding pro
29	41	51.9	199	2	UC5718	tenascin precursor
						superoxide dismutase

30	41	51.9	268	2	F64101	proliporotein dia
31	41	51.9	287	2	H70923	probable hg transp
32	41	51.9	349	2	A83094	conserved hypothet
33	41	51.9	349	2	H98192	hypothetical prote
34	41	51.9	366	2	C83789	hypothetical prote
35	41	51.9	405	2	F96505	probable nucleolin
36	41	51.9	754	2	B86592	general secretion
37	41	51.9	754	2	D72032	general secretion
38	41	51.9	1123	2	S36845	myosin-binding pro
39	41	51.9	1138	2	S24614	myosin-binding pro
40	41	51.9	1557	2	D41214	protein-tyrosine-p
41	41	51.9	1630	2	C41214	protein-tyrosine-p
42	41	51.9	1742	2	S24600	proectin - fruit
43	41	51.9	1825	2	C88400	protein H19M22.1 l
44	41	51.9	1825	2	T32828	hypothetical prote
45	41	51.9	6658	2	T13931	proectin - fruit

ALIGNMENTS

RESULT 1

146162
fibronectin ED-B - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
C:Accession: I46162
R:Zhang, D.W.; Burron-Wuester, N.; Lust, G.
J. Biol. Chem. 270, 1817-1822, 1995
A>Title: Alternative splicing of ED-A and ED-B sequences of fibronectin pre-mRNA differ
A:Reference number: 146161; MUID:9513063; PMID:782518
A:Accession: I46162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-90 <ZHA>
A:Cross-references: EMBL:U16208; NID:9562168; PIDN:AA67749.1; PID:9562169
C:Superfamily: fibronectin, fibronectin type I repeat homology; fibronectin type II rep

Query Match 100.0%; Score 79; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDIITDSSIGLRWTP 15
DB 10 VDIITDSSIGLRWTP 24

RESULT 2
fibronectin, transformation-associated splice form - human (fragment)

S00848
N:Alternate names: fibronectin ED-B
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jul-2000
C:Accession: S00848; I59102; A28347
R:Paolletta, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
A>Title: Sequence analysis and in vivo expression show that alternative splicing of ED-
A:Reference number: S00848; MUID:88233940; PMID:3375063
A:Accession: S00848
A:Molecule type: DNA
A:Residues: 1-147 <PAO>
A:Cross-references: EMBL:X07117; NID:931406; PIDN:CAB52437.1; PID:95725425
R:Gutman, A.; Kornblith, A.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7179-7182, 1987
A>Title: Identification of a third region of cell-specific alternative splicing in huma
A:Reference number: I59102; MUID:88041070; PMID:3478690
A:Accession: I59102
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 26-134 <GUT>
A:Cross-references: GB:M8179; NID:9182693; PIDN:AA52461.1; PID:9182695
R:Zardi, L.; Canemolla, B.; Siri, A.; Petersen, T.E.; Paolletta, G.; Sebastio, G.; Bara
EMBO J. 6, 2337-2342, 1987

A>Title: Transformed human cells produce a new fibronectin isoform by preferential altered
 A/Reference number: A28347; MUID:88029324; PMID:2822387
 A/Accession: A28347
 A/Molecule type: Protein
 A/Residues: 3-146 <ZAR>
 C/Genetics:
 A/Gene: GDB:FNI
 A/Cross-references: GDB:119135; OMIM:135600
 A/Map position: 2q34-2q34
 A/Introns: 35/1; 126/1
 C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat
 C/Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter
 F/33-112/Region: transformation-associated insert
 F/35-118/Domain: fibronectin type III repeat homology <3PR>

Query Match 100.0%; Score 79; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDIRSSIGLRWPL 15
 Db 45 VDIRSSIGLRWPL 59

RESULT 3
 A29355
 fibronectin - chicken (fragment)
 C/Species: Gallus gallus (chicken)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 12-Feb-1999
 C/Accession: A29355
 R/Norton, P.A.; Hynes, R.O.
 Mol. Cell. Biol. 7, 4297-4307, 1987
 A>Title: Alternative splicing of chicken fibronectin in embryos and in normal and transf
 A/Reference number: A29355; MUID:88142820; PMID:2830487
 A/Accession: A29355
 A/Molecule type: mRNA
 A/Residues: 1-1020 <NOR>
 C/Genetics:
 A/Introns: 176/3
 C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
 C/Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter
 F/1-86/Domain: fibronectin type III repeat homology <FN3>
 F/92-177/Domain: fibronectin type III repeat homology <FN3>
 F/180-262/Region: cell attachment (R-G-D) motif
 F/257-259/Region: cell attachment (R-G-D) motif
 F/274-356/Domain: fibronectin type III repeat homology <FN3K>
 F/364-446/Domain: fibronectin type III repeat homology <FN3L>
 F/454-536/Domain: fibronectin type III repeat homology <FN3M>
 F/546-628/Domain: fibronectin type III repeat homology <FN3N>
 F/636-718/Domain: fibronectin type III repeat homology <FN3O>
 F/837-917/Domain: fibronectin type III repeat homology <FN3P>
 F/940-979/Domain: fibronectin type I repeat homology <1F10>
 F/940-969,967-979,985-1012/Dissulfide bonds: #status predicted

Query Match 100.0%; Score 79; DB 2; Length 1020;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDIRSSIGLRWPL 15
 Db 104 VDIRSSIGLRWPL 118

RESULT 4
 S14428

fibronectin precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Aug-1999
 C/Accession: S14428; S12455; R22319; S46203; S00459; A27252; I59049
 R/Hynes, R.O.
 submitted to the EMBL Data Library, July 1989
 A/Reference number: S14428
 A/Accession: S14428

A/Molecule type: mRNA
 A/Residues: 1-2477 <HYN>
 A/Cross-references: EMBL:X15906; NID:956163; PIDN:CAA34020.1; PID:956164
 R/Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
 EMBO J. 6, 2573-2580, 1987
 A>Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
 A/Reference number: S12455; MUID:88054951; PMID:2445560
 A/Accession: S12455
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 609-1810, 'T', 1812-2283 <SCH>
 A/Cross-references: EMBL:X15906
 R/Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
 A>Title: A single rat fibronectin gene generates three different mRNAs by alternative sp
 A/Reference number: A2319; MUID:84298097; PMID:6089177
 A/Accession: A2319
 A/Molecule type: DNA
 A/Residues: 2052-2237 <TAM>
 R/Falkenberg, C.; Englund, J.J.; Thøgersen, I.B.; Salvesen, G.; Akertroem, B.
 Biochem. J. 301, 745-751, 1994
 A>Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in
 A/Reference number: S46203; MUID:94330948; PMID:7519849
 A/Accession: S46203
 A/Status: preliminary
 A/Molecule type: Protein
 A/Residues: 1183-1192, 'GLN', 1268, 'P', 1270-1271, 'D', 1273, 'CF', 1276, 'PY', 1385-1399 <FAL>
 R/Patel, R.S.; Odermatt, E.; Schwarzbauer, J.E.; Hynes, R.O.
 EMBO J. 6, 2565-2572, 1987
 A>Title: Organization of the fibronectin gene provides evidence for exon shuffling during
 A/Reference number: S00459; MUID:88054950; PMID:3119323
 A/Accession: S00459
 A/Molecule type: DNA
 A/Residues: 1-139; 2382-2477 <PAT>
 A/Cross-references: EMBL:X05831
 A/Note: the authors translated the codon CCG for residues 51 and 94 as Ala
 R/Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
 Cell 35, 421-431, 1983
 A>Title: Three different fibronectin mRNAs arise by alternative splicing within the codi
 A/Reference number: A27252; MUID:84082067; PMID:6317187
 A/Accession: A27252
 A/Molecule type: mRNA
 A/Residues: 1586-1720, 'T', 1722, 1813-2477 <SC2>
 R/Odermatt, E.; Tamkun, J.W.; Hynes, R.O.
 Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
 A>Title: Repeating modular structure of the fibronectin gene: Relationship to protein st
 A/Reference number: I59049; MUID:86016741; PMID:3863113
 A/Accession: I59049
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1722-1810 <RBS>
 A/Cross-references: GB:M1750; NID:G204164; PIDN:AAA41170.1; PID:9554437
 C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
 C/Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; dupli
 F/1-33/Domain: signal sequence #status predicted <SIG>
 F/11-33/Domain: signal sequence #status predicted <SIG>
 F/53-447/Product: fibronectin #status predicted <NAT>
 F/533-88/Domain: fibronectin type I repeat homology <1F1>
 F/598-136/Domain: fibronectin type I repeat homology <1F2>
 F/142-180/Domain: fibronectin type I repeat homology <1F3>
 F/187-226/Domain: fibronectin type I repeat homology <1F4>
 F/232-271/Domain: fibronectin type I repeat homology <1F5>
 F/308-342/Domain: fibronectin type I repeat homology <1F6>
 F/360-401/Domain: fibronectin type II repeat homology <2F1>
 F/420-461/Domain: fibronectin type II repeat homology <2F2>
 F/470-508/Domain: fibronectin type I repeat homology <1F7>
 F/518-555/Domain: fibronectin type I repeat homology <1F8>
 F/561-599/Domain: fibronectin type I repeat homology <1F9>
 F/609-697/Domain: fibronectin type III repeat homology <FN3A>
 F/718-800/Domain: fibronectin type III repeat homology <FN3B>
 F/809-890/Domain: fibronectin type III repeat homology <FN3C>
 F/905-987/Domain: fibronectin type III repeat homology <FN3D>

F,1995-1076/Domain: fibronectin type III repeat homology <FN3>
 F,1085-1164/Domain: fibronectin type III repeat homology <FN3F>
 F,1172-1257/Domain: fibronectin type III repeat homology <FN3G>
 F,1125-1348/Domain: fibronectin type III repeat homology <FN3H>
 F,1336-1439/Domain: fibronectin type III repeat homology <FN3I>
 F,1447-1529/Domain: fibronectin type III repeat homology <FN3J>
 F,1537-1619/Domain: fibronectin type III repeat homology <FN3K>
 F,1614-1616/Region: cell attachment (R-G-D) motif
 F,1631-1713/Domain: fibronectin type III repeat homology <FN3L>
 F,1721-1803/Domain: fibronectin type III repeat homology <FN3M>
 F,1811-1893/Domain: fibronectin type III repeat homology <FN3N>
 F,1903-1984/Domain: fibronectin type III repeat homology <FN3O>
 F,1992-2074/Domain: fibronectin type III repeat homology <FN3P>
 F,2181-2183/Region: cell attachment (R-G-D) motif
 F,2193-2273/Domain: fibronectin type III repeat homology <FN3Q>
 F,2286-2335/Domain: fibronectin type I repeat homology <F10>
 F,2341-2378/Domain: fibronectin type I repeat homology <F11>
 F,2385-2420/Domain: fibronectin type I repeat homology <F12>
 F,53-79,77-88,98-126,124-136,142-170,168-180,187-216,214-226,232-261,259-271,308-335,333
 368,2366-2378,2385-2411,2409-2420/Disulfide bonds: #status predicted
 F,2458/Disulfide bonds: interchain (to 2462) #status predicted
 F,2462/Disulfide bonds: interchain (to 2458) #status predicted

Query Match 100.0%; Score 79; DB 2; Length 2477;
 Best Local Similarity 100.0%; Pred. No. 7,6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VDIRSIGRWPPL 15
 Db 1275 VDIRSIGRWPPL 1289

RESULT 5
 A,3908
 C,Species: Xenopus laevis (African clawed frog)
 C,Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 12-Feb-1999
 C,Accession: A43908
 Dev. Biol. 149, 357-369, 1992
 A,Title: Identification and characterization of alternatively spliced fibronectin mRNAs
 A,Reference number: A43908; MUID:211194; PMID:1703030
 A,Accession: A43908
 A,Status: nucleic acid sequence not shown; not compared with conceptual translation
 A,Molecule type: mRNA
 A,Residues: 1-2481 <DES>
 A,Note: sequence extracted from NCBI backbone (NCBIP:77473)
 C,Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat homology; duplication; extracellular matrix; glycoprotein; heterodimer
 F,55-90/Domain: fibronectin type I repeat homology <F1>
 F,100-138/Domain: fibronectin type I repeat homology <F2>
 F,144-182/Domain: fibronectin type I repeat homology <F3>
 F,189-228/Domain: fibronectin type I repeat homology <F4>
 F,234-273/Domain: fibronectin type I repeat homology <F5>
 F,309-343/Domain: fibronectin type I repeat homology <F6>
 F,351-402/Domain: fibronectin type II repeat homology <F7>
 F,421-462/Domain: fibronectin type II repeat homology <F8>
 F,471-509/Domain: fibronectin type I repeat homology <F9>
 F,519-556/Domain: fibronectin type I repeat homology <F10>
 F,562-600/Domain: fibronectin type I repeat homology <F11>
 F,610-693/Domain: fibronectin type III repeat homology <F12>
 F,719-801/Domain: fibronectin type III repeat homology <F13>
 F,810-891/Domain: fibronectin type III repeat homology <F14>
 F,906-988/Domain: fibronectin type III repeat homology <F15>
 F,996-1077/Domain: fibronectin type III repeat homology <F16>
 F,1086-1165/Domain: fibronectin type III repeat homology <F17>
 F,1173-1258/Domain: fibronectin type III repeat homology <F18>
 F,1266-1349/Domain: fibronectin type III repeat homology <F19>
 F,1357-1440/Domain: fibronectin type III repeat homology <F20>
 F,1448-1530/Domain: fibronectin type III repeat homology <F21>
 F,1538-1620/Domain: fibronectin type III repeat homology <F22>
 F,1615-1617/Region: cell attachment (R-G-D) motif

F,1632-1714/Domain: fibronectin type III repeat homology <FN3L>
 F,1722-1804/Domain: fibronectin type III repeat homology <FN3M>
 F,1812-1894/Domain: fibronectin type III repeat homology <FN3N>
 F,1904-1985/Domain: fibronectin type III repeat homology <FN3O>
 F,1993-2075/Domain: fibronectin type III repeat homology <FN3P>
 F,2197-2277/Domain: fibronectin type III repeat homology <FN3Q>
 F,2301-2340/Domain: fibronectin type I repeat homology <F10>
 F,2346-2383/Domain: fibronectin type I repeat homology <F11>
 F,2390-2455/Domain: fibronectin type I repeat homology <F12>
 F,55-81,79-90,100-128,126-138,144-172,170-182,189-218,216-228,234-263,261-273,309-336,3
 2373,2371-2393,2390-2416,2414-2425/Disulfide bonds: #status predicted
 F,2459/Disulfide bonds: interchain (to 2463) #status predicted
 F,2463/Disulfide bonds: interchain (to 2459) #status predicted

Query Match 81.0%; Score 64; DB 2; Length 2481;
 Best Local Similarity 78.6%; Pred. No. 0.029;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

2 DITDSIGRWPPL 15
 Db 1277 DITDSIGRWPPL 1290

RESULT 6
 A,4020
 C,Alternate names: fibronectin
 C,Species: Gallus gallus (chicken)
 C,Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 15-Sep-2003
 C,Accession: A40020; A34485; B34485; A28037; S28014; S22254; S28011
 R,Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shimomura, T.; Tanaka, H.; Nishida, Y.; Oba
 J. Cell Biol. 115, 209-221, 1991
 A,Title: The complete primary structure of type XII collagen shows a chimeric molecule
 non-region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site
 A,Reference number: A40020; MUID:92011862; PMID:1918137
 A,Accession: A40020
 A,Molecule type: mRNA
 A,Residues: 1-3124 <YAM>
 A,Cross-references: GB:D00824; NID:9222810; PIDN:BA00701.1; PID:9222811
 A,Note: in the authors' translation residues 1236-1219 are shown after residue 1235 and
 R,Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
 J. Biol. Chem. 264, 19772-19778, 1989
 A,Title: Type XII collagen. A large multidomain molecule with partial homology to type
 A,Reference number: A34485; MUID:90062079; PMID:2584192
 A,Accession: A34485
 A,Molecule type: mRNA
 A,Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
 A,Cross-references: EMBL:U05137; NID:9211284; PIDN:AAA4835.1; PID:9211285
 A,Accession: B34485
 A,Molecule type: protein
 A,Residues: 2772-2792,2846-2873 <GOR2>
 R,Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
 A,Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA
 A,Reference number: A28037; MUID:87317590; PMID:3476925
 A,Accession: A28037
 A,Molecule type: mRNA
 A,Residues: 2960-2976, 'F', 2978-3074, 'AG' <GOR3>
 A,Cross-references: EMBL:M1375; NID:9211649; PIDN:AAA48718.1; PID:9211650
 A,Note: this sequence has been revised in reference A34485
 R,Koch, M.; Bernasconi, C.; Chiquet, M.
 Eur. J. Biochem. 207, 847-856, 1992
 A,Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of
 A,Reference number: S28014; MUID:92352621; PMID:1333460
 A,Accession: S28014
 A,Molecule type: protein
 A,Residues: 'X', 1333, 'O', 1335-1347, 1914-1928, 2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-2517
 R,Dublet, B.; van der Rest, M.
 J. Biol. Chem. 262, 17724-17727, 1987
 A,Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepin
 A,Reference number: S22254; MUID:88087065; PMID:3121603
 A,Accession: S22254
 A,Molecule type: protein

A:Residues: 2831-2837, 'T', 2834, 'R', 2836-2843;3002-3014 <DUB>
A:Trnab, U.; Trnab, B. 1171, 97-98, 1992
Biochim. Biophys. Acta 1171, 97-98, 1992
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Aug-1999
C:Species: Gallus gallus (chicken)
A:Title: The two splice variants of collagen XII share a common 5' end.
A:Reference number: S28811; MUID:93042014; PMID:1420368
A:Accession: S28811
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-24, 1189-1257, 'S', 1259-1263, 'E', 1265-1280 <TRU>
A:Cross-references: EMBL:X67327
C:Genetics:
A:Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
C:Keywords: alternative splicing; cell binding; cold coil; connective tissue; disulfid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-3124/Product: collagen alpha 1(XII) chain #status predicted <MAT>
F:24-1189-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted
F:24-114/Domain: IIA #status predicted <IIA>
F:24-105/Domain: fibronectin type III repeat homology <FN3A>
F:137-301/Domain: von Willebrand factor type A repeat homology <VMA1>
F:332-425/Domain: IIB #status predicted <IIB>
F:332-414/Domain: fibronectin type III repeat homology <FN3B>
F:437-601/Domain: von Willebrand factor type A repeat homology <VMA2>
F:629-1178/Domain: IIC #status predicted <IIC>
F:630-711/Domain: fibronectin type III repeat homology <FN3C>
F:721-802/Domain: fibronectin type III repeat homology <FN3D>
F:812-895/Domain: fibronectin type III repeat homology <FN3E>
F:905-986/Domain: fibronectin type III repeat homology <FN3F>
F:995-1076/Domain: fibronectin type III repeat homology <FN3G>
F:1065-1169/Domain: fibronectin type III repeat homology <FN3H>
F:1197-1361/Domain: von Willebrand factor type A repeat homology <VMA3>
F:1384-2295/Domain: IID #status predicted <IID>
F:1474-1557/Domain: fibronectin type III repeat homology <FN3I>
F:1565-1647/Domain: fibronectin type III repeat homology <FN3J>
F:1565-1738/Domain: fibronectin type III repeat homology <FN3K>
F:1766-1838/Domain: fibronectin type III repeat homology <FN3M>
F:1847-1928/Domain: fibronectin type III repeat homology <FN3N>
F:1937-2019/Domain: fibronectin type III repeat homology <FN3O>
F:2028-2110/Domain: fibronectin type III repeat homology <FN3P>
F:2119-2199/Domain: fibronectin type III repeat homology <FN3Q>
F:2207-2294/Domain: fibronectin type III repeat homology <FN3R>
F:2325-2490/Domain: von Willebrand factor type A repeat homology <VMA4>
F:2428-2440/Region: cell adhesion #status predicted
F:2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted
F:2751-2902/Domain: collagenous COL2 #status predicted <COL2>
F:2899-2901/Region: cell attachment (R-G-D) motif
F:2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F:2946-3048/Domain: collagenous COL1 #status predicted <COL1>
F:3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F:312, 1006, 1032, 1044, 1512, 1767, 2210, 2273, 2532, 2683/Binding site: carboxyproline (Asn) (cov)
F:2780, 2789, 2836, 2842, 2850, 2865, 2869, 3004, 3007/Modified site: hydroxyproline (Pro) #stat
Query Match 73.4%; Score 58; DB 2; Length 3124;
Best Local Similarity 69.2%; Pred. No. 0.39;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 DITDSTGLRWT 14
Db 916 DITDTVGLSWTP 928

RESULT 7
A28512
fibronectin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Aug-1999
C:Accession: A28512
R:Kubomura, S.; Obara, M.; Karsaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, K.
Biochim. Biophys. Acta 910, 171-181, 1987
A:Title: Genetic analysis of the cell binding domain region of the chicken fibronectin g
A:Reference number: A28512; MUID:86050950; PMID:2823895
A:Accession: A28512
A:Molecule type: DNA

A:Residues: 1-273 <RTB>
A:Cross-references: GB:X06533; NID:963393; PIDN:CAA29781.1; PID:G295716
A:Note: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C:Genetics:
A:Introns: 90/1; 129/1; 184/1; 236/1
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter
F:1-82/Domain: fibronectin type II repeat homology (fragment) <FN3I>
F:90-172/Domain: fibronectin type III repeat homology <FN3J>
F:167-169/Region: cell attachment (R-G-D) motif
F:184-266/Domain: fibronectin type III repeat homology <FN3K>
Query Match 59.5%; Score 47; DB 2; Length 273;
Best Local Similarity 53.8%; Pred. No. 2.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 DITDSTGLRWT 14
Db 195 DVQNSISIRWTP 207

RESULT 8
151027
type XII collagen alpha-1 chain - eastern newt (fragment)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 15-Sep-2003
C:Accession: 151027
R:Wei, Y.; Yang, E.V.; Klatte, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A:Title: Monoclonal antibody M2 identifies the urodele alpha 1 chain of type XII collag
A:Reference number: 151027; MUID:95246925; PMID:7729585
A:Accession: 151027
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-929 <WEI>
A:Cross-references: EMBL:U19494; NID:9632647; PIDN:AAA80217.1; PID:9632648
F:631-795/Domain: von Willebrand factor type A repeat homology <VMA3>
Query Match 59.5%; Score 47; DB 2; Length 929;
Best Local Similarity 66.7%; Pred. No. 8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DITDSTGLRWT 13
Db 350 DITDTTTSWT 361

RESULT 9
T42629
tenascin-X - bovine
N:Alternate names: flexillin
C:Species: Bos primigenius taurus (cattle)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42629
R:Eleftheriou, F.; Exposito, J.Y.; Garrone, R.; Lethias, C.
J. Biol. Chem. 272, 22866-22874, 1997
A:Title: Characterization of the bovine tenascin-X.
A:Reference number: 222180; MUID:97426436; PMID:9278449
A:Accession: T42629
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-4135 <ELE>
A:Cross-references: EMBL:Y11915; NID:G2462978; PIDN:CAA72671.1; PID:G2462979
C:Genetics:
A:Gene: TN-X
C:Superfamily: tenascin-X; BGF homology; fibrinogen beta/gamma homology; fibronectin typ
C:Keywords: extracellular matrix; glycoprotein; heparin repeat
Query Match 59.5%; Score 47; DB 2; Length 4135;
Best Local Similarity 58.3%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DITDSIGLRWT 13
Db 1616 DVTNPSVGLRWT 1627

RESULT 10

fibronectin - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 20-Oct-2000
C/Accession: A26452; B21165; F23292
R/Skorsengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.
Eur. J. Biochem. 161, 441-453, 1986

A/Title: Complete primary structure of bovine plasma fibronectin.
A/Reference number: A26452; MUID:87054047; PMID:3780752
A/Accession: A26452

A/Molecule type: protein
A/Residues: 1-2265 <SKO>
R/Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983

A/Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A/Reference number: A21165; MUID:83221567; PMID:6304699
A/Accession: B21165

A/Molecule type: mRNA
A/Residues: 2170-2265 <KOR>
A/Cross-references: GB:X00800; NID:g163055; PIDN:AAA30521.2; PID:95713323
R/Petersen, T.E.; Thogersen, H.C.; Skorsengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottrup
Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983

A/Title: Partial primary structure of bovine plasma fibronectin: three types of internal
A/Reference number: A23392; MUID:83117805; PMID:6218503
A/Accession: A23392

A/Molecule type: protein
A/Residues: 1-16, 'C', 18-20, 'S', 22-432, 447-463, 1367-1517, 1567-1673, 2062-2176, 'N', 2178-226
C/Comment: Cys-1201 and Cys-2015 have free sulphydryl groups.
C/Comment: The plasma fibronectin molecule consists of two chains, which are connected b
C/Comment: Fibronectins bind cell surfaces and various compounds including collagen, fib
aling, and maintenance of cell shape.
C/Comment: Plasma fibronectin is synthesized by hepatocytes.
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C/Keywords: acute phase; alternative splicing; collagen binding; duplication; extracellular
F/21-241/Domain: fibronectin type I repeat homology <FBR>
F/21-56/Domain: fibronectin type I repeat homology <F11>
F/66-104/Domain: fibronectin type I repeat homology <F12>
F/110-148/Domain: fibronectin type I repeat homology <F13>
F/155-194/Domain: fibronectin type I repeat homology <F14>
F/200-239/Domain: fibronectin type I repeat homology <F15>
F/277-577/Domain: collagen binding <CBR>
F/277-511/Domain: fibronectin type I repeat homology <F16>
F/339-370/Domain: fibronectin type II repeat homology <F21>
F/389-430/Domain: fibronectin type II repeat homology <F22>
F/439-477/Domain: fibronectin type I repeat homology <F17>
F/487-524/Domain: fibronectin type I repeat homology <F18>
F/530-568/Domain: fibronectin type I repeat homology <F19>
F/578-561/Domain: fibronectin type III repeat homology <F23>
F/688-770/Domain: fibronectin type III repeat homology <F24>
F/779-860/Domain: fibronectin type III repeat homology <F25>
F/875-957/Domain: fibronectin type III repeat homology <F26>
F/965-1046/Domain: fibronectin type III repeat homology <F27>
F/1055-1134/Domain: fibronectin type III repeat homology <F28>
F/1142-1221/Domain: fibronectin type III repeat homology <F29>
F/1235-1318/Domain: fibronectin type III repeat homology <F30>
F/1326-1404/Domain: fibronectin type III repeat homology <F31>
F/1410-1517/Domain: cell attachment <CAD>
F/1416-1502/Domain: fibronectin type III repeat homology <F32>
F/1493-1498/Region: cell attachment (R-G-D) motif
F/1510-1582/Domain: fibronectin type III repeat homology <F33>
F/1600-1870/Domain: heparin binding <HB2>
F/1600-1682/Domain: fibronectin type III repeat homology <F34>
F/1692-1773/Domain: fibronectin type III repeat homology <F35>
F/1781-1863/Domain: fibronectin type III repeat homology <F36>
F/1970-1972/Region: cell attachment (R-G-D) motif
F/1982-2062/Domain: fibronectin type III repeat homology <F37>
F/1985-2216/Domain: fibrin binding <FB2>

F/2085-2124/Domain: fibronectin type I repeat homology <F10>
F/2130-2167/Domain: fibronectin type I repeat homology <F11>
F/2174-2209/Domain: fibronectin type I repeat homology <F12>
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/3/Cross-Link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status experim
F/21-47, 45-56, 66-94, 92-104, 110-138, 136-148, 155-184, 182-194, 200-229, 227-239, 277-304, 302-
7, 2155-2167, 2174-2200, 2198-2209/Disulfide bonds: #status predicted
F/339, 497, 511, 846, 976, 1213, 1987/Binding site: carboxylate (Asn) (covalent) #status exp
F/1205, 1692/Binding site: carboxylate (Asn) (covalent) #status absent
F/1243, 1944/Binding site: carboxylate (Thr) (covalent) #status experimental
F/2246/Disulfide bonds: interchain (to 2250) #status predicted
F/2250/Disulfide bonds: interchain (to 2246) #status predicted
F/2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 58.2% Score 46; DB 1; Length 2265;
Best Local Similarity 53.8% Pred. No. 32;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DITDSIGLRWT 14
Db 1521 DVQDNISVRWLP 1533

RESULT 11

FNHU
fibronectin precursor [validated] - human
N/Alternate names: fibronectin splice form ED-A
C/Species: Homo sapiens (man)
C/Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text_change 06-Dec-2000
C/Accession: A26460; A26284; S03917; A24854; A24476; A20108; A93529; A21011; A90435; A2
R/Dean, D.C.; Bowls, C.L.; Bougeais, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987

A/Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A/Reference number: A26460; MUID:87175578; PMID:3031656
A/Accession: A26460

A/Molecule type: DNA
A/Residues: 1-49 <DBA>
A/Cross-references: GB:M15801; NID:g182686; PIDN:AAA53376.1; PID:9553293
R/Oldery, A.; Rucsaltili, E.
J. Biol. Chem. 261, 2113-2116, 1986

A/Title: Evolution of the fibronectin gene.
A/Reference number: A26284; MUID:86111901; PMID:3003095
A/Accession: A26284

A/Molecule type: DNA
A/Residues: 1447-1540 <OID>
A/Cross-references: GB:M12549; NID:g182688
A/Note: The authors translated the codon TTC for residue 1494 as Gln
R/Paciolla, G.; Henschliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988

A/Title: Sequence analysis and in vivo expression show that alternative splicing of ED-
A/Reference number: S00848; MUID:88233940; PMID:3375063
A/Accession: S03917

A/Molecule type: DNA
A/Residues: 1594-1767, 'V', 1769-1783 <PAO>
A/Cross-references: EMBL:X07718; NID:g31402
A/Note: The authors translated the codon AAC for residue 1631 as Asp
R/Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986

A/Title: Donor and acceptor splice signals within an exon of the human fibronectin gene
A/Reference number: A24854; MUID:87030929; PMID:3770201
A/Accession: A24854

A/Molecule type: DNA
A/Residues: 1992-2147 <VTB>
A/Cross-references: GB:X04530; NID:g31436
R/Gutman, A.; Yamada, K.M.; Kornblith, A.
FEBS Lett. 207, 145-148, 1986

A/Title: Human fibronectin is synthesized as a pre-propolypeptide.
A/Reference number: A24476; MUID:87030890; PMID:3770189
A/Accession: A24476

A/Status: not compared with conceptual translation
A/Molecule type: RNA
A/Residues: 1-14, 'Q', 16-38 <GUT>
R/Kornblith, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.

EMBO J. 4, 1755-1759, 1985
A:Title: Primary structure of human fibronectin: differential splicing may generate at l
A:Reference number: A91008; MUID:85284965; PMID:2992939
A:Accession: A91008
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 32-1344,1346-2080,2112-2386 <KOR>
A:Cross-references: GB:X02761
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5868, 1984
A:Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A:Reference number: A93529; MUID:84272255; PMID:6462919
A:Accession: A93529
A:Molecule type: mRNA
A:Residues: 973-2080,2112-2386 <KO2>
A:Cross-references: GB:X00739
R:Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A:Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a
A:Reference number: A21011; MUID:83290923; PMID:6688418
A:Accession: A21011
A:Molecule type: mRNA
A:Residues: 1434-1537 <OL2>
A:Cross-references: GB:K00055; NID:g182680; PIDN:AAA52459.1; PID:g182683
R:Bernard, M.P.; Kolbe, M.; Weill, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A:Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with re
A:Reference number: A90495; MUID:85280409; PMID:2992573
A:Accession: A90495
A:Molecule type: mRNA
A:Residues: 1594-2386 <BBR>
A:Cross-references: GB:M10905; NID:g182696; PIDN:AAA52462.1; PID:g182697
R:Umezawa, K.; Kornblith, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A:Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A:Reference number: A22245; MUID:85231203; PMID:2989004
A:Accession: A22245
A:Molecule type: mRNA
A:Residues: 1948-2067 <DME>
A:Cross-references: GB:M27589; NID:g182705; PIDN:AAA52465.1; PID:g182706
A:Accession: B22245
A:Molecule type: mRNA
A:Residues: 1975-1991,2017-2039 <DM2>
A:Cross-references: GB:M27590
R:Seikiuchi, K.; Kios, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A:Title: Human liver fibronectin complementary DNAs: identification of two different mes
A:Reference number: 152394; MUID:87026578; PMID:3021206
A:Accession: 165273
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1978-1990,2016-2018,'N',2020-2081,2113-2127 <SEK>
A:Cross-references: GB:M4060; NID:g182701; PIDN:AAA52464.1; PID:g182704
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectins
A:Reference number: A21165; MUID:83221567; PMID:6304659
A:Accession: A21165
A:Molecule type: mRNA
A:Residues: 2291-2386 <KO3>
A:Cross-references: GB:K00799; NID:g182681; PIDN:AAA52460.1; PID:g182684
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
U. Biol. Chem. 258, 12670-12674, 1983
A:Title: Primary structure of human plasma fibronectin.
A:Reference number: A92398; MUID:84032463; PMID:6650202
A:Accession: A92398
A:Molecule type: protein
A:Residues: 32-47,'C',49-51,'S',53-72,'A',74-290 <GAR1>
R:Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A:Title: Further characterization of the binding of fibronectin to gelatin reveals the F

A:Molecule type: protein
A:Residues: 291-300,551-560 <GAR2>
R:Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A:Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A:Reference number: A60904; MUID:87019725; PMID:3532418
A:Accession: A60904
A:Molecule type: protein
A:Residues: 293-301 <GR1>
R:Calaycay, J.; Pandey, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A:Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pl
A:Reference number: A23901; MUID:86008277; PMID:3900070
A:Accession: A23901
A:Molecule type: protein
A:Residues: 616-677,'Q',679-703,'PT' <CA1>
R:Pferschbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A:Title: The cell attachment domain of fibronectin. Determination of the primary structu
A:Reference number: A92386; MUID:82265604; PMID:7050098
A:Accession: A92386
A:Molecule type: protein
A:Residues: 1541-1548 <PIE>
A:Note: residues 1524-1527 are responsible for the cell-binding activity
R:Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A:Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dom
A:Reference number: A32517; MUID:87241275; PMID:3593230
A:Accession: A32517
A:Molecule type: protein
A:Residues: 1589-1630,'T',1722-2058 <GAR3>
R:Tresselt, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pand
Biochem. J. 274, 731-738, 1991
A:Title: Human plasma fibronectin. Demonstration of structural differences between the A
A:Reference number: S14357; MUID:91190085; PMID:2012601
A:Accession: S14357
A:Molecule type: protein
A:Residues: 1614-1630,'T',1722-2081,2113-2244 <TRB>
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A:Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dal
A:Reference number: A23891; MUID:86261459; PMID:4019516
A:Accession: A23891
A:Molecule type: protein
A:Residues: 2071-2080,2112-2356 <GAR4>
C:Comment: The extra domain and connecting strand 3 are subject to developmental and tis
C:Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
action, and transformation.
C:Genetics:
A:Gene: GDB:FNI
A:Cross-references: GDB:119135; OMTM:135600
A:Map position: 2q34-2q34
A:Insertion: 49/3;1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C:Superfamily: fibronectin; fibronectin type I repeat homology <1F1>
C:Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicat
F1:1-26/Domain: signal sequence #status predicted <PRO>
F1:27-31/Domain: propeptide #status predicted <PRO>
F1:32-336/Domain: fibronectin #status experimental <AMT>
F1:32-336/Product: fibronectin #status experimental <FHE>
F1:52-87/Domain: fibronectin type I repeat homology <1F1>
F1:52-87/Domain: fibronectin type I repeat homology <1F2>
F1:141-179/Domain: fibronectin type I repeat homology <1F3>
F1:186-225/Domain: fibronectin type I repeat homology <1F4>
F1:231-270/Domain: fibronectin type I repeat homology <1F5>
F1:308-608/Domain: collagen binding <CBR>
F1:308-608/Domain: fibronectin type I repeat homology <1F6>
F1:360-401/Domain: fibronectin type II repeat homology <2F1>
F1:420-461/Domain: fibronectin type II repeat homology <2F2>
F1:470-508/Domain: fibronectin type I repeat homology <1F7>
F1:518-555/Domain: fibronectin type I repeat homology <1F8>
F1:561-595/Domain: fibronectin type I repeat homology <1F9>

F:719-801/Domain: fibronectin type III repeat homology <3FB>
 F:810-891/Domain: fibronectin type III repeat homology <3FC>
 F:906-988/Domain: fibronectin type III repeat homology <3FD>
 F:996-1077/Domain: fibronectin type III repeat homology <3FE>
 F:1086-1164/Domain: fibronectin type III repeat homology <3FF>
 F:1173-1258/Domain: fibronectin type III repeat homology <3FG>
 F:1266-1349/Domain: fibronectin type III repeat homology <3FH>

Query Match 58.2% Score 46; DB 1; Length 2386;
 Best Local Similarity 57.1%; Pred. No. 34;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DITDSSIGLRWT 14
 Db 1006 VNERTSTVLVLRWT 1019

RESULT 12
 A:40701
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Dec-1999
 C:Accession: A40701; A33725; G42175
 R:Brilow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.
 J. Cell Biol. 122, 265-278, 1993
 A:Title: Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene
 A:Reference number: A40701; MUID:93300909; PMID:7686164
 A:Accession: A40701
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-3566 <BRI>
 A:Cross-references: EMBL:X11937
 R:Morel, Y.; Brilow, J.; Gitelman, S.E.; Miller, W.L.
 Proc. Natl. Acad. Sci. U.S.A. 86, 6582-6586, 1989
 A:Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/c
 A:Reference number: A33725; MUID:93672293; PMID:2475872
 A:Accession: A33725
 A:Molecule type: mRNA
 A:Residues: 2748-3199, 'V', 3201-3298, 'E', 3299-3314, 'G', 3316-3566 <MOR>
 A:Cross-references: GB:G25513; NID:G183069; PIDN:AA35884.1; PID:G183070
 R:Matsumoto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.
 Genomics 12, 485-491, 1992
 A:Title: Cluster of fibronectin type III repeats found in the human major histocompatibility
 A:Reference number: A42175; MUID:92217969; PMID:1373119
 A:Accession: C42175
 A:Molecule type: DNA
 A:Residues: 1849-1936 <MAT>
 A:Experimental source: clone 3.9KX3-1
 A>Note: sequence extracted from NCBI backbone (NCBIP:95634)
 C:Genetic:
 A:Gene: GDB:TNXA, D6103E; TNX, XA; XB
 A:Cross-references: GDB:568487; OMIM:600261
 A:Map position: 6p21.3-6p21.3
 C:Keywords: extracellular matrix; glycoprotein
 F:748-828/Domain: EGF homology <EGF>
 F:748-828/Domain: fibronectin type III repeat homology <3FI>
 F:829-856/Domain: fibronectin type III repeat homology #status atypical <3F2>
 F:873-953/Domain: fibronectin type III repeat homology <3F3>
 F:975-1055/Domain: fibronectin type III repeat homology <3F4>
 F:1078-1158/Domain: fibronectin type III repeat homology <3F5>
 F:1167-1247/Domain: fibronectin type III repeat homology <3F6>
 F:1248-1317/Domain: fibronectin type III repeat homology #status atypical <3F7>
 F:1323-1403/Domain: fibronectin type III repeat homology <3F8>
 F:1412-1482/Domain: fibronectin type III repeat homology <3F9>
 F:1510-1590/Domain: fibronectin type III repeat homology <3F10>
 F:1618-1676/Domain: fibronectin type III repeat homology #status atypical <3F11>
 F:1678-1749/Domain: fibronectin type III repeat homology #status atypical <3F12>
 F:1751-1831/Domain: fibronectin type III repeat homology <3F13>
 F:1849-1929/Domain: fibronectin type III repeat homology <3F14>
 F:1955-2035/Domain: fibronectin type III repeat homology <3F15>
 F:2061-2141/Domain: fibronectin type III repeat homology <3F16>

F:2167-2246/Domain: fibronectin type III repeat homology <3F17>
 F:2274-2354/Domain: fibronectin type III repeat homology <3F18>
 F:2382-2462/Domain: fibronectin type III repeat homology <3F19>
 F:2488-2568/Domain: fibronectin type III repeat homology <3F20>
 F:2584-2664/Domain: fibronectin type III repeat homology <3F21>
 F:2677-2757/Domain: fibronectin type III repeat homology <3F22>
 F:2771-2851/Domain: fibronectin type III repeat homology <3F23>
 F:2878-2958/Domain: fibronectin type III repeat homology <3F24>
 F:2977-3067/Domain: fibronectin type III repeat homology #status atypical <3F25>
 F:3078-3159/Domain: fibronectin type III repeat homology <3F26>
 F:3167-3247/Domain: fibronectin type III repeat homology <3F27>
 F:3255-3334/Domain: fibronectin type III repeat homology <3F28>
 F:3349-3557/Domain: fibronectin type III repeat homology <3F29>

Query Match 58.2% Score 46; DB 1; Length 3566;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 DITDSSIGLRWT 13
 Db 1178 DITPDVGLSWT 1189

RESULT 13
 A:18344
 C:Species: Homo sapiens (man)
 C:Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 15-Sep-2000
 C:Accession: 18344; 18345; S20898; S20899; S63665; S37393
 R:Labat, S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A:Reference number: A57430; MUID:96026330; PMID:7569978
 A:Accession: 18344
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
 A:Molecule type: mRNA
 A:Residues: 1-26926 <LAB1>
 A:Cross-references: EMBL:X90568; NID:G1017424; PID:G1017425
 R:Musco, G.; Tzafaris, C.; Schuck, P.; Pastore, A.
 Biochemistry 34, 553-561, 1995
 A:Title: Dissecting titin into its structural motifs: identification of an alpha-helix
 A:Reference number: 18345; MUID:95119041; PMID:7819249
 A:Accession: 18345
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1977-2014 <MUS>
 A:Cross-references: EMBL:X83270; NID:G602579; PIDN:CAA58243.1; PID:G602580
 A>Note: conformation and properties are reported for a synthetic peptide corresponding
 R:Labat, S.; Gaulet, M.; Lahey, A.; Trinck, J.
 EMBO J. 11, 1711-1716, 1992
 A:Title: Towards a molecular understanding of titin.
 A:Reference number: S20897; MUID:92258380; PMID:1582406
 A:Accession: S20898
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 13597-14200, 'I', 14202-14696 <LAB2>
 A:Cross-references: EMBL:X64698; NID:G37192; PIDN:CAA45930.1; PID:G37193
 A:Accession: S20897
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 16330-16382, 'S', 16384-16756, 'F', 16758-16860 <LAB3>
 A:Cross-references: EMBL:X64699; NID:G37190; PIDN:CAA45940.1; PID:G37191
 A:Accession: S20899
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 'P', 22278-22431, 'R', 22433-22448, 'G', 22450-22453, 'Q', 22455-22480, 'NR', 22483-
 A:Cross-references: EMBL:X64697; NID:G37190; PIDN:CAA45938.1; PID:G37195
 R:Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labat, S.
 J. Mol. Biol. 256, 556-563, 1996
 A:Title: Genomic organization of M line titin and its tissue-specific expression in two
 A:Reference number: S63665; MUID:96177761; PMID:8604138

A:Accession: S63665
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 26729-26825 <KOL>
A:Cross-references: EMBL:X92412; NID:G1236761
R:Gautel, M.; Leonard, K.; Labelle, S.
EMBO J. 12, 3827-3834, 1993
A>Title: Phosphorylation of KSP motifs in the C-terminal region of citin in differentiat
A:Reference number: S37393; MUID:94008990; PMID:8404852
A:Accession: S37393
A:Molecule type: mRNA
A:Residues: 26831-26926 <GAV>
R:Improta, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A:Reference number: A66736; PDB:1IT1
A:Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
R:Finhl, M.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66201; PDB:1NCT
A:Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
C:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q32
C:Function:
A:Description: structural protein forming filaments in striated muscle
C:Superfamily: titin fibronectin type III repeat homology; immunoglobulin homology; pro
C:Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glyco
structural protein
F:24752-25008/Domain: protein kinase homology <KIN>
F:841177,995,2276,2378,2459,2481,2553,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068,
98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,1
tatus predicted
F:16780,16876,17579,17602,17667,17681,17845,17899,18121,18188,18209,18336,18670,18680,18
21900,21955,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,248
F:26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 57.0%; Score 45; DB 1; Length 26926;
Best Local Similarity 53.8%; Pred. No. 7,2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DITDSIGLRWTP 14
Db 20084 DITESTYLRWTP 20096

RESULT 14
T00764
hypothetical protein T22J18.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C:Accession: T00764
R:Vysotskaja, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Oji, O.; Kwan, A.; Liu, S.; Li,
rtz, D.D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N
submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence.
A:Reference number: Z14202
A:Accession: T00764
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-357 <YVS>
A:Cross-references: EMBL:AC003979; NID:G5172156; PID:G3287661; GSPDB:GN00059; ATSP:T22J1
C:Genetics:
A:Gene: ATSP:T22J18.3
A:Map position: 1
A:introns: 64/3; 92/3; 107/1; 154/2; 177/3; 199/2; 225/3; 255/1; 306/3

Query Match 55.7%; Score 44; DB 2; Length 357;
Best Local Similarity 61.5%; Pred. No. 9.1;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDTDSIGLRWTP 13

Db 156 VDLTSSIGLRWTP 168

RESULT 15
FOHUMP
macrophage colony-stimulating factor precursor - human
N:Alternate names: colony-stimulating factor 1; M-CSF-1
N:Contents: macrophage colony-stimulating factor precursor alpha splice form; macrophage
ice form
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 18-Aug-1995 #text_change 22-Jun-1999
C:Accession: A47583; S00304; JH0088; A44191; I57708; A27698; S02615
R:Wong, G.G.; Temple, P.A.; Leary, A.C.; Witek-Gianotti, J.S.; Yang, Y.C.; Ciardetta, A
tk, S.C.; Yandi, N.; Yokoye, H.; Yamada, M.; Saito, M.; Mochiyoshi, K.; Takaku, F.
Science 235, 1504-1508, 1987
A>Title: Human CSF-1: molecular cloning and expression of 4-kb cDNA encoding the human u
A:Reference number: A47583; MUID:87149084; PMID:3493529
A:Accession: A47583
A:Molecule type: mRNA
A:Residues: 1-554 <MON>
A:Cross-references: GB:M37435
A>Note: pairs of this sequence, including the amino end of the mature protein, were dete
A>Note: evidence suggests that as many as 333 carboxyl-terminal residues may be removed
R:Ladner, M.B.; Martin, G.A.; Noble, J.A.; Nikolett, D.M.; Tal, R.; Kawasaki, E.S.; Whit
EMBO J. 6, 2693-2698, 1987
A>Title: Human CSF-1: gene structure and alternative splicing of mRNA precursors.
A:Reference number: S00304; MUID:88054965; PMID:3500041
A:Accession: S00304
A:Molecule type: DNA, mRNA
A:Residues: 1-13,19-554 <LAD>
A:Cross-references: EMBL:X06106; EMBL:X05825
R:Takahashi, M.; Hirata, T.; Takano, M.; Nishida, T.; Nagamura, K.; Kamogashira, T.; Nak
Biochem. Biophys. Res. Commun. 161, 892-901, 1989
A>Title: Amino-terminal region of human macrophage colony-stimulating factor (M-CSF) is
mutants of human M-CSF
A:Reference number: A33256; MUID:89286601; PMID:2660794
A:Accession: A33256
A:Molecule type: mRNA
A:Residues: 1-407, 'P', 409-554 <TX>
A:Cross-references: GB:M27087
A>Note: termination mutants lacking 377 carboxyl-terminal residues remain active
R:Gerretti, D.P.; Wignall, J.; Anderson, D.; Tushinski, R.J.; Gallis, B.M.; Styra, M.; Gi
Mol. Immunol. 25, 761-770, 1988
A>Title: Human macrophage-colony stimulating factor: alternative RNA and protein process
A:Reference number: JH0088; MUID:89039923; PMID:2460758
A:Accession: JH0088
A:Molecule type: mRNA
A:Residues: 1-364,481-554 <CER>
A:Cross-references: GB:U22386
R:Kawasaki, E.S.; Ladner, M.B.; Wang, A.M.; Van Arcsdel, J.; Warren, M.K.; Coyne, M.Y.;
Science 230, 291-296, 1985
A>Title: Molecular cloning of a complementary DNA encoding human macrophage-specific col
A:Reference number: A44191; MUID:86018828; PMID:2996129
A:Accession: A44191
A:Molecule type: mRNA
A:Residues: 1-90, 'Y', 92-181,480-554 <RY>
A:Cross-references: GB:M10108; GB:M11295; GB:M11296; NID:G181142; PID:AA55957.1; PID:G
A>Note: part of this sequence, including the amino end of the mature protein, were deter
R:Pamper, S.; Tabibzadeh, S.; Chuan, F.C.; Pollard, J.W.
Mol. Endocrinol. 5, 1931-1938, 1991
A>Title: Expression of colony-stimulating factor-1 (CSF-1) messenger RNA in human endome
om of CSF-1.
A:Reference number: I57708; MUID:92168031; PMID:1791839
A:Accession: I57708
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 33-90, 'Y', 92-181,480-554 <RES>
A:Cross-references: GB:M76453; NID:G933119; PID:AAA52120.1; PID:G933120
R:Takahashi, M.; Hong, Y.M.; Yasuda, S.; Takano, M.; Kawai, K.; Nakai, S.; Hirai, Y.
Biochem. Biophys. Res. Commun. 152, 1401-1409, 1988
A>Title: Macrophage colony-stimulating factor is produced by human T lymphoblastoid cell
A:Reference number: A27698; MUID:88240361; PMID:3259875

A/Molecule type: protein
 A/Residues: 35-38,'X','40-46','XX','49-52','XX','55-61 <TA2>
 A/Experimental source: leukemic cell line CCRF-CEM. ATCC CCL119
 A/Note: one other peptide was found with an additional amino-terminal Glu-Glu, and a sec
 R/Sakai, N.; Umeda, T.; Suzuki, H.; Ishimatsu, Y.; Shikita, M.
 FEBS Lett 222:341-344, 1987
 A/Title: Macrophage colony-stimulating factor purified from normal human urine. Amino-te
 A/Reference number: S02615; MUID:88005180; PMID:3498652
 A/Accession: S02615
 A/Molecule type: protein
 A/Residues: 33-38,'X','40-62','X','64-68','S','70-76 <SAK>
 C/Genetics:
 A/Gene: GDB:CSF1
 A/Cross-references: GDB:119811; OMIM:120420
 A/Map position: 1p21-1p13
 A/Introns: 13/3; 54/3; 75/3; 132/3; 182/1; 523/3; 541/2
 C/Complex: homodimer, disulfide linked
 C/Function:
 A/Description: stimulates the differentiation and proliferation of hematopoietic progeni
 C/Superfamily: macrophage colony-stimulating factor
 C/Keywords: alternative splicing; cytokine; glycoprotein; growth factor; homodimer; lymph
 F/1-554/Product: macrophage colony-stimulating factor precursor beta splice form #status
 F/1-364,481-554/Product: macrophage colony-stimulating factor precursor gamma splice for
 F/1-181,480-554/Product: macrophage colony-stimulating factor precursor alpha splice for
 F/1-32/Domain: signal sequence #status predicted <SIG>
 F/497-518/Domain: transmembrane #status predicted <TM>
 F/154,172/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 55.7%; Score 44; DB 1; Length 554;
 Best Local Similarity 53.8%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 DITDSATGLRWTP 14
 Db 293 DITDSAMGNNWVP 305

Search completed: September 21, 2004, 05:48:41
 Job time : 8.75 secs

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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:37 ; Search time 4.30147 Seconds

(without alignments)
181.578 Million cell updates/sec

Title: US-10-676-049-1

Sequence: 79

Sequence: 1 VDIITDSIGKRTPL 15

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	1256	1 FINC_CHICK	P11722 gallus gall
2	79	100.0	2477	1 FINC_MOUSE	P11276 mus musculu
3	79	100.0	2477	1 FINC_MOUSE	P04937 rattus norv
4	68	86.1	1328	1 FINC_PLEMA	O91289 pleurodeles
5	64	81.0	2481	1 FINC_XENLA	O91740 xenopus lae
6	58	73.4	3124	1 CALIC_CHICK	P13944 gallus gall
7	49	62.0	3063	1 CALIC_HUMAN	O09275 homo sapien
8	49	62.0	3119	1 CALIC_MOUSE	O60847 mus musculu
9	47	59.5	929	1 CALIC_NOTVI	O91145 notophthalm
10	46	58.2	2265	1 FINC_BOVIN	P07589 bos taurus
11	46	58.2	2386	1 FINC_HUMAN	P02751 homo sapien
12	46	58.2	4289	1 TENX_HUMAN	P22105 homo sapien
13	44	55.7	331	1 DFEA_HUMAN	O00273 homo sapien
14	44	55.7	357	1 V180_ARATH	O08053 arabidopsis
15	44	55.7	554	1 CSF1_HUMAN	P09603 homo sapien
16	44	55.7	621	1 MYPS_RAT	O63518 rattus norv
17	44	55.7	1270	1 MYPC_MOUSE	O70468 mus musculu
18	44	55.7	1271	1 MYPC_CHICK	O90688 gallus gall
19	44	55.7	1274	1 MYPC_HUMAN	O14896 homo sapien
20	44	55.7	1329	1 KP10_HUMAN	O90218 homo sapien
21	43	54.4	1241	1 NPHN_HUMAN	O60550 homo sapien
22	42.5	53.8	261	1 BUB2_YEAST	P53323 saccharomyc
23	42	53.2	369	1 DHDO_DICDI	O8VCC8 mus musculu
24	42	53.2	876	1 EPAC_MOUSE	O95398 homo sapien
25	42	53.2	884	1 EPAC_HUMAN	O92138 rattus norv
26	42	53.2	884	1 EPAC_RAT	O14324 homo sapien
27	42	53.2	1142	1 MYPF_HUMAN	P10059 gallus gall
28	42	53.2	1808	1 TENA_CHICK	P124702 actinobacti
29	41	51.9	190	1 SODC_ACTPL	P459432 haemophilus
30	41	51.9	199	1 SODC_HABDU	O54930 haemophilus
31	41	51.9	268	1 LGT_HAELN	O00872 homo sapien
32	41	51.9	1141	1 MYPS_HUMAN	O91044 rattus norv
33	41	51.9	1234	1 NPHN_RAT	

ALIGNMENTS

RESULT 1	ID	FINC_CHICK	STANDARD	PRT	1256 AA.
AC	P11722	O90921			
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Fibronectin (FN) (Fragments).				
GN	FN1				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RP	[1]				
RP	SEQUENCE OF 1-50 FROM N.A.				
RX	MEDLINE=83117650; PubMed=6572007;				
RA	Hirano H., Yamada Y., Sullivan M., de Crombrughe B., Paetan I.,				
RA	Yamada K.M.;				
RT	"Isolation of genomic DNA clones spanning the entire fibronectin				
RT	gene.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 80:46-50(1983).				
RN	[2]				
RP	SEQUENCE OF 51-1256 FROM N.A.				
RC	STRAIN=White leghorn;				
RA	Norton P.A.;				
RL	Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.				
RN	[3]				
RP	SEQUENCE OF 227-415 FROM N.A.				
RX	MEDLINE=96183558; PubMed=8603103;				
RA	Genlis A.L., Brandli D.W., Lewis S.D., Bennett V.D.;				
RT	"The exon encoding the fibronectin type III-9 repeat is				
RT	constitutively included in the mRNA from chick limb mesenchyme and				
RT	cartilage.";				
RL	Biochim. Biophys. Acta 1311:5-12(1996).				
RN	[4]				
RP	SEQUENCE OF 327-599 FROM N.A.				
RX	MEDLINE=88050950; PubMed=2823899;				
RA	Kubomura S., Obara K., Karasaki Y., Taniguchi H., Gotoh S.,				
RA	Tsuda T., Higashi K., Ohsato K., Hirano H.;				
RT	"Genetic analysis of the cell binding domain region of the chicken				
RT	fibronectin gene.";				
RL	Biochim. Biophys. Acta 910:171-181(1987).				
RN	[5]				
RP	SEQUENCE OF 413-1256 FROM N.A.				
RX	MEDLINE=88142820; PubMed=2830487;				
RA	Norton P.A., Hyatt R.O.;				
RT	"Alternative splicing of chicken fibronectin in embryos and in normal				
RT	and transformed cells.";				
RL	Mol. Cell. Biol. 7:4297-4307(1987).				
CC	- FUNCTION: Fibronectins bind cell surfaces and various compounds				
CC	including collagen, fibrin, heparin, DNA, and actin. Fibronectins				
CC	are involved in cell adhesion, cell motility, opsonization, wound				
CC	healing, and maintenance of cell shape.				
CC	- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED				
CC	VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;				

34	41	51.9	1631	1 PRP1_DROME	P35992 drosophila
35	40	50.6	271	1 KKA8_ECOLI	P14509 escherichia
36	40	50.6	308	1 PEX7_SCHPO	P78798 schizosach
37	40	50.6	535	1 SSNH_HUMAN	P51649 homo sapien
38	40	50.6	567	1 KOGE_HUMAN	P52429 homo sapien
39	40	50.6	833	1 CUD4_CABEL	O17392 caenorhabdi
40	40	50.6	988	1 STJ3_YEAST	O06010 saccharomyc
41	40	50.6	1131	1 MYPF_CHICK	P16419 gallus gall
42	40	50.6	1242	1 NPHN_MOUSE	O94257 mus musculu
43	40	50.6	1370	1 DP2L_HAELN	O9hm88 halobacteri
44	40	50.6	2069	1 DOC9_HUMAN	O9b229 homo sapien
45	39.5	50.0	572	1 HEMA_P13H4	P08492 human parat

CC TO A LESSER EXTEND HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1.
 CC Comment=A number of isoforms are produced. Each of the "extra
 CC domain" and the connecting strand 3 are present in some forms of
 CC fibronectin and absent in others;
 CC Name=1;
 CC -1- IsoId=P11722-1; Sequence=Displayed;
 CC TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 CC forms), made by fibroblasts, epithelial and other cell types, is
 CC deposited as fibrils in the extracellular matrix.
 CC -1- PFM: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains at least 2 fibronectin type I domains.
 CC -1- SIMILARITY: Contains at least 8 fibronectin type III domains.
 CC -----
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 CC or send an email to license@sb-sib.ch).
 CC -----
 CC EMBL; V00432; CAA23714.1; -;
 CC EMBL; U21327; AAA73566.1; -;
 CC EMBL; X06533; CAA29781.1; -;
 CC EMBL; M26186; AAA48772.1; ALT_SEQ.
 CC EMBL; U20386; AAB01062.1; -;
 CC PIR; A28512; A28512.
 CC PIR; A29355; A29355.
 CC PIR; S71465; S71465.
 CC HSSP; P02751; 1FNH.
 CC Interpro: IPR000083; Fibrnctn1.
 CC Interpro: IPR008957; FN_III-like.
 CC Interpro: IPR003961; FN_Type_II.
 CC Interpro: IPR000562; FN_Type_II.
 CC Interpro: IPR003962; FNIII_subd.
 CC PRINTS; PR0014; FNTYPEIII.
 CC SMART; SM00058; FN1; 3.
 CC SMART; SM00060; FN3; 9.
 CC PROSITE; PS00023; FIBRONECTIN_2; PARTIAL.
 CC PROSITE; PS01253; FIBRONECTIN_1; 2.
 CC GlycoPost: Plasma; Heparin-binding; Acute phase; Cell adhesion;
 CC Repeat; Sulfation; Alternative splicing.
 CC KW
 CC NON_TER 1
 CC NON_CONS 51
 CC DOMAIN 236 509
 CC DOMAIN 690 961
 CC DOMAIN 1153 1226
 CC DOMAIN 327 415
 CC DOMAIN 416 509
 CC DOMAIN 510 599
 CC DOMAIN 600 689
 CC DOMAIN 690 781
 CC DOMAIN 782 871
 CC DOMAIN 872 961
 CC DOMAIN 962 1082
 CC DOMAIN 1083 1152
 CC DOMAIN 1174 1218
 CC DOMAIN 1219 >1256
 CC SITE 493 495
 CC DISULFID 1176 1205
 CC DISULFID 1203 1215
 CC DISULFID 1221 1248
 CC CARBOHYD 122 122
 CC CARBOHYD 1078 1078
 CC CARBOHYD 1034 1034
 CC CARBOHYD 1035 1035
 CC CONFLICT 516 516
 CC CONFLICT 569 572
 CC NON_TER 1256 1256

SQL SEQUENCE 1256 AA; 137435 MW; 345A4C0AE4D71D9B CRC64;
 Query Match 100.0%; Score 79; DB 1; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VDITDSIGLRWTP 15
 DB 154 VDITDSIGLRWTP 168
 RESULT 2
 ID FINE_MOUSE STANDARD; PRT; 2477 AA.
 AC P11276; Q61567; Q61568; Q61569; Q64233; Q80U14;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin precursor (FN).
 GN FN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE OF 1-920 FROM N.A.
 RC STRAIN=FVB/N-3; TISSUE=Breast tumor;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diachenko L., Varnauskas K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huljic S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903 (2002).
 RL [2]
 RP SEQUENCE OF 1-28 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=941313; PubMed=8299972;
 RA Polly P., Nicholson R.C.;
 RT "Sequence of the mouse fibronectin-encoding gene promoter region";
 RL Gene 137:353-354 (1993).
 RP [3]
 RP SEQUENCE OF 562-834 FROM N.A.
 RC STRAIN=NMRI;
 RX MEDLINE=95403556; PubMed=7673336;
 RA Tals J.F., Wellner A., Timpl R., Ekblom M., Ekblom P.;
 RT "Regulation of mesenchymal extracellular matrix protein synthesis by
 RT transforming growth factor-beta and glucocorticoids in tumor
 RT stroma";
 RL J. Cell Sci. 108:2153-2162 (1995).
 RP [4]
 RP SEQUENCE OF 899-2376 FROM N.A.
 RA Gurski G., Aros M., Norton P.;
 RX Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RX MEDLINE=88124987; PubMed=3124113;
 RA Blatti S.P., Foster D.N., Ranganathan G., Moses H.L., Getz M.J.;
 RT "Induction of fibronectin gene transcription and mRNA is a primary

Query Match	Similarity	Score	DB 1:	Length	DB 2:	Length	DB 3:	Length	DB 4:	Length	DB 5:	Length	DB 6:	Length	DB 7:	Length	DB 8:	Length	DB 9:	Length	DB 10:	Length	DB 11:	Length	DB 12:	Length	DB 13:	Length	DB 14:	Length	DB 15:	Length	DB 16:	Length	DB 17:	Length	DB 18:	Length	DB 19:	Length	DB 20:	Length	DB 21:	Length	DB 22:	Length	DB 23:	Length	DB 24:	Length	DB 25:	Length	DB 26:	Length	DB 27:	Length	DB 28:	Length	DB 29:	Length	DB 30:	Length	DB 31:	Length	DB 32:	Length	DB 33:	Length	DB 34:	Length	DB 35:	Length	DB 36:	Length	DB 37:	Length	DB 38:	Length	DB 39:	Length	DB 40:	Length	DB 41:	Length	DB 42:	Length	DB 43:	Length	DB 44:	Length	DB 45:	Length	DB 46:	Length	DB 47:	Length	DB 48:	Length	DB 49:	Length	DB 50:	Length	DB 51:	Length	DB 52:	Length	DB 53:	Length	DB 54:	Length	DB 55:	Length	DB 56:	Length	DB 57:	Length	DB 58:	Length	DB 59:	Length	DB 60:	Length	DB 61:	Length	DB 62:	Length	DB 63:	Length	DB 64:	Length	DB 65:	Length	DB 66:	Length	DB 67:	Length	DB 68:	Length	DB 69:	Length	DB 70:	Length	DB 71:	Length	DB 72:	Length	DB 73:	Length	DB 74:	Length	DB 75:	Length	DB 76:	Length	DB 77:	Length	DB 78:	Length	DB 79:	Length	DB 80:	Length	DB 81:	Length	DB 82:	Length	DB 83:	Length	DB 84:	Length	DB 85:	Length	DB 86:	Length	DB 87:	Length	DB 88:	Length	DB 89:	Length	DB 90:	Length	DB 91:	Length	DB 92:	Length	DB 93:	Length	DB 94:	Length	DB 95:	Length	DB 96:	Length	DB 97:	Length	DB 98:	Length	DB 99:	Length	DB 100:	Length	DB 101:	Length	DB 102:	Length	DB 103:	Length	DB 104:	Length	DB 105:	Length	DB 106:	Length	DB 107:	Length	DB 108:	Length	DB 109:	Length	DB 110:	Length	DB 111:	Length	DB 112:	Length	DB 113:	Length	DB 114:	Length	DB 115:	Length	DB 116:	Length	DB 117:	Length	DB 118:	Length	DB 119:	Length	DB 120:	Length	DB 121:	Length	DB 122:	Length	DB 123:	Length	DB 124:	Length	DB 125:	Length	DB 126:	Length	DB 127:	Length	DB 128:	Length	DB 129:	Length	DB 130:	Length	DB 131:	Length	DB 132:	Length	DB 133:	Length	DB 134:	Length	DB 135:	Length	DB 136:	Length	DB 137:	Length	DB 138:	Length	DB 139:	Length	DB 140:	Length	DB 141:	Length	DB 142:	Length	DB 143:	Length	DB 144:	Length	DB 145:	Length	DB 146:	Length	DB 147:	Length	DB 148:	Length	DB 149:	Length	DB 150:	Length	DB 151:	Length	DB 152:	Length	DB 153:	Length	DB 154:	Length	DB 155:	Length	DB 156:	Length	DB 157:	Length	DB 158:	Length	DB 159:	Length	DB 160:	Length	DB 161:	Length	DB 162:	Length	DB 163:	Length	DB 164:	Length	DB 165:	Length	DB 166:	Length	DB 167:	Length	DB 168:	Length	DB 169:	Length	DB 170:	Length	DB 171:	Length	DB 172:	Length	DB 173:	Length	DB 174:	Length	DB 175:	Length	DB 176:	Length	DB 177:	Length	DB 178:	Length	DB 179:	Length	DB 180:	Length	DB 181:	Length	DB 182:	Length	DB 183:	Length	DB 184:	Length	DB 185:	Length	DB 186:	Length	DB 187:	Length	DB 188:	Length	DB 189:	Length	DB 190:	Length	DB 191:	Length	DB 192:	Length	DB 193:	Length	DB 194:	Length	DB 195:	Length	DB 196:	Length	DB 197:	Length	DB 198:	Length	DB 199:	Length	DB 200:	Length	DB 201:	Length	DB 202:	Length	DB 203:	Length	DB 204:	Length	DB 205:	Length	DB 206:	Length	DB 207:	Length	DB 208:	Length	DB 209:	Length	DB 210:	Length	DB 211:	Length	DB 212:	Length	DB 213:	Length	DB 214:	Length	DB 215:	Length	DB 216:	Length	DB 217:	Length	DB 218:	Length	DB 219:	Length	DB 220:	Length	DB 221:	Length	DB 222:	Length	DB 223:	Length	DB 224:	Length	DB 225:	Length	DB 226:	Length	DB 227:	Length	DB 228:	Length	DB 229:	Length	DB 230:	Length	DB 231:	Length	DB 232:
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Db 1275 VDIRSSIGLRWPL 1289

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RESULT 3
FIND RAT STANDARD; PRT; 2477 AA.
AC P04937;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin precursor (FN).
GN FN1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer; TISSUE=Liver;
RX MEDLINE=88054951; PubMed=2445560;
RA Schwarzauer J.E., Patel R.S., Fonda D., Hynes R.O.;
RT "Multiple sites of alternative splicing of the rat fibronectin gene
transcript."
RL EMBL J. 6:2573-2580(1987).
RN [2]
RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.
RC STRAIN=Fischer; TISSUE=Liver;
RX MEDLINE=88054950; PubMed=3119323;
RA Patel R.S., Odermatt E., Schwarzauer J.E., Hynes R.O.;
RT "Organization of the fibronectin gene provides evidence for exon
shuffling during evolution."
RL EMBO J. 6:2565-2572(1987).
RN [3]
RP SEQUENCE OF 1586-2477 FROM N.A.
RX MEDLINE=84082067; PubMed=6317187;
RA Schwarzbauer J.E., Tankun J.W., Lemischka I.R., Hynes R.O.;
RT "Three different fibronectin mRNAs arise by alternative splicing
within the coding region."
RL Cell 35:421-431(1983).
CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
including collagen, fibrin, heparin, DNA, and actin. Fibronectins
are involved in cell adhesion, cell motility, opsonization, wound
healing, and maintenance of cell shape.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS,
TO A LESSER EXTENT HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Comment=Each of the "extra domain" and the connecting strand 3
are present in some forms of fibronectin and absent in others;
CC Name=1;
CC IsoId=P04937-1; Sequence=Displayed;
CC Name=2; Synonyms=FNII-13-less;
CC IsoId=P04937-2; Sequence=VSP_003258;
CC Name=3; Synonyms=Lambda-RLR4-5;
CC IsoId=P04937-3; Sequence=VSP_003259;
CC Name=4; Synonyms=Lambda-RLR6;
CC IsoId=P04937-4; Sequence=VSP_003260;
CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
forms), made by fibroblasts, epithelial and other cell types, is
deposited as fibrils in the extracellular matrix.
CC -1- PM: Sulfated (By similarity).
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
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CC -----
DR EMBL; X15906; CAA34020.1; -
DR EMBL; L29191; AAA41166.1; -
DR EMBL; L29191; AAA41166.1; JOINED.
DR EMBL; L29191; AAA41167.1; -
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DR EMBL; L29191; AAA41168.1; -
DR EMBL; L29191; AAA41168.1; JOINED.
DR EMBL; X05831; CAA29278.1; -
DR EMBL; X05832; CAA29279.1; -
DR EMBL; X05833; CAA29280.1; -
DR EMBL; X05834; CAA29281.1; -
DR PIR; S14428; S14428.
DR HSPD; P02751; IFBR.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibrinctn.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR003962; FNII_subd.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 13.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR GlycoProtex; P01253; FIBRONECTIN;
KW Sulfation; Cell adhesion; Repeat; Alternative splicing; Signal.
FT SIGNAL 1 32
FT CHAIN 33 2477
FT DOMAIN 53 273
FT DOMAIN 308 608
FT DNA_BIND 906 1171
FT DOMAIN 1357 1630
FT DOMAIN 1811 2081
FT DOMAIN 2296 2427
FT DOMAIN 51 91
FT DOMAIN 96 139
FT DOMAIN 140 183
FT DOMAIN 185 229
FT DOMAIN 230 274
FT DOMAIN 306 345
FT DOMAIN 345 404
FT DOMAIN 405 469
FT DOMAIN 468 511
FT DOMAIN 516 558
FT DOMAIN 559 602
FT DOMAIN 609 706
FT DOMAIN 707 808
FT DOMAIN 809 903
FT DOMAIN 904 994
FT DOMAIN 995 1084
FT DOMAIN 1085 1172
FT DOMAIN 1173 1264
FT DOMAIN 1265 1355
FT DOMAIN 1356 1446
FT DOMAIN 1447 1536
FT DOMAIN 1537 1630
FT DOMAIN 1631 1720
FT DOMAIN 1721 1810
FT DOMAIN 1811 1902
FT DOMAIN 1903 1991
FT DOMAIN 1992 2081
FT DOMAIN 2082 2201
FIBRONECTIN.
FIBRIN- AND HEPARIN-BINDING 1.
COLLAGEN-BINDING.
CELL-ATTACHMENT.
HEPARIN-BINDING 2.
FIBRIN-BINDING 2.
FIBRONECTIN TYPE-I 1.
FIBRONECTIN TYPE-I 2.
FIBRONECTIN TYPE-I 3.
FIBRONECTIN TYPE-I 4.
FIBRONECTIN TYPE-I 5.
FIBRONECTIN TYPE-I 6.
FIBRONECTIN TYPE-II 1.
FIBRONECTIN TYPE-II 2.
FIBRONECTIN TYPE-II 7.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8 (EXTRA DOMAIN 1).
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 10.
FIBRONECTIN TYPE-III 11.
FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 13 (EXTRA DOMAIN 2).
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
CONNECTING STRAND 3 (CS-3) (V REGION).
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FT DOMAIN 2202 2383 FIBRONECTIN TYPE-III 17.
FT DOMAIN 2294 2338 FIBRONECTIN TYPE-I 10.
FT DOMAIN 2339 2381 FIBRONECTIN TYPE-I 11.
FT DOMAIN 2383 2426 FIBRONECTIN TYPE-I 12.
FT SITE 1614 1616 CELL ATTACHMENT SITE.
FT SITE 2181 2183 CELL ATTACHMENT SITE.
FT DISULFID 53 79 BY SIMILARITY.
FT DISULFID 77 88 BY SIMILARITY.
FT DISULFID 98 126 BY SIMILARITY.
FT DISULFID 124 136 BY SIMILARITY.
FT DISULFID 142 170 BY SIMILARITY.
FT DISULFID 168 180 BY SIMILARITY.
FT DISULFID 187 216 BY SIMILARITY.
FT DISULFID 214 226 BY SIMILARITY.
FT DISULFID 232 261 BY SIMILARITY.
FT DISULFID 259 271 BY SIMILARITY.
FT DISULFID 308 335 BY SIMILARITY.
FT DISULFID 333 342 BY SIMILARITY.
FT DISULFID 360 386 BY SIMILARITY.
FT DISULFID 374 401 BY SIMILARITY.
FT DISULFID 420 446 BY SIMILARITY.
FT DISULFID 434 461 BY SIMILARITY.
FT DISULFID 470 498 BY SIMILARITY.
FT DISULFID 496 508 BY SIMILARITY.
FT DISULFID 518 545 BY SIMILARITY.
FT DISULFID 543 555 BY SIMILARITY.
FT DISULFID 561 589 BY SIMILARITY.
FT DISULFID 587 599 BY SIMILARITY.
FT DISULFID 2296 2325 BY SIMILARITY.
FT DISULFID 2323 2335 BY SIMILARITY.
FT DISULFID 2341 2368 BY SIMILARITY.
FT DISULFID 2366 2378 BY SIMILARITY.
FT DISULFID 2385 2409 BY SIMILARITY.
FT DISULFID 2407 2423 BY SIMILARITY.
FT DISULFID 2458 2458 INTERCHAIN (WITH C-2458).
FT DISULFID 2462 2462 SULFATION (POTENTIAL).
FT MOD RES 875 875 SULFATION (POTENTIAL).
FT MOD RES 880 880 SULFATION (POTENTIAL).
FT MOD RES 2392 2392 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 2475 2475 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 528 528 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1006 1006 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 2154 2154 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT VARSPLIC 1720 1809 Missing (in isoform 2).
FT VARSPLIC 2082 2106 /FTid=VSP_003258.
FT VARSPLIC 2082 2200 Missing (in isoform 3).
FT CONFLICT 2318 2318 /FTid=VSP_003259.
FT CONFLICT 2318 2318 Missing (in isoform 4).
SQ SEQUENCE 2477 AA; 272510 MM; B4391A472ECDEB5 CRC64;
Query Match 100.0%; Score 79; DB 1; Length 2477;
Best Local Similarity 100.0%; Pred. No. 3; 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
DE Fibronectin (FN) (Fragment).
OS Pleurodeles waltl (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae;
OC Pleurodeles.
OX NCBI_TaxID=8319;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94363379; PubMed=8081872;
RX Cavalier L., Rieu J., Desimone D.W.;
RT "Amphibian pleurodeles waltl fibronectin: cDNA cloning and
developmental expression of spliced variants."
RL Cell Adhes. Commun. 1:83-91(1993).
CC -1- FUNCTION: Fibronection binds cell surfaces and various compounds
including collagen, fibrin, heparin, DNA, and actin. Fibronections
are involved in cell adhesion, cell motility, opsonization, wound
healing, and maintenance of cell shape (by similarity).
CC -1- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
SIMILARITY).
CC -1- SIMILARITY: Contains at least 3 fibronection type III domains.
CC -1- SIMILARITY: Contains at least 10 fibronection type III domains.
CC -----
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CC -----
DR EMBL; X66813; CAA47292.1; -.
DR HSRP; P02751; FNH.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR006083; Fibrinectn.
DR InterPro; IPR008857; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FNIII_subd.
DR Pfam; PF00039; fn3; 3.
DR Pfam; PF00041; fn3; 11.
DR PRINTS; PR00014; FNTPR111.
DR SMART; SMO0056; FN1; 3.
DR SMART; SMO0060; FN3; 9.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
Repeat.
FT NON_TER 1 1
FT DNA_BIND <1 13
FT DOMAIN 203 477 CELL-ATTACHMENT.
FT DOMAIN 658 929 HEPARIN-BINDING 2 (BY SIMILARITY).
FT DOMAIN 1157 1288 FIBRIN-BINDING 2 (BY SIMILARITY).
FT DOMAIN <1 14 FIBRONECTIN TYPE-III.
FT DOMAIN 15 110 FIBRONECTIN TYPE-III.
FT DOMAIN 111 201 FIBRONECTIN TYPE-III (EXTRA DOMAIN).
FT DOMAIN 202 292 FIBRONECTIN TYPE-III.
FT DOMAIN 293 383 FIBRONECTIN TYPE-III.
FT DOMAIN 384 477 FIBRONECTIN TYPE-III.
FT DOMAIN 478 567 FIBRONECTIN TYPE-III.
FT DOMAIN 568 657 FIBRONECTIN TYPE-III (EXTRA DOMAIN).
FT DOMAIN 658 749 FIBRONECTIN TYPE-III.
FT DOMAIN 750 838 FIBRONECTIN TYPE-III.
FT DOMAIN 839 929 FIBRONECTIN TYPE-III.
FT DOMAIN 930 1064 CONNECTING STRAND 3 (CS-3) (V REGION).
FT DOMAIN 1065 1143 FIBRONECTIN TYPE-III.
FT DOMAIN 1145 1199 FIBRONECTIN TYPE-I.
FT DOMAIN 1200 1243 FIBRONECTIN TYPE-I.
FT DOMAIN 1245 1287 FIBRONECTIN TYPE-I.
FT DISULFID 1184 1186 BY SIMILARITY.
FT DISULFID 1187 1196 BY SIMILARITY.
FT DISULFID 1202 1229 BY SIMILARITY.
FT DISULFID 1227 1240 BY SIMILARITY.
FT DISULFID 1247 1270 BY SIMILARITY.
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FT DISUFLD 1268 1284 BY SIMILARITY.
FT DISUFLD 1320 1320 INTERCHAIN (WITH C-1324) (BY SIMILARITY).
FT DISUFLD 1324 1324 INTERCHAIN (WITH C-1320) (BY SIMILARITY).
FT SITE 461 463 CELL ATTACHMENT SITE.
FT CARBOXID 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1328 AA; 145037 MW; E31BF7968A1DE74 CRC64;

Query March 86.1%; Score 68; DB 1; Length 1328;
Best Local Similarity 80.0%; Pred. No. 0.0013; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 1;

QY 1 VDIITSSIGLRWTP 15
Db 121 VDVITRISLRWTP 135

RESULT 5
FINC_XENLA STANDARD; PRT; 2481 AA.
AC 091740;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibronectin precursor.
GN FN1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=9211942; PubMed=1730390;
RA Desimone D.W., Norton P.A., Hynes R.O.;
RT "Identification and characterization of alternatively spliced
RT fibronectin mRNAs expressed in early Xenopus embryos."
RU Dev. Biol. 149:357-369(1992).
CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC are involved in cell adhesion, cell motility, opsonization, wound
CC healing, and maintenance of cell shape (by similarity).
CC -1- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
CC CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC domain=A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC -1- IsoId=091740-1; Sequence=Displayed;
CC -1- TISSUE SPECIFICITY: IN EARLY XENOPUS EMBRYO. CELLULAR FORMS OF
CC FIBRONECTIN PREDOMINATE WHICH INCLUDE BOTH EXTRA DOMAINS. IN
CC FIBRONECTIN OF EMBRYONIC AND ADULT LIVER THE CONNECTING STRAND 3
CC CAN BE EITHER COMPLETELY EXCLUDED OR INCLUDED.
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M77820; AAA49707.1; -.
CC HSSP; P02751; 2FN2.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR000083; Fibrinctl.
CC InterPro; IPR009957; FN III-like.
CC InterPro; IPR003961; FN_III.

DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PFO00039; fn1; 12.
DR Pfam; PFO00040; fn2; 2.
DR Pfam; PFO00041; fn3; 17.
DR PRINTS; PRO0013; FNYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 17.
DR PROSITE; PS00023; EGF_1; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 11.
DR Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
KW Repeat; Alternative splicing; Signal.
KM SIGNAL 1 31
FT CHAIN 32 2481
FT DOMAIN 55 275
FT DOMAIN 309 609
FT DNA BIND 907 1172
FT DOMAIN 1358 1631
FT DOMAIN 1812 2082
FT DOMAIN 2301 2432
FT DOMAIN 53 93
FT DOMAIN 98 141
FT DOMAIN 142 185
FT DOMAIN 187 231
FT DOMAIN 232 276
FT DOMAIN 307 346
FT DOMAIN 346 405
FT DOMAIN 406 470
FT DOMAIN 469 512
FT DOMAIN 517 559
FT DOMAIN 560 603
FT DOMAIN 610 707
FT DOMAIN 708 809
FT DOMAIN 810 904
FT DOMAIN 905 995
FT DOMAIN 996 1085
FT DOMAIN 1086 1173
FT DOMAIN 1174 1265
FT DOMAIN 1266 1356
FT DOMAIN 1357 1447
FT DOMAIN 1448 1537
FT DOMAIN 1538 1631
FT DOMAIN 1632 1721
FT DOMAIN 1722 1811
FT DOMAIN 1812 1903
FT DOMAIN 1904 1992
FT DOMAIN 1993 2082
FT DOMAIN 2083 2205
FT DOMAIN 2206 2287
FT DOMAIN 2289 2343
FT DOMAIN 2344 2386
FT DOMAIN 2388 2431
FT SITE 1615 1617
FT DISULF 55 81
FT DISULF 79 90
FT DISULF 100 128
FT DISULF 126 138
FT DISULF 144 172
FT DISULF 170 182
FT DISULF 189 218
FT DISULF 216 228
FT DISULF 234 263
FT DISULF 261 273
FT DISULF 309 336
FT DISULF 334 343
FT DISULF 361 387
FT DISULF 375 402
FT DISULF 421 447
FT DISULF 471 499
FT DISULF 497 509
FT DISULF 519 546
FT DISULF 544 556
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FT DISULFID 562 590 BY SIMILARITY.
FT DISULFID 588 600 BY SIMILARITY.
FT DISULFID 2301 2330 BY SIMILARITY.
FT DISULFID 2328 2340 BY SIMILARITY.
FT DISULFID 2346 2373 BY SIMILARITY.
FT DISULFID 2371 2383 BY SIMILARITY.
FT DISULFID 2390 2414 BY SIMILARITY.
FT DISULFID 2412 2428 BY SIMILARITY.
FT DISULFID 2459 2459 INTERCHAIN (WITH C-2463) (BY SIMILARITY).
FT DISULFID 2463 2463 INTERCHAIN (WITH C-2459) (BY SIMILARITY).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 543 543 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 877 877 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1244 1244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1291 1291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2202 2202 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 2481 AA; 272678 MW; 7547D4F6CE7C93 CRC64;

Query Match 81.0%; Score 64; DB 1; Length 2481;
Best Local Similarity 78.6%; Pred. No. 0.012;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 DITDSIGLRWTP 15
Db 1277 DVTDSIDLRWTP 1290

RESULT 6
ID CAIC CHICK STANDARD; PRT; 3124 AA.
AC P13944; 004509;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Collagen alpha 1(XII) chain precursor (Fibrochimerin).
GN COL12A1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn;
RX MEDLINE=82011863; Pubmed=1918137;
RA Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H.,
RA Nishida Y., Obata M., Kimata K.;
RT "The complete primary structure of type XII collagen shows a chimeric
RT molecule with reiterated fibronectin type III motifs, von Willebrand
RT factor A motifs, a domain homologous to a noncollagenous region of
RT type IX collagen, and short collagenous domains with an Arg-Gly-Asp
RT site.";
RU J. Cell Biol. 115:209-221(1991).
RN [2]
RP SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
RP 2846-2873.
RX MEDLINE=90062079; Pubmed=2584192;
RA Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.;
RT "Type XII collagen. A large multidomain molecule with partial
RT homology to type IX collagen.";
RU J. Biol. Chem. 264:19772-19778(1989).
RN [3]
RP SEQUENCE OF 2960-3076 FROM N.A.
RX MEDLINE=87317590; Pubmed=3476925;
RA Gordon M.K., Gerecke D.R., Olsen B.R.;
RT "Type XII collagen: distinct extracellular matrix component
RT discovered by cDNA cloning.";
RU Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
RN [4]
RP SEQUENCE OF 1-1283 FROM N.A. (ISOFORM SHORT), AND ALTERNATIVE
RP SPLICING.
RC TISSUE=Embryo;
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RX MEDLINE=93042014; Pubmed=1420368;
RA Trueb J., Trueb B.;
RT "The two splice variants of collagen XII share a common 5' end.";
RU Biochim. Biophys. Acta 1171:97-98(1992).
RN [5]
RP ALTERNATIVE SPLICING.
RX MEDLINE=95370352; Pubmed=7642694;
RA Koch M., Bohmann B., Mathison M., Hagios C., Trueb B., Chiquet M.;
RT "Large and small splice variants of collagen XII: differential
RT expression and ligand binding.";
RU J. Cell Biol. 130:1005-1014(1995).
CC -1- FUNCTION: Type XII collagen interacts with type I collagen-
CC containing fibrils, the COL1 domain could be associated with the
CC surface of the fibrils, and the COL2 and NC3 domains may be
CC localized in the pericellular matrix.
CC -1- SUBUNIT: Trimer of identical chains each containing 190 kDa of
CC nontriple-helical sequences.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=The final tissue form of collagen XII may contain
CC homocollimers of either isoform long or isoform short or any
CC combination of isoform long and isoform short. Only isoform long
CC is a proteoglycan. Isoform long has more restricted expression
CC in embryonic tissue than isoform short;
CC Name=Long;
CC . IsoId=P13944-1; Sequence=Displayed;
CC Name=Short;
CC . IsoId=P13944-2; Sequence=VSP 001148;
CC -1- TISSUE SPECIFICITY: Type XII collagen is present in tendons,
CC ligaments, perichondrium, and pericardium, all dense connective
CC tissues containing type I collagen.
CC -1- DOMAIN: This sequence defines five distinct domains, two triple-
CC helical domains (COL1 and COL2) and three nontriple-helical
CC domains (NC1, NC2, and NC3).
CC -1- PTM: The triple-helical tail is stabilized by disulfide bonds at
CC each end.
CC -1- PTM: Proline at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -1- PTM: O-glycosylated; glycosaminoglycan of chondroitin-sulfate type
CC (By similarity).
CC -1- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
CC INTERRUPTED HELICES (FACIT) FAMILY.
CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -1- SIMILARITY: Contains 4 VWF domains.
CC -1- SIMILARITY: Contains 18 fibronectin type III domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; D00824; BAA00701.1; -
DR EMBL; X61024; CAA43358.1; -
DR EMBL; M17375; AAA48718.1; -
DR EMBL; J05137; AAA48635.1; -
DR EMBL; X67327; CAA47744.1; -
DR PIR; A40020; A40020.
DR HSSP; P20701; 1LEPA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003861; FN_III.
DR InterPro; IPR003129; TSPN.
DR Pfam; PF01391; Collagen_4.
DR Pfam; PF00041; FN3; 17.
DR Pfam; PF02210; TSPN; 1.
DR Pfam; PF00092; VWA; 4.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SMO0060; FN3; 16.
DR SMART; SMO0210; TSPN; 1.
```

DR SMART, SM00327; VMA: 4.
 DR PROSITE; PSS0234; VMA: 4.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 3124
 FT DOMAIN 25 114
 FT DOMAIN 139 311
 FT DOMAIN 332 425
 FT DOMAIN 439 615
 FT DOMAIN 629 720
 FT DOMAIN 721 811
 FT DOMAIN 812 904
 FT DOMAIN 905 998
 FT DOMAIN 999 1085
 FT DOMAIN 1086 1178
 FT DOMAIN 1199 1371
 FT DOMAIN 1384 1473
 FT DOMAIN 1474 1565
 FT DOMAIN 1566 1654
 FT DOMAIN 1655 1755
 FT DOMAIN 1756 1846
 FT DOMAIN 1847 1936
 FT DOMAIN 1937 2027
 FT DOMAIN 2028 2118
 FT DOMAIN 2119 2206
 FT DOMAIN 2207 2295
 FT DOMAIN 2327 2500
 FT DOMAIN 2524 2716
 FT DOMAIN 2455 2750
 FT DOMAIN 2751 2902
 FT DOMAIN 2903 2945
 FT DOMAIN 2946 3048
 FT DOMAIN 3049 3124
 FT DOMAIN 3086 3096
 FT DOMAIN 3111 3123
 FT SITE 2438 2440
 FT SITE 2899 2901
 FT SITE 32 32
 FT CARBOHYD 797 797
 FT CARBOHYD 890 890
 FT CARBOHYD 981 981
 FT CARBOHYD 1006 1006
 FT CARBOHYD 1032 1032
 FT CARBOHYD 1044 1044
 FT CARBOHYD 1512 1512
 FT CARBOHYD 1767 1767
 FT CARBOHYD 2210 2210
 FT CARBOHYD 2273 2273
 FT CARBOHYD 2532 2532
 FT CARBOHYD 2683 2683
 FT VARSPLIC 25 1188
 FT CONFLICT 1258 1258
 FT CONFLICT 1264 1264
 FT CONFLICT 2759 2759
 FT CONFLICT 2803 2803
 FT CONFLICT 2977 2977
 FT CONFLICT 3075 3076
 FT SEQUENCE 3124 AA; 340578 MW; 094285AFEF7346CF CRC64;
 Query Match 73.4%; Score 58; DB 1; Length 3124;
 Best Local Similarity 69.2%; Pred. No. 0.16;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DITDSSIGLRWTP 14
 DB 916 DITDTVGLSWTP 928

RESULT 7
 CAIC HUMAN STANDARD; PRT; 3063 AA.
 ID 099715; Q99716;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Collagen alpha 1(XII) chain precursor.
 GN COL12A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 [1]
 SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.
 RP MEDLINE=97288521; PubMed=9143499;
 RA Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,
 RA Hudson D.L., Champlaud M.-F., Olsen B.R., Burgeson R.E.;
 RT "Complete primary structure of two splice variants of collagen XII,
 RT and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX)
 RT collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human
 RT chromosome 6q12-q13."
 RL Genomics 41:236-242(1997).
 CC -! FUNCTION: Type XII collagen interacts with type I collagen-
 CC containing fibrils, the COL1 domain could be associated with the
 CC surface of the fibrils, and the COL2 and NC3 domains may be
 CC localized in the pericellular matrix (By similarity).
 CC -! SUBUNIT: Trimer of identical chains each containing 190 kDa of
 CC nontriple-helical sequences.
 CC -! ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=The final tissue form of collagen XII may contain
 CC homotrimers of either isoform long or isoform short or any
 CC combination of isoform long and isoform short;
 CC Name=Long;
 CC IsoId=Q99715-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=Q99715-2; Sequence=VSP 001149;
 CC -! TISSUE SPECIFICITY: Found in collagen I-containing tissues; both
 CC short and long isoforms appear in amnion, chorion, skeletal
 CC muscle, small intestine, and in cell culture of dermal
 CC fibroblasts, keratinocytes and endothelial cells. Only the short
 CC isoform is found in lung, placenta, kidney and a squamous cell
 CC carcinoma cell line.
 CC -! PTM: The triple-helical tail is stabilized by disulfide bonds at
 CC each end (By similarity).
 CC -! PTM: Prolines at the third position of the tripeptide repeating
 CC unit (G-X-Y) are hydroxylated in some or all of the chains (By
 CC similarity).
 CC -! PTM: O-glycosylation of isoform long; glycosaminoglycan of
 CC chondroitin-sulfate type (By similarity).
 CC -! SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
 CC INTERRUPTED HELICES (FACIT) FAMILY.
 CC -! SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -! SIMILARITY: Contains 4 VMPA domains.
 CC -! SIMILARITY: Contains 18 fibronectin type III domains.
 CC
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 CC
 CC EMBL: U73778; AAC51244.1; -;
 CC EMBL: U73779; AAD40483.1; -;
 CC HSSP: P02751; ITTF.
 CC Genep: HGNC:2168; COL12A1.
 CC MIM: 120320; -;
 CC GO: GO:0005595; C:collagen type XII; TAS.

DR GO: 0001501; P:skeletal development; TAs.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003129; TSEN.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF01391; Collagen; 4.
 DR Pfam; PF00041; Collagen; 4.
 DR Pfam; PF02210; TSEN; 1.
 DR Pfam; PF00092; Vwf; 4.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SMO0060; FN3; 16.
 DR SMART; SMO0210; TSPN; 1.
 DR PROSITE; PS50234; VWF; 4.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
 FT SIGNAL 1
 FT CHAIN 24
 FT DOMAIN 25 3063 COLLAGEN ALPHA 1(XII) CHAIN.
 FT DOMAIN 25 114 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 140 316 VWF 1.
 FT DOMAIN 333 426 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 440 616 VWF 2.
 FT DOMAIN 630 721 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 722 812 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 813 903 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 904 998 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 999 1085 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 1086 1178 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 1199 1371 VWF 3.
 FT DOMAIN 1384 1473 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1474 1564 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 1565 1652 FIBRONECTIN TYPE-III 11.
 FT DOMAIN 1654 1751 FIBRONECTIN TYPE-III 12.
 FT DOMAIN 1752 1842 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 1843 1932 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 1933 2023 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 2024 2114 FIBRONECTIN TYPE-III 16.
 FT DOMAIN 2115 2202 FIBRONECTIN TYPE-III 17.
 FT DOMAIN 2203 2291 FIBRONECTIN TYPE-III 18.
 FT DOMAIN 2292 2496 VWF 4.
 FT DOMAIN 2520 2712 TSP N-TERMINAL.
 FT DOMAIN 2451 2746 NONHELIICAL REGION (NC3).
 FT DOMAIN 2747 2898 TRIPLE-HELICAL REGION
 FT DOMAIN 2899 2941 (COL2) WITH 1 IMPERFECTION.
 FT DOMAIN 2942 3044 NONHELIICAL REGION (NC2).
 FT DOMAIN 3045 3063 (COL1) WITH 2 IMPERFECTIONS.
 FT SITE 862 864 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 2779 2781 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 2895 2897 CELL ATTACHMENT SITE (POTENTIAL).
 FT MOD_RES 2944 2944 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2947 2947 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2950 2950 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2959 2959 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2965 2965 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2968 2968 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2971 2971 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2983 2983 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3000 3000 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3003 3003 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3014 3014 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3023 3023 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3026 3026 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3029 3029 HYDROXYLATION (BY SIMILARITY).
 FT CARBOHYD 700 700 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 798 798 O-LINKED (XYL. . .) (CHONDROITIN SULFATE) (POTENTIAL).
 FT CARBOHYD 889 889 O-LINKED (XYL. . .) (CHONDROITIN SULFATE) (POTENTIAL).
 FT CARBOHYD 981 981 O-LINKED (XYL. . .) (CHONDROITIN SULFATE) (POTENTIAL).

FT CARBOHYD 1763 1763 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2206 2206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2528 2528 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2679 2679 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 25 1188 Missing (in isoform Short).
 FT SQ SEQUENCE 3063 AA; 333189 MW; 75FEA78FA8E48293 CRC64;
 Query Match 62.0%; Score 49; DB 1; Length 3063;
 Best Local Similarity 75.0%; Pred. No. 5;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 DTTDSIGLRWT 13
 Db 915 DTTDSIGAYWT 926
 RESULT 8
 ID CALC_MOUSE STANDARD; PRT; 3119 AA.
 AC Q60847; P70322;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1(XII) chain precursor.
 GN COL12A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-1 AND XIIA-2).
 RP STRAIN=Swiss Webster; and C57BL/6J; TISSUE=Skin;
 RX MEDLINE=96170761; PubMed=8601036;
 RA Boehme K., Li Y., Oh P.S., Olsen B.R.;
 RT "Primary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic development";
 RT Dev. Dyn. 204:432-445 (1995).
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-2 AND XIIA-2).
 RP STRAIN=C57BL/6J; TISSUE=Skin fibroblast;
 RX MEDLINE=99348349; PubMed=10419532;
 RA Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R.W., Olsen B.R., Nishimura I.;
 RT "Structural variation of type XII collagen at its carboxyl-terminal NC1 domain generated by tissue-specific alternative splicing";
 RT J. Biol. Chem. 274:22053-22059 (1999).
 RL -1- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the pericollagenous matrix (By similarity).
 CC -1- SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=The final tissue form of collagen XII may contain homotrimers or any combination of the various isoforms;
 CC Name=XIIA-1;
 CC IsoId=Q60847-1; Sequence=Displayed;
 CC Name=XIIA-2; Synonyms=ERK;
 CC IsoId=Q60847-2; Sequence=VSP_001151, VSP_001152;
 CC Name=XIIB-1;
 CC IsoId=Q60847-3; Sequence=VSP_001150;
 CC Name=XIIB-2;
 CC IsoId=Q60847-4; Sequence=VSP_001150, VSP_001151, VSP_001152;
 CC -1- TISSUE SPECIFICITY: Highest expression in tendons, perichondrium, skin, cornea, sclera, blood vessels, and pericardium.
 CC -1- DEVELOPMENTAL STAGE: The long NC3 XIIA isoforms are predominant at early stages (E9.5 and 11); at later stages of development (E18.5 and 17) the short NC3 XIIB forms become the major forms. As the

XII collagen, a developmentally regulated extracellular matrix protein in regenerating newt limbs.",
 RL Dev. Biol. 168:503-513(1995).
 CC -I- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the pericollagen matrix (By similarity). Could play a developmental role in regeneration.
 CC -I- SUBUNIT: Trimer of identical chains, each containing 190 kDa of nontriple-helical sequences (By similarity).
 CC -I- DEVELOPMENTAL STAGE: Expression starts at 3 days after amputation in cells of the basal layer of the wound epithelium. At day 10, expression is found in both the basal wound epithelial cells and the distal mesenchyme cells. At mid-bud and late-bud blastema stages, wound epithelium expression has decreased, whereas the mesenchyme remains strongly active in transcription and showed a tendency toward distal regionalization. Condensing cartilage shows largely restricted to the perichondrium.
 CC -I- PTM: The triple-helical tail is stabilized by disulfide bonds at each end (By similarity).
 CC -I- PTM: Proline at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By similarity).
 CC -I- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
 CC -I- SIMILARITY: Contains 2 VMPA domains.
 CC -----
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 CC -----
 DR EMBL: U19494; AAA80217.1; -.
 DR PIR: I51027; I51027.
 DR HSBP: P02751; IENA.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR02035; VWF_A.
 DR Pfam: PF00041; FN3; 7.
 DR Pfam: PF00042; FN3; 2.
 DR PRINTS: PR00453; VWFADOMAIN.
 DR SMART: SM00060; FN3; 4.
 DR SMART: SM00327; VMA; 1.
 DR PROSITE: PS50234; VMPA; 2.
 KM Extracellular matrix; Connective tissue; Repeat; Cell adhesion;
 KM Collagen; Glycoprotein.
 FT NON TER 1
 FT DOMAIN 1
 FT 63 49 VMA 1.
 FT 154 154 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 155 245 FIBRONECTIN TYPE-III 2.
 FT 246 338 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 339 432 FIBRONECTIN TYPE-III 4.
 FT 433 519 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 520 612 FIBRONECTIN TYPE-III 6.
 FT 612 805 VMA 2.
 FT 805 907 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 908 929 FIBRONECTIN TYPE-III 8.
 FT 929 929 O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
 FT CARBOHYD 231 231 (POTENTIAL).
 FT 324 324 O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
 FT CARBOHYD 415 415 O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
 FT 98 98 CARBOHYD
 FT NON TER 929 929 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 929 AA; 101647 MW; AE5D7485254FD954 CRC64;
 Query Match Score 47; DB 1; Length 929;
 Best Local Similarity 66.7%; Pred. No. 3.6;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 DITDSSIGLRMT 13
 Db 350 DITDTRIGSWT 361
 RESULT 10
 ID FINC_BOVIN STANDARD; PRT; 2265 AA.
 AC P07589;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin (FN).
 GN FN1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_Taxid:9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87054047; PubMed=3780752;
 RA Skoretengard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
 RT "Complete primary structure of bovine plasma fibronectin.",
 RL Eur. J. Biochem. 161:441-453(1986).
 RN [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=83117805; PubMed=6218503;
 RA Petersen T.E., Thorgersen H.C., Skoretengard K., Vibe-Pedersen K.,
 RA Sahl P., Soltup-Jensens L., Magnusson S.;
 RT "Partial primary structure of bovine plasma fibronectin: three types of internal homology",
 RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
 RN [3]
 RP SEQUENCE OF 2170-2265 FROM N.A.
 RX MEDLINE=83221567; PubMed=6304699;
 RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
 RT "Isolation and characterization of cDNA clones for human and bovine fibronectins",
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
 CC -I- FUNCTION: Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape.
 CC -I- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS. CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
 CC NO A LESSER EXTEND HOMODIMERS.
 CC -I- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced. Each of the "extra domain" and the connecting strand 3 are present in some forms of fibronectin and absent in others;
 CC Name=1;
 CC -I- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted by hepatocytes. Cellular FN (dimeric or cross-linked multimeric forms), made by fibroblasts, epithelial and other cell types, is deposited as fibrils in the extracellular matrix.
 CC -I- PTM: Sulfated (By similarity).
 CC -I- SIMILARITY: Contains 12 fibronectin type I domains.
 CC -I- SIMILARITY: Contains 2 fibronectin type II domains.
 CC -I- SIMILARITY: Contains 15 fibronectin type III domains.
 CC -----
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RX MEDLINE=87030890; PubMed=3770189;
RA Gutman A., Yamada K.M., Kornblith A.R.;
RT "Human fibronectin is synthesized as a pre-polypeptide.";
RL FEBS Lett. 207:145-148(1986).
RN [4]
RP SEQUENCE OF 1-49 FROM N.A.
RX MEDLINE=87175578; PubMed=3031656;
RA Dean D.C., Bowlin C.L., Bourgeois S.;
RT "Cloning and analysis of the promoter region of the human fibronectin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).
RN [5]
RP SEQUENCE OF 28-2386 FROM N.A. (ISOFORM 3).
RX MEDLINE=85264965; PubMed=2992939;
RA Kornblith A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;
RT "Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene.";
RL EMO J. 4:1755-1759(1985).
RN [6]
RP SEQUENCE OF 103-481 AND 2228-2386 FROM N.A. (ISOFORMS 1, 3, 8 AND 9).
RC TISSUE=Periphereal blood T-cell, and umbilical vein endothelial cells;
RA Godfrey H.P., Ebrahim A.A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 973-2386 FROM N.A. (ISOFORM 3).
RX MEDLINE=84272258; PubMed=6462919;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats.";
RL Nucleic Acids Res. 12:5853-5868(1984).
RN [8]
RP SEQUENCE OF 1232-1782 FROM N.A. (ISOFORM 7).
RX MEDLINE=88233940; PubMed=3375063;
RA Palella G., Henschliffe C., Sebastio G., Baralle F.E.;
RT "Sequence analysis and in vivo expression show that alternative splicing of ED-B and ED-A regions of the human fibronectin gene are independent events.";
RL Nucleic Acids Res. 16:3545-3557(1988).
RN [9]
RP SEQUENCE OF 1257-1365 FROM N.A. (ISOFORM 11).
RX MEDLINE=88041070; PubMed=3478690;
RA Gutman A., Kornblith A.R.;
RT "Identification of a third region of cell-specific alternative splicing in human fibronectin mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7179-7182(1987).
RN [10]
RP SEQUENCE OF 1441-1548.
RX MEDLINE=82265604; PubMed=7050098;
RA Pletschbacher W.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
RT "The cell attachment domain of fibronectin. Determination of the primary structure.";
RL J. Biol. Chem. 257:9593-9597(1982).
RN [11]
RP SEQUENCE OF 1448-1540 FROM N.A.
RX MEDLINE=83290929; PubMed=6686418;
RA Oldberg A., Linney E., Ruoslahti E.;
RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell attachment domain in human fibronectin.";
RL J. Biol. Chem. 258:10193-10196(1983).
RN [12]
RP SEQUENCE OF 1448-1540 FROM N.A.
RX MEDLINE=86111901; PubMed=3003095;
RA Oldberg A., Ruoslahti E.;
RT "Evolution of the fibronectin gene. Exon structure of cell attachment domain.";
RL J. Biol. Chem. 261:2113-2116(1986).
RN [13]
RP SEQUENCE OF 1594-2386 FROM N.A. (ISOFORM 1).
RX MEDLINE=85280409; PubMed=292573;
RA Bernard M.P., Kolbe M., Weil D., Chu M.-L.;
RT "Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat identifies primary structural domains separated by hypervariable regions.";

RL Biochemistry 24:2698-2704(1985).
RN [14]
RP SEQUENCE OF 1712-1739 FROM N.A.
RX MEDLINE=87026578; PubMed=3021206;
RA Sekiguchi K., Kios A.M., Kurauchi K., Yoshitake S., Hakomori S.;
RT "Human liver fibronectin complementary DNAs: identification of two different messenger RNAs possibly encoding the alpha and beta subunits of plasma fibronectin.";
RL Biochemistry 25:4936-4941(1986).
RN [15]
RP SEQUENCE OF 1788-2386 FROM N.A. (ISOFORMS 4, 5 AND 6).
RC TISSUE=Cartilage;
RX MEDLINE=22126816; PubMed=12127832;
RA Parker A.E., Bourell J., Carr A., Maciewicz R.A.;
RT "Novel cartilage-specific splice variants of fibronectin.";
RL Osteoarthritis Cartilage 10:528-534(2002).
RN [16]
RP SEQUENCE OF 32-290.
RX MEDLINE=84032463; PubMed=6630202;
RA Garcia-Pardo A., Pearlsrein B., Pangione B.;
RT "Primary structure of human plasma fibronectin. The 29,000-dalton NH2-terminal domain.";
RL J. Biol. Chem. 258:12670-12674(1983).
RN [17]
RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
RX MEDLINE=87080265; PubMed=3024962;
RA Owens R.J., Baralle F.E.;
RT "Mapping the collagen-binding site of human-fibronectin by expression in Escherichia coli.";
RL EMO J. 5:2825-2830(1986).
RN [18]
RP SULFATION.
RX MEDLINE=86042625; PubMed=2414772;
RA Liu M.C., Yu S., Sy U., Redman C.M., Lipmann F.;
RT "Tyrosine sulfation of proteins from the human hepatoma cell line HepG2.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
RN [19]
RP O-GLYCOSYLATION OF THR-2064.
RX MEDLINE=91190085; PubMed=2012601;
RA Tresselt T., McCarthy J.B., Calaycay J., Lee T.D., Legesse K., Shively J.E., Pande H.;
RT "Human plasma fibronectin. Demonstration of structural differences between the A- and B-chains in the III CS region.";
RL Biochem. J. 274:731-738(1991).
RN [20]
RP FBIN1-BINDING SITE.
RX MEDLINE=93015879; PubMed=1400330;
RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K., Argaves W.S.;
RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding region of fibronectin.";
RL J. Biol. Chem. 267:20120-20125(1992).
RN [21]
RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
RX MEDLINE=9508153; PubMed=7989369;
RA Rosagano A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
RT "Further characterization of the NH2-terminal fibrin-binding site on fibronectin.";
RL J. Biol. Chem. 269:31938-31945(1994).
RN [22]
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=92162710; PubMed=1311202;
RA Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J., Campbell I.D.;
RT "1H NMR assignment and secondary structure of the cell adhesion type III module of fibronectin.";
RL Biochemistry 31:2068-2073(1992).
RN [23]
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=93046665; PubMed=1423622;
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;
RT "The three-dimensional structure of the tenth type III module of

RT fibronectin: an insight into RGD-mediated interactions.";
 RL Cell 71:671-678(1992).
 RP STRUCTURE BY NMR OF 182-275.
 RX MEDLINE=94141923; PubMed=8308892.
 RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,
 RA Campbell I.D.;
 RT "Solution structure of a pair of fibronectin type 1 modules with
 RT fibrin binding activity.";
 RL J. Mol. Biol. 235:1302-1311(1994).
 RP STRUCTURE BY NMR OF 32-92.
 RX MEDLINE=96065779; PubMed=7583666;
 RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;
 RT "High-resolution structural studies of the factor XIIIa crosslinking
 RT site and the first type 1 module of fibronectin.";
 RL Nat. Struct. Biol. 2:946-950(1995).
 RP STRUCTURE BY NMR OF 406-464.
 RX MEDLINE=96179558; PubMed=9514732;
 RA Sticht H., Pickford A.R., Potts J.R., Campbell I.D.;
 RT "Solution structure of the glycosylated second type 2 module of
 RT fibronectin.";
 RL J. Mol. Biol. 276:177-187(1998).
 RP STRUCTURE BY NMR OF EXTRA ED-B DOMAIN FROM ISOFORM 7.
 Query Match 58.2%; Score 46; DB 1; Length 2386;
 Best Local Similarity 57.1%; Pred. No. 14;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

1 VDIRSSIGRMP 14
 1006 VNEDTSVLVWRMP 1019

RESULT 12
 TENX HUMAN STANDARD; PRT; 4289 AA.
 ID TENX_HUMAN P22105; P78530; Q08424; Q9DUG7;
 AC P22105; P78530; Q08424; Q9DUG7;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tenascin X precursor (TN-X) (Hexabrachion-like).
 GN TNXB OR TNX OR XB OR HXBL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_Taxid=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Dalkers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,
 RA Banta A., Schwartz S., Smith T.M., Spies T., Hood L.;
 RT "Sequence determination of 300 kilobases of the human class III MEC
 RT locus.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE OF 1-747 AND 1687-1944 FROM N.A.
 RC TISSUE=Leukocyte; PubMed=7686164;
 RX MEDLINE=93300909; PubMed=7686164;
 RA Bristow J., Tee M.K., Gitelman S.E., Mellon S.H., Miller W.L.;
 RT "Tenascin-X: a novel extracellular matrix protein encoded by the human
 RT XB gene overlapping P450C21B.";
 RL J. Cell Biol. 122:265-278(1993).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM XB-SHORT).
 RC TISSUE=Adrenal gland;
 RX MEDLINE=96015044; PubMed=8530023;
 RA Tee M.K., Thomson A.A., Bristow J., Miller W.L.;
 RT "Sequences promoting the transcription of the human XB gene
 RT overlapping P450C21B correctly predict the presence of a novel,
 RT adrenal-specific, truncated form of tenascin-X.";
 RL Genomics 28:171-178(1995).

RP SEQUENCE OF 1-23 FROM N.A.
 RC TISSUE=Fetal adrenal gland;
 RX MEDLINE=97081760; PubMed=8923003;
 RA Speck M., Barry F., Miller W.L.;
 RT "Alternate promoters and alternate splicing of human tenascin-X, a
 RT gene with 5' and 3' ends buried in other genes.";
 RL Hum. Mol. Genet. 5:1749-1758(1996).
 RP SEQUENCE OF 3470-4289 FROM N.A.
 RX MEDLINE=89367293; PubMed=2475872;
 RA Morel Y., Bristow J., Gitelman S.E., Miller W.L.;
 RT "Transcript encoded on the opposite strand of the human steroid 21-
 RT hydroxylase/complement component C4 gene locus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:6582-6586(1989).
 RP DISEASE.
 RX MEDLINE=21468843; PubMed=11642233;
 RA Schalkwijk J., Zweers M.C., Steijlen P.M., Dean W.B., Taylor G.,
 RA van Vlijmen I.M., van Haren B., Miller W.L., Bristow J.;
 RT "A recessive form of the Ehlers-Danlos syndrome caused by tenascin-X
 RT deficiency.";
 RL New Engl. J. Med. 345:1167-1175(2001).
 CC -1- FUNCTION: Appears to mediate interactions between cells and the
 CC extracellular matrix. Substrate-adhesion molecule that appears to
 CC inhibit cell migration. May play a role in supporting the growth
 CC of epithelial tumors.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=XB;
 CC IsoId=P22105-1; Sequence=Displayed;
 CC Name=XB-short;
 CC IsoId=P22105-2; Sequence=VSP_001418;
 CC -1- TISSUE SPECIFICITY: Highly expressed in fetal adrenal, in fetal
 CC testis, fetal smooth, striated and cardiac muscle. Isoform XB-
 CC short is only expressed in the adrenal gland.
 CC -1- DISEASE: Association with congenital adrenal hyperplasia.
 CC -1- DISEASE: Defects in TNXB are the cause of Ehlers-Danlos-like
 CC syndrome [MIM:606408]. This clinically distinct form of Ehlers-
 CC Danlos syndrome is characterized by hyperextensible skin,
 CC hypermobile joints, and tissue fragility, but it lacks atrophic
 CC scars and delayed wound healing. Inheritance is autosomal
 CC recessive.
 CC -1- SIMILARITY: Contains 19 EGF-like domains.
 CC -1- SIMILARITY: Contains 32 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 fibronectin C-terminal domain.
 CC -1- CAUTION: There are two genes for TN-X: TNXA and TNXB.
 CC partial gene which can sometimes recombine with TNXB.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, U89337; AA847488.1; -;
 DR EMBL, AF019413; AA857981.1; -;
 DR EMBL, X71923; CA850739.1; -;
 DR EMBL, Y13783; CA874109.1; -;
 DR EMBL, Y13783; CA874110.1; -;
 DR EMBL, U24488; AA841287.1; -;
 DR EMBL, U52696; AAC50889.1; -;
 DR EMBL, M25813; AA835884.1; -;
 DR FIR, A40701; A40701.
 DR HSSP, P02671; 1F2D.
 DR GeneW, HGNC:11976; TNXB.
 DR MIM, 600985; -;
 DR GO, GO:0005578; C:extracellular matrix; NAS.

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DR GO:0007160; P:cell-matrix adhesion; NAS.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR002049; Laminin_EGF.
 DR Pfam; PF00008; EGF_8.
 DR Pfam; PF00147; fibrinogen_C_1.
 DR Pfam; PF00041; fn3_33.
 DR PRINTS; PRO0011; EGF_LAMININ.
 DR SMART; SM00181; EGF_7.
 DR SMART; SM00186; FBG_1.
 DR SMART; SM00060; FN3_30.
 DR PROSITE; PS00022; EGF_1_18.
 DR PROSITE; PS01186; EGF_3_19.
 DR PROSITE; PS00026; EGF_5_8.
 DR PROSITE; PS00514; FIBRIN_Ag_C_DOMAIN_1.
 DR GlycoProtein; Cell adhesion; Repeat; EGF-like domain; Coiled coil;
 KW Extracellular matrix; Alternative splicing; Signal;
 KW Ehlers-Danlos syndrome.
 FT SIGNAL 1 23
 FT CHAIN 24 4289
 FT DOMAIN 156 168 EGF-Like 1 (INCOMPLETE).
 FT DOMAIN 183 213 EGF-Like 2.
 FT DOMAIN 214 244 EGF-Like 3.
 FT DOMAIN 245 275 EGF-Like 4.
 FT DOMAIN 276 306 EGF-Like 5.
 FT DOMAIN 307 337 EGF-Like 6.
 FT DOMAIN 338 368 EGF-Like 7.
 FT DOMAIN 369 399 EGF-Like 8.
 FT DOMAIN 400 430 EGF-Like 9.
 FT DOMAIN 431 461 EGF-Like 10.
 FT DOMAIN 462 492 EGF-Like 11.
 FT DOMAIN 493 523 EGF-Like 12.
 FT DOMAIN 524 554 EGF-Like 13.
 FT DOMAIN 555 585 EGF-Like 14.
 FT DOMAIN 586 616 EGF-Like 15.
 FT DOMAIN 617 647 EGF-Like 16.
 FT DOMAIN 648 679 EGF-Like 17.
 FT DOMAIN 684 714 EGF-Like 18.
 FT DOMAIN 715 746 EGF-Like 19.
 FT DOMAIN 746 776 EGF-Like 19.
 FT DOMAIN 792 822 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 922 952 COILED COIL (POTENTIAL).
 FT DOMAIN 951 1021 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 1047 1127 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 1149 1226 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 1246 1327 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 1348 1429 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 1459 1540 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 1561 1642 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 1659 1736 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1756 1836 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 1856 1939 FIBRONECTIN TYPE-III 11.
 FT DOMAIN 1962 2039 FIBRONECTIN TYPE-III 12.
 FT DOMAIN 2069 2150 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 2167 2248 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 2266 2347 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 2365 2446 FIBRONECTIN TYPE-III 16.
 FT DOMAIN 2471 2552 FIBRONECTIN TYPE-III 17.
 FT DOMAIN 2582 2663 FIBRONECTIN TYPE-III 18.
 FT DOMAIN 2688 2769 FIBRONECTIN TYPE-III 19.
 FT DOMAIN 2794 2875 FIBRONECTIN TYPE-III 20.
 FT DOMAIN 2889 2972 FIBRONECTIN TYPE-III 21.
 FT DOMAIN 2997 3078 FIBRONECTIN TYPE-III 22.
 FT DOMAIN 3105 3186 FIBRONECTIN TYPE-III 23.
 FT DOMAIN 3211 3292 FIBRONECTIN TYPE-III 24.
 FT DOMAIN 3307 3384 FIBRONECTIN TYPE-III 25.
 FT DOMAIN 3399 3481 FIBRONECTIN TYPE-III 26.
 FT DOMAIN 3494 3575 FIBRONECTIN TYPE-III 27.
 FT DOMAIN 3601 3682 FIBRONECTIN TYPE-III 28.
 FT DOMAIN 3699 3787 FIBRONECTIN TYPE-III 29.
 FT DOMAIN 3801 3879 FIBRONECTIN TYPE-III 30.

FT DOMAIN 3890 3971 FIBRONECTIN TYPE-III 31.
 FT DOMAIN 3978 4059 FIBRONECTIN TYPE-III 32.
 FT DOMAIN 4071 4289 FIBRINOGEN C-TERMINAL.
 FT SITE 1748 1750 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 187 197 BY SIMILARITY.
 FT DISULFID 191 202 BY SIMILARITY.
 FT DISULFID 204 213 BY SIMILARITY.
 FT DISULFID 218 228 BY SIMILARITY.
 FT DISULFID 222 233 BY SIMILARITY.
 FT DISULFID 235 244 BY SIMILARITY.
 FT DISULFID 249 259 BY SIMILARITY.
 FT DISULFID 253 264 BY SIMILARITY.
 FT DISULFID 266 275 BY SIMILARITY.
 FT DISULFID 280 290 BY SIMILARITY.
 FT DISULFID 284 295 BY SIMILARITY.
 FT DISULFID 297 306 BY SIMILARITY.
 FT DISULFID 311 321 BY SIMILARITY.
 FT DISULFID 315 326 BY SIMILARITY.
 FT DISULFID 328 337 BY SIMILARITY.

Query Match 58.2%; Score 46; DB 1; Length 4289;
 Best Local Similarity 58.3%; Pred. No. 25;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 DITDSIGLRWT 13
 Db 1571 DVTNSVGLSWT 1582

RESULT 13
 ID DFFA HUMAN STANDARD; PRT; 331 AA.
 AC 000273; Q96197; Q96C6;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 15-MAR-2004 (Rel. 43; Last annotation update)
 DE DNA fragmentation factor alpha subunit (DNA fragmentation factor 45
 kDa subunit) (DFF-45) (inhibitor of CAD) (ICAD).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Carnivora; Homiidae; Homo.
 OC NCBI_Taxid=9606;
 RX MEDLINE=99339996; PubMed=10409614;
 RA Gu J.J., Dong R.P., Zhang C., McLaughlin D.F., Wu M.X.,
 RT "DFF, a heterodimeric protein that functions downstream of caspase-3
 to trigger DNA fragmentation during apoptosis.";
 RL Cell 89:175-184(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFOR DFF45), AND SEQUENCE OF 171-181; 190-201;
 RP 214-218 AND 230-242.
 RX MEDLINE=97262059; PubMed=9108473;
 RA Liu X., Zou H., Slaughter C., Wang X.;
 RT "DFF, a heterodimeric protein that functions downstream of caspase-3
 to trigger DNA fragmentation during apoptosis.";
 RL Cell 89:175-184(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFOR DFF45).
 RX MEDLINE=99339996; PubMed=10409614;
 RA Gu J.J., Dong R.P., Zhang C., McLaughlin D.F., Wu M.X.,
 RT "Functional interaction of DFF45 and DFF45 with caspase-activated DNA
 fragmentation nuclease DFF40.";
 RL J. Biol. Chem. 274:20759-20762(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFOR DFF45).
 RX MEDLINE=99339996; PubMed=10409614;
 RA Oh J.J., Grosshans D.R., Wong S.G., Slamon D.J.;
 RT "Identification of differentially expressed genes associated with
 HER-2/neu overexpression in human breast cancer cells.";
 RL Nucleic Acids Res. 27:4008-4017(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFOR DFF45).
 RX TISSUE=Eye, Kidney, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schneetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman W., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP STRUCTURE BY NMR OF 11-100.
RX MEDLINE=21265459; PubMed=11371636;
RA Zhou P., Lugovskoy A.A., McCarthy J.S., Li P., Wagner G.;
RT "Solution structure of DFP40 and DFP45 N-terminal domain complex and
RT mutual chaperone activity of DFP40 and DFP45.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:6051-6055(2001).
CC -1- FUNCTION: Inhibitor of the caspase-activated DNase (DFF40).
CC -1- SUBUNIT: Heterodimer of a 45 kDa and a 40 kDa subunit.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=DFF45;
CC IsoId=000273-1; Sequence=Displayed;
CC Name=DFF35;
CC IsoId=000273-2; Sequence=VSP_001085, VSP_001086;
CC -1- PM: CASPASE-3 CLEAVES DFF45 AT 2 SITES TO GENERATE AN ACTIVE
CC FACTOR.
CC -1- SIMILARITY: Contains 1 CIDB-N domain.
CC -----
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CC -----
CC EMBL; U91985; AAC51249.1; -;
CC DR EMBL; AF087573; AAD32953.1; -;
CC DR EMBL; AF103799; AAF02419.1; -;
CC DR EMBL; BC000037; AAH00037.1; -;
CC DR EMBL; BC007112; AAH07112.1; -;
CC DR EMBL; BC007721; AAH07721.1; -;
CC DR PDB; 1IBX; 30-MAY-01.
CC DR PDB; 1IYR; 25-SEP-02.
CC DR PDB; 1KOY; 18-SEP-02.
CC DR Genew: HGNC:2772; DFFA.
CC MIM: 601882;
CC DR GO; GO:0005829; C:cytosol; TAS.
CC DR GO; GO:0005634; C:nucleus; TAS.
CC DR GO; GO:0004537; F:caspase-activated deoxyribonuclease activity; TAS.
CC DR GO; GO:0006309; P:DNA fragmentation; TAS.
CC DR GO; GO:0007242; P:intracellular signaling cascade; TAS.
CC DR InterPro: IPR003508; CAD.
CC DR Pfam: PF02017; CIDB-N; 1.
CC DR SMART; SM00286; CAD; 1.
CC DR Apoptosis; Alternative splicing; 3D-structure.
CC DR DOMAIN 17 96
CC FT SITE 117 118 CLEAVAGE (BY CASPASE-3).
CC FT SITE 224 225 CLEAVAGE (BY CASPASE-3).
CC FT VARSPLC 262 268 LVTKEAD -> VGSNGOH (in isoform DFF35).
CC FT VARSPLC 269 331 /FTId=VSP_001085.
CC FT VARSPLC 269 331 Missing (in isoform DFF35).
CC FT VARSPLC 269 331 /FTId=VSP_001086.
CC FT VARSPLC 269 331 R -> W (in REF. 4; AAH07721).
CC FT CONFLICT 291 291

FT STRAND 22 22
FT STRAND 24 24
FT STRAND 31 31
FT HELIX 39 50
FT TURN 51 51
FT TURN 55 56
FT STRAND 60 63
FT TURN 64 66
FT STRAND 69 69
FT HELIX 73 78
FT STRAND 84 88
SQ SEQUENCE 331 AA; 36521 MW; 8656FE45DB003DF3 CRC64;
Query Match 55.7%; Score 44; DB 1; Length 331;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 VDITDSSTGLRW 12
DB 113 VDITDSGAGLKW 124
RESULT 14
ID Y180_ARATH STANDARD; PRT; 357 AA.
AC 080543;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein At1g22800.
DE AT1G22800 OR T22Y18.3.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Bueller E., Chan A., Chen Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huzar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.B., Kremenetskaia I., Kurtz D.B., Kwan S., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
RA Miltner J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Tatum M.J., Town C.D.,
RA Utechtback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana".
RL Nature 408:816-820 (2000).
CC -1- SIMILARITY: TO R.FROMAZEKII RP459.
CC -----
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CC -----
CC EMBL; AC003979; AAC25509.1; -;
CC DR EMBL; T00764; T00764.
CC DR PIR; T00764; T00764.
CC DR Hypothetical protein.
SQ SEQUENCE 357 AA; 39972 MW; C249EC58130F8944 CRC64;

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us-10-676-049-1.open.rsp

Page 18

Db 293 DIDSAMGTWVP 305
Search completed: September 21, 2004, 05:47:28
Job time : 8.30147 secs

RA Retenmier C.W., Rousset M.F.;
RT "Differential processing of colony-stimulating factor 1 precursors
RT encoded by two human cDNAs.";
RL Mol. Cell. Biol. 8:5026-5034(1988).
RN (13)
RP CHARACTERIZATION; PubMed=1531650;
RX MEDLINE=92165782; PubMed=1531650;
RA Suzu S., Ohtsuki T., Yanai N., Takatsu Z., Kawashima T., Takaku F.,
RA Nagata N., Motoyoshi K.;
RT "Identification of a high molecular weight macrophage colony-
RT stimulating factor as a glycosaminoglycan-containing species.";
RL J. Biol. Chem. 267:4345-4348(1992).
RN (14)
RP DISULFIDE BONDS;
RX MEDLINE=91136140; PubMed=8422357;
RA Glocker M.O., Arbogast B., Schreurs J., Deiner M.L.;
RT "Assignment of the inter- and intramolecular disulfide linkages in
RT recombinant human macrophage colony stimulating factor using fast
RT atom bombardment mass spectrometry.";
RL Biochemistry 32:482-488(1993).
RN (15)
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 33-190.
RX MEDLINE=93088061; PubMed=1455231;
RA Pandit J., Bohm A., Jancarik J., Halenbeck R., Koehn K., Kim S.H.;
RT "Three-dimensional structure of dimeric human recombinant macrophage
RT colony-stimulating factor.";
RL Science 258:1358-1362(1992).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. CSF-
CC 1 induces cells of the monocyte/macrophage lineage. It plays a
CC role in immunological defenses, bone metabolism, lipoproteins
CC clearance, fertility and pregnancy.
CC -1- SUBUNIT: Homodimer or heterodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Predominantly extracellular. Isoform 3
CC exists as an integral membrane protein, only slowly released by
CC proteolytic cleavage.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=P09603-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P09603-2; Sequence=VSP_001188;
CC Name=3;
CC IsoId=P09603-3; Sequence=VSP_001187;
CC -1- PTM: Glycosylation and proteolytic cleavage yield different
CC soluble forms. A high molecular weight soluble form is a
CC proteoglycan containing chondroitin sulfate.
CC -1- PTM: Isoform 1 is N- and O-glycosylated. Isoform 3 is N-
CC glycosylated.
CC -----
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CC -----
DR EMBL, M11286; AAB59527.1; -
DR EMBL, M11038; AAB59527.1; JOINED.
DR EMBL, M11295; AAB59527.1; JOINED.
DR EMBL, M37435; AAB52117.1; -
DR EMBL, M64592; AAB59572.1; -
DR EMBL, U22386; AAB64849.1; -

Query Match 55.7%; Score 44; DB 1; Length 554;
Best Local Similarity 53.8%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

2 DITDSIGRMT 14

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53 ; Search time 23.6029 Seconds
(without alignments)
200.516 Million cell updates/sec

Title: US-10-676-049-1

Perfect score: 79

Sequence: 1 VDIRDSSIGLRMTPL 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organella:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	90	Q28253	Q28253 canis fam11
2	67	84.8	134	Q9M232	Q9M232 bos taurus
3	59	74.7	2478	Q93406	Q93406 brachydanio
4	48	60.8	1282	Q90X86	Q90X86 xenopus lae
5	47	59.5	4135	Q18977	Q18977 bos taurus
6	47	59.5	19066	Q801W8	Q801W8 brachydanio
7	46	58.2	253	Q9XSG0	Q9XSG0 oryctolagus
8	46	58.2	865	Q9NPK7	Q9NPK7 homo sapien
9	46	58.2	865	Q9Y464	Q9Y464 homo sapien
10	46	58.2	4288	Q9NPK9	Q9NPK9 homo sapien
11	45	57.0	26926	Q8WZB3	Q8WZB3 homo sapien
12	45	57.0	26926	Q10466	Q10466 homo sapien
13	45	57.0	34350	Q8WZ42	Q8WZ42 homo sapien
14	44	55.7	355	Q84MB4	Q84MB4 arabidopsis
15	44	55.7	395	Q887F7	Q887F7 pseudomonas
16	44	55.7	637	Q81VX1	Q81VX1 homo sapien

17	44	55.7	1274	Q9UM53	Q9UM53 homo sapien
18	44	55.7	4006	Q35452	Q35452 mus musculus
19	44	55.7	4114	Q54796	Q54796 mus musculus
20	43.5	55.1	323	Q8DKK6	Q8DKK6 synechococ
21	43.5	55.1	392	Q8DXD0	Q8DXD0 escherichia
22	43.5	55.1	392	Q8FE61	Q8FE61 escherichia
23	43	54.4	320	P72908	P72908 synechocyst
24	43	54.4	340	Q8CKX2	Q8CKX2 streptomyces
25	43	54.4	374	Q7UI13	Q7UI13 rhodospirillum
26	43	54.4	521	Q8LEB1	Q8LEB1 arabidopsis
27	43	54.4	523	Q8LPR6	Q8LPR6 arabidopsis
28	43	54.4	529	Q8SM78	Q8SM78 arabidopsis
29	43	54.4	623	Q7SZG1	Q7SZG1 tuiga rubrip
30	43	54.4	1115	Q9HD43	Q9HD43 homo sapien
31	43	54.4	1118	Q15426	Q15426 homo sapien
32	43	54.4	1402	Q9Y7G6	Q9Y7G6 neurospora
33	43	54.4	4621	Q7VHE6	Q7VHE6 mus musculus
34	42.5	53.8	1121	Q7UKC6	Q7UKC6 rhodospirillum
35	42	53.2	973	Q8P148	Q8P148 xanthomonas
36	42	53.2	1136	Q8K2V0	Q8K2V0 mus musculus
37	42	53.2	1136	Q8C109	Q8C109 mus musculus
38	42	53.2	1532	Q90994	Q90994 gallus galli
39	42	53.2	1714	Q90995	Q90995 gallus galli
40	42	53.2	1810	Q90824	Q90824 gallus galli
41	42	53.2	4039	Q7ZZ46	Q7ZZ46 brachydanio
42	42	53.2	18412	Q7ZZ61	Q7ZZ61 brachydanio
43	41.5	52.5	2313	Q8WHW9	Q8WHW9 psilocybe nu
44	41	51.9	81	Q8PBW8	Q8PBW8 xanthomonas
45	41	51.9	114	Q8NPF29	Q8NPF29 homo sapien

ALIGNMENTS

RESULT 1
ID Q28253 PRELIMINARY; PRT; 90 AA.

AC Q28253;
DT 01-NOV-1996 (TRENBERG, 01, Created)
DT 01-NOV-1996 (TRENBERG, 01, Last sequence update)
DT 01-OCT-2003 (TRENBERG, 25, Last annotation update)
DE Fibronectin ED-B (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Carnivora; Fissipedata; Canidae; Canis.
NCBI_Taxid=9615;
RN [1]
RP
RX MEDLINE=95130563; PubMed=7829518;
RA Zhang D.W., Burton-Murster N., Just G.;
RT "Alternative splicing of ED-A and ED-B sequences of fibronectin pre-
RT mRNA differs in chondrocytes from different cartilaginous tissues and
RT can be modulated by biological factors";
RL J. Biol. Chem. 270:1817-1822(1995).
DR EMBL; U16208; AA67749.1; -.
DR PIR; I46162; I46162.
DR HSSP; P02751; ITPF.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; FN3; 1.
DR SMART; SM00060; FN3; 1.
FT NON_TER
FT TER
SQ SEQUENCE 90 AA; 9585 MW; 766781BDF6511848 CRC64;

Query Match 100.0%; Score 79; DB 6; Length 90;
Best local similarity 100.0%; Pred. No. 6,4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDIRDSSIGLRMTPL 15
DB 10 VDIRDSSIGLRMTPL 24

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RESULT 2
09MZ32 . PRELIMINARY; PRT; 134 AA.
ID 09WZ32 AC
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fibronectin ED-B+ region (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA De Candia L.M., Rodgers R.J.;
RT "Characterization of the expression of the alternative splicing of ED-
RT A, ED-B and V regions of fibronectin mRNA in bovine ovarian follicles
RT and corpora lutea."
RL Reprod. Fertil. Dev. 0:0-0(2000).
DR EMBL; AF260304; AAF91380.1; -.
DR HSSP; P02751; 1ENF.
DR InterPro; IPR003961; FN_II.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR NON TER 1
FT NON TER 134
FT NON TER 134
SQ SEQUENCE 134 AA; 14408 MW; 820971B2619A48A5 CRC64;

Query Match 84.8%; Score 67; DB 6; Length 134;
Best Local Similarity 86.7%; Pred. NO. 0.0012;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDIIDSSIGLRWTP 15
DB 39 VDISDSIGLRWTP 53

RESULT 3
ID 093406 PRELIMINARY; PRT; 2478 AA.
AC 093406;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fibronectin.
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao Q., Colloidi P.;
RT "Characterization and expression of zebrafish fibronectin.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081128; AAC31947.1; -.
DR HSSP; P02751; 1FBR.
DR ZFIN; ZDB-GENE-000426-1; fn1.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibrinctn.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17

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DR Prodom; PD000995; FN_Type_11; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 14.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 11.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
SQ SEQUENCE 2478 AA; 271652 MW; A034475C5A3B5750 CRC64;

Query Match 74.7%; Score 59; DB 13; Length 2478;
Best Local Similarity 60.8%; Pred. No. 0.73;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDITDSIGLRWTP 15
:::|||:|||:|
Db 1274 INVTDSTIGLSWSPL 1288

RESULT 4
Q90X86 PRELIMINARY; PRT; 1282 AA.
AC Q90X86;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cardiac myosin-binding protein C.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Heart;
RC Duan L.-J., George M.E., Drysdale T.A.;
RT "Developmental Expression of Cardiac Myosin-Binding Protein C in
RT Xenopus."
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF417472; AAI15871.1; -
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FNIII.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; IG_II-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00041; FN3; 3.
DR Pfam; PF00047; Ig; 8.
DR PRINTS; PR00014; FNTPPEIIT.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PSS0835; IG_LIKE; 5.
KW Immunoglobulin domain; Repeat.
KV SEQUENCE 1282 AA; 144076 MW; 11E649F0CF3C2D40 CRC64;

Query Match 60.8%; Score 48; DB 13; Length 1282;
Best Local Similarity 53.8%; Pred. NO. 28;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 DIITSIGLRWTP 14
||:|||:|||
Db 888 DVSDTISILKWRP 900

RESULT 5
O18977 PRELIMINARY; PRT; 4135 AA.
AC O18977;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tenascin-X.
GN TN-X.
OS Bos taurus (Bovine).

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QY 2 DITDSIGLRWTP 14
|:|:|:|:|
Db 91 DVQDNISVRLWLP 103

RESULT 8

Q9NPK7 PRELIMINARY; PRT; 865 AA.
AC Q9NPK7;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE DJ34F7.1.3 (Tenascin XB (isoform 3)) (Fragment).
GN DJ34F7.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049547; CAB89298.1; -
DR HSSP; P02751; ITTP.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; FN3; 8.
DR SMART; SM00060; FN3; 7.
FT NON TER 1
FT NON TER 865
SQ SEQUENCE 865 AA; 94083 MW; 66612C9901F6B05E CRC64;

Query Match 58.2%; Score 46; DB 4; Length 865;
Best Local Similarity 58.3%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 9

Q9Y464 PRELIMINARY; PRT; 865 AA.
AC Q9Y464;
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Tenascin-X (Fragment).
GN XB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Exposito J.Y., Eleftheriou F., Garrone R., Lethias C.,
RT "Human tenascin-X. Detection of new fibronectin-type III coding units
and alternative splicing of its pre-mRNA";
RL Submitted (UTL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=93300909; PubMed=7686164;
RA Bristol J., Tee M.K., Gitelman S.E., Mellon S.H., Miller W.L.;
RT "Tenascin-X: a novel extracellular matrix protein encoded by the human
XL XB gene overlapping P450C21B";
RL J. Cell Biol. 122:265-278(1993).
DR EMBL; Y1866; CAA76900.1; -
DR HSSP; P02751; ITTP.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.

DR SMART; SM00060; FN3; 7.
FT NON TER 1
FT NON TER 20
FT CONFLICT 20
FT CONFLICT 534 534 A -> D (IN REF. 2).
FT VARIANT 854 854 T -> S (IN REF. 2).
FT VARIANT 854 854 A -> G.
FT NON TER 865
SQ SEQUENCE 865 AA; 94027 MW; 723C942248DE440F CRC64;

Query Match 58.2%; Score 46; DB 4; Length 865;
Best Local Similarity 58.3%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DITDSIGLRWTP 13
|:|:|:|:|
Db 156 DVTNPSVGLSWT 167

RESULT 10

Q9NPK9 PRELIMINARY; PRT; 4288 AA.
AC Q9NPK9;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE DJ34F7.1.1 (Tenascin XB (isoform 1)).
GN DJ34F7.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049547; CAB89296.1; -
DR HSSP; P02751; ITTP.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002181; Fibrirogen_C.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR006210; IBSF.
DR InterPro; IPR002045; Laminin_EGF.
DR Pfam; PF00008; EGF; 8.
DR Pfam; PF00147; fibrirogen_C; 1.
DR Pfam; PF00041; FN3; 33.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00181; EGF; 7.
DR SMART; SM00186; FBG; 1.
DR SMART; SM00060; FN3; 31.
DR PROSITE; PS00022; EGF_1; 18.
DR PROSITE; PS01186; EGF_2; 19.
DR PROSITE; PS00514; FIBRIN_AG_C_DOWAIN; 1.
KW EGF-like domain.

Query Match 58.2%; Score 46; DB 4; Length 4288;
Best Local Similarity 58.3%; Pred. No. 2,46+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DITDSIGLRWTP 13
|:|:|:|:|
Db 1570 DVTNPSVGLSWT 1581

RESULT 11

Q8WZB3 PRELIMINARY; PRT; 26926 AA.
AC Q8WZB3;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)


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GN TTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=20309627; PubMed=10850961;
RA Freiburg A., Tremblais K., Heil W., Gaziola C., Fougereuse F.,
RA Genter T., Kolmer B., Witt C., Beckmann J.S., Gregorio C.C.,
RA Granzler H., Labelt S.;
RT "Series of exon-skipping events in the elastic spring region of titin
RT as the structural basis for myofibrillar elastic diversity.";
RL CIRC. Res. 86:1114-1121(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=21573839; PubMed=11717165;
RA Bang M.L., Centner T., Fornoff F., Geach A.J., Gotthardt M.,
RA McNabb M., Witt C.C., Labelt D., Gregorio C.C., Granzler H.,
RA Labelt S.;
RT "The complete gene sequence of titin, expression of an unusual -700
RT kDa titin isoform and its interaction with obscurin identify a novel
RT Z-line to I-band linking system.";
RL CIRC. Res. 89:1065-1072(2001).
CC -1 SIMILARITY: CONTAINS 91 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
DR EMBL; AJ277892; CAD12455.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006979; P:response to oxidative stress; IEA.
DR InterPro; IPR002822; Cytok_receptor_2.
DR InterPro; IPR005777; FGfy_kin.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR010921; HLH_basic.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR007119; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00041; fn3_133.
DR Pfam; PF00047; ig_93.
DR Pfam; PF00069; pkinase_1.
DR Pfam; PF00001; Prot_kinase_1.
DR SMART; SM00060; FN3_132.
DR SMART; SM00408; IGC2_22.
DR SMART; SM00220; S_TKc_1.
DR PROSITE; PS00933; FGfy_KINASES_1; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00835; IG_LIKE; 88.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Transferase.
SQ SEQUENCE 26926 AA; 299285 MW; 169AB42637A7C1FB CRC64;

Query Match 57.0%; Score 45; DB 4; Length 26926;
Best Local Similarity 53.8%; Pred. No. 2.8e+03;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

CY 2 DITDSIGLWTP 14
DB 20084 DITDSVTLKWP 20096

RESULT 12
Q10466 PRELIMINARY; PRT; 26926 AA.
AC Q10466;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Titin, heart isoform N2-B (EC 2.7.1.1-) (Connectin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=HEART;
RA MEDLINE=96026330; PubMed=7569978;
RA Labelt S., Kolmer B.;
RT "Titins: giant proteins in charge of muscle ultrastructure and
RT elasticity.";
RL Science 270:293-296(1995).
RN [2]
RP SEQUENCE OF 22277-25376 FROM N.A.
RA MEDLINE=92258380; PubMed=1582406;
RA Labelt S., Gautel M., Lakey A., Trinick J.;
RT "Towards a molecular understanding of titin.";
RL EMO J. 11:1711-1716(1992).
RN [3]
RP SEQUENCE OF 1576-2014 FROM N.A.
RA Labelt S.;
RT Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RA MEDLINE=95331314; PubMed=7607248;
RA Gautel M., Castiglione-Morelli M.A., Pfuhl M., Motta A., Pastore A.;
RT "A calmodulin-binding sequence in the C-terminus of human cardiac
RT titin kinase.";
RL Eur. J. Biochem. 230:752-759(1995).
CC -1 FUNCTION: THIS GIANT MUSCLE PROTEIN MAY BE INVOLVED IN MUSCLE
CC ASSEMBLY AND IN MAINTAINING THE STRUCTURAL INTEGRITY OF
CC SARCOMERES. MAY HAVE PROTEIN KINASE ACTIVITY.
CC -1 TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
CC -1 SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
CC KINASES.
CC -1 SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 112
CC IMMUNOGLOBULIN C2-LIKE DOMAINS AND 132 FIBRONECTIN TYPE III-LIKE
CC DOMAINS.
DR EMBL; X64593; CAA45939.1; -.
DR EMBL; X83270; CAA58243.1; -.
DR EMBL; X64677; CAA45938.1; -.
DR EMBL; X90568; CAA62188.1; -.
DR EMBL; X64639; CAA45940.1; -.
DR PIR; I38344; I38344.
DR PDB; 1BPV; 12-AUG-99.
DR PDB; 1G1C; 12-OCT-01.
DR PDB; 1NCT; 08-NOV-96.
DR PDB; 1NCU; 08-NOV-96.
DR PDB; 1T1T; 11-JUL-96.
DR PDB; 1T1U; 11-JUL-96.
DR PDB; 1TKI; 08-JUN-99.
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005516; F:calmodulin binding; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-claes (D200-domain. . .); IEA.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.
DR GO; GO:0007517; P:muscle development; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006979; P:response to oxidative stress; IEA.

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DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR000577; FG_Y_Kin.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003598; Ig_Like.
DR InterPro; IPR003005; IG_MHC.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00041; fn3; 132.
DR Pfam; PF00047; Ig; 91.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00060; FN3; 127.
DR SMART; SM00408; IGC2; 23.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00933; FG_Y_KINASES_1; 1.
DR PROSITE; PS00038; HLH_1; 1..c2.
DR PROSITE; PS50835; IG_LIKE; 87.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR Muscle protein; Cytoskeleton; structural protein; Alternatve splicing; Repeat;
KW Serine/threonine-protein kinase; Alternatve splicing; Repeat;
KW Immunoglobulin domain; Phosphorylation
FT DOMAIN 1370 1389 4 X 3 AA TANDEM REPEATS OF R-M-S-P-A.
FT DOMAIN 4429 4614 GLU/LYS/PRO/VAL-RICH.
FT DOMAIN 24731 25070 CATALYTIC.
FT MOD_RES 1372 1372 CALMODULIN-BINDING.
FT MOD_RES 1372 1372 PHOSPHORYLATION (BY PDBK) (POTENTIAL).
FT MOD_RES 1377 1377 PHOSPHORYLATION (BY PDBK) (POTENTIAL).
FT MOD_RES 1382 1382 PHOSPHORYLATION (BY PDBK) (POTENTIAL).
FT MOD_RES 1387 1387 PHOSPHORYLATION (BY PDBK) (POTENTIAL).
FT MOD_RES 26171 26171 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 26178 26178 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 26184 26184 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 26190 26190 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 22377 22377 T -> P (IN REF. 2).
FT MOD_RES 22377 22377 T -> Q (IN REF. 2).
FT MOD_RES 22449 22449 E -> Q (IN REF. 2).
FT MOD_RES 22454 22454 T -> Q (IN REF. 2).
FT MOD_RES 23324 23324 S -> L (IN REF. 2).
FT MOD_RES 23324 23324 S -> L (IN REF. 2).
SQ SEQUENCE 26926 AA; 2993428 MW; D5EEDC3454DF5523 CRC64;

Query Match 57.0%; Score 45; DB 4; Length 26926;
Best Local Similarity 53.8%; Pred. No. 2.8e+03;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

RA Gentner T., Kolmerer B., Witt C., Beckmann J.S., Gregorio C.C.,
RA Granzier H., Labitt S.;
RT "Series of exon-skipping events in the elastic spring region of titin
RT as the structural basis for myofibrillar elastic diversity.";
RL Circ. Res. 86:1114-1121(2000).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=21573839; PubMed=1171165;
RA Band M.L., Gentner T., Fornoff F., Geach A.J., Gethardt M.,
RA McElabb M., Witt C.C., Labitt D., Gregorio C.C., Granzier H.,
RA Labitt S.;
RT "The complete gene sequence of titin, expression of an unusual -700
RT kDa titin isoform and its interaction with obscurin identify a novel
RT Z-line to I-band linking system.";
RL Circ. Res. 89:1065-1072(2001).
CC -1- SIMILARITY: CONTAINS 146 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
DR EMBL; AJ277692; CAD12456.1; .
DR PDB; 1TNM; 20-APR-95.
DR PDB; 1TNM; 20-APR-95.
DR Genew; HGNC:12403; TTN.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0008307; F:structural constituent of muscle; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0007517; P:muscle development; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006979; P:response to oxidative stress; IEA.
DR InterPro; IPR00282; Cytok_receptor_2.
DR InterPro; IPR00577; FG_Y_Kin.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003598; Ig_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR004168; PAK motif.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00041; fn3; 132.
DR Pfam; PF00047; Ig; 148.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF02818; PAK; 53.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00060; FN3; 132.
DR SMART; SM00408; IGC2; 63.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00933; FG_Y_KINASES_1; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS50835; IG_LIKE; 143.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR ATP-binding; Immunoglobulin domain; Transferase.
SQ SEQUENCE 34350 AA; 3816262 MW; SB1120058A7CE56A CRC64;

Query Match 57.0%; Score 45; DB 4; Length 34350;
Best Local Similarity 53.8%; Pred. No. 3.6e+03;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

Q84MB4
ID Q84MB4 PRELIMINARY; PRT; 355 AA.
AC Q84MB4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Atig22800.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCB1_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shin P., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL "Arabidopsis ORF clones."
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT006429; AAP21237.1; -
SQ SEQUENCE 355 AA; 39365 MW; C912P235B4486435 CRC64;

Query Match 55.7%; Score 44; DB 10; Length 355;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDIITSSIGLRWT 13
||: ||: ||: ||
Db 168 VDIITSSIGLRWT 180

RESULT 15
Q887F7
ID Q887F7 PRELIMINARY; PRT; 395 AA.
AC Q887F7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Membrane protein, putative.
GN PSP10139.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCB1_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouli H., Fedorova N., Tran B., Russell D.,
RA Berry K., Uettermann T., Van Aken S., Feldblyum T., Gwin M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M.W., Haft D., Selengut J., Nelson W., Davidsen T.,
RA White O., Fraser C., Collier A.;
RT "Complete sequence of Pseudomonas syringae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016860; AA054861.1; -
DR TIGR; PSP10139; -
KM Complete proteome.
SQ SEQUENCE 395 AA; 42618 MW; 42375205B92D0234 CRC64;

Query Match 55.7%; Score 44; DB 16; Length 395;
Best Local Similarity 46.7%; Pred. No. 37;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDIITSSIGLRWT 15
: ||: ||: ||: ||
Db 189 LIDACDPVGIWQPL 203

Search completed: September 21, 2004, 05:57:04
Job time : 26.6029 secs

PD / AN K

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53 ; Search time 30.2206 Seconds
(without alignments)
140.243 Million cell updates/sec

Title: US-10-676-049-1

Perfect score: 79

Sequence: 1 VDIRSSIGLRWPL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries:

Database :
1: geneseq_29Jan04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	15	AA017875	AA017875 EDB fibro
2	79	100.0	30	AAU79566	AAU79566 Eptope #
3	79	100.0	91	AA025405	AA025405 ED-B. 1/1
4	79	100.0	91	AA023838	AA023838 The ED2 d
5	79	100.0	91	ABG98132	ABG98132 Anti-neov
6	79	100.0	91	AA017878	AA017878 EDB fibro
7	79	100.0	91	ABP74705	ABP74705 Human ED-
8	79	100.0	91	AD009564	AD009564 Eptope w
9	79	100.0	146	AD009565	AD009565 Eptope w
10	79	100.0	147	ABG98133	ABG98133 Human fib
11	79	100.0	147	ABP74706	ABP74706 Human ED-
12	79	100.0	1336	AA060019	AA060019 Tissue-bi
13	79	100.0	2220	AB001289	AB001289 Human pro
14	79	100.0	2446	AA060021	AA060021 Fibronoge
15	79	100.0	2446	AA050377	AA050377 Human fib
16	79	100.0	2477	AAW95955	AAW95955 Human fib
17	79	100.0	2477	AD063323	AD063323 Rat Prote
18	79	100.0	2477	ABG98133	ABG98133 Anti-neov
19	50	63.3	9	ABP74400	ABP74400 Human ED-
20	50	63.3	9	AD009259	AD009259 Eptope w
21	49	62.0	92	AA016010	AA016010 Peptide #
22	49	62.0	92	AB035003	AB035003 Peptide #
23	49	62.0	92	AA028511	AA028511 Peptide #
24	49	62.0	92	AB029626	AB029626 Peptide #
25	49	62.0	92	AB020415	AB020415 Protein #

26	49	62.0	92	4	AA068188	AA068188 Human bot
27	49	62.0	92	4	AA058814	AA058814 Human bra
28	49	62.0	92	4	ABG49839	ABG49839 Human liv
29	49	62.0	92	4	AA003744	AA003744 Peptide #
30	49	62.0	92	5	ABG37717	ABG37717 Human pep
31	49	62.0	3063	5	AB090762	AB090762 Human tum
32	49	62.0	3063	6	AB054469	AB054469 Human tum
33	49	62.0	3063	6	ABR47415	ABR47415 Breast ca
34	49	62.0	3063	6	ABR47415	ABR47415 Breast ca
35	49	62.0	3118	4	AAU27790	AAU27790 Human ful
36	46	58.2	8	5	ABG98138	ABG98138 Anti-neov
37	46	58.2	8	7	AD009258	AD009258 Human ED-
38	46	58.2	8	7	AD009258	AD009258 Peptide #
39	46	58.2	88	4	AA029663	AA029663 Peptide #
40	46	58.2	88	4	AA029663	AA029663 Protein #
41	46	58.2	88	4	ABG51016	ABG51016 Human liv
42	46	58.2	88	4	AA004865	AA004865 Peptide #
43	46	58.2	88	5	ABG38958	ABG38958 Human pep
44	46	58.2	223	4	ABG22276	ABG22276 Novel hum
45	46	58.2	223	4	ABG22276	ABG22276 Novel hum

ALIGNMENTS

RESULT 1
AA017875
ID AA017875 standard; peptide, 15 AA.
XX
AC AA017875;
XX
DT 20-AUG-2002 (first entry)
XX
DE EDB fibronectin domain binding peptide #1.
XX
KW EDB fibronectin domain, EDBFD, angiogenesis; gene therapy; transplant;
XX implant; receptor molecule interaction.
XX
OS Unidentified.
XX
PN WO200220563-A2.
XX
PD 14-MAR-2002.
XX
PF 30-AUG-2001; 2001WO-EP010016.
XX
PR 07-SEP-2000; 2000DE-01045803.
XX
PR 02-MAY-2001; 2001DE-01023133.
XX
XX (SCHD) SCHERING AG.
XX (REDL) REDLITZ A.
XX (KOPP) KOPPEITZ M.
XX (EGNE) EGNER U.
XX (BAHR) BAHR I.
XX (MENR) MENRAD A.
XX
XX Menrad A;
XX
XX WPI; 2002-479458/51.
XX
XX New proteins binding specifically to the ED-b fibronectin domain, are
XX cell adhesion and proliferation mediators useful e.g. in screening tests.
XX
XX Claim 2, Page 40; 66pp; German.
XX
XX The present invention relates to a new protein which binds specifically
XX to the EDB fibronectin domain (EDbFD), is specifically expressed or
XX activated in endothelial cells, stromal cells of a tumour and tumour
XX cells, and has an apparent molecular weight of 120-130 kDa for the light
XX chain and 150-160 kDa for the heavy chain. The protein can be used to
XX screen compounds which bind to EdbFD or its receptor, for coating
XX surfaces to which endothelial cells bind, in cell cultures, in
XX combination with transplants or in combination with implants


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PR      07-MAR-2001; 2001US-0274063P.
XX
XX      (CTL)- CTL IMMUNOTHERAPIES CORP.
XX
PI      Simard JLL, Diamond DC;
XX
XX      WPI, 2002-750433/81.
XX
PT      Evaluating cell-mediated immunity, in particular cytotoxic T lymphocyte
PT      responses, by implanting vascular cells, useful for treatment and
PT      research models for directly targeting tumor neovasculature.
XX
PS      Example 5; Page 25; 73pp; English.
XX
XX      The invention describes a method of evaluating cell-mediated immunity
CC      comprising implanting vascular cells into an immunodeficient mammal,
CC      establishing an immune response in the mammal, and assaying a
CC      characteristic to determine cell-mediated immunity in the mammal. The
CC      methods and compositions of the present invention are useful for the
CC      generation of a cellular immune response, in particular a CTL response,
CC      for treatment directly against a tumour neovasculature. They can also be
CC      used for making research models targeting tumour neovasculature. The
CC      present invention using the anti-angiogenesis approach takes advantage of
CC      the need of tumours to recruit a blood supply to support their continued
CC      growth. This approach aims to disrupt a tumour's supply of nutrients to
CC      cause it to die or at least limit its growth. This is the amino acid
CC      sequence of a peptide associated with the neo-vasculature preparation
CC      for treatment of cancer described in the invention
XX
SQ      Sequence 91 AA;
XX
XX      Query Match          100.0%; Score 79; DB 5; Length 91;
XX      Best Local Similarity 100.0%; Pred. NO. 2.7e-06;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 VDIITSSIGLRWPL 15
DB      11 VDIITSSIGLRWPL 25
XX
XX      |||||
XX      |||||
XX      |||||
XX      |||||
XX      |||||
XX
RESULT 6
AA017878
ID      AA017878 standard; protein; 91 AA.
XX
XX      AA017878;
XX
XX      20-AUG-2002 (first entry)
XX
DE      EDB fibronectin domain binding protein.
XX
XX      EDB fibronectin domain; EDBPD; angiogenesis; gene therapy; transplant;
XX      implant; receptor molecule interaction.
XX
XX      Unidentified.
XX
XX      WO200220563-A2.
XX
XX      14-MAR-2002.
XX
XX      30-AUG-2001; 2001WO-EP010016.
XX
XX      07-SEP-2000; 2000DE-01045803.
XX      02-MAY-2001; 2001DE-01023133.
XX
XX      (SCHD ) SCHERING AG.
XX      (REDL ) REDLITZ A.
XX      (KOPF ) KOPRITZ M.
XX      (EGNE ) EGNER U.
XX      (BAHR ) BAHR I.
XX      (MENR ) MENRAD A.
XX
XX      Menrad A;
XX

```

DR WPI; 2002-479456/51.
XX
PT New proteins binding specifically to the ED-B fibronectin domain, are
XX cell adhesion and proliferation mediators useful e.g. in screening tests.
PS
XX Claim 18; Page 41-42; 66pp; German.
XX
CC The present invention relates to a new protein which binds specifically
CC to the ED-B fibronectin domain (EDBPD), is specifically expressed or
CC activated in endothelial cells, stromal cells of a tumour and tumour
CC cells, and has an apparent molecular weight of 120-130 kDa for the light
CC chain and 150-160 kDa for the heavy chain. The protein can be used to
CC screen compounds which bind to EDBPD or its receptor, for coating
CC surfaces to which endothelial cells bind, in cell cultures, in
CC combination with transplants or in combination with implants
CC (specifically lung implants, artificial heart pacemakers or valves,
CC vascular implants, endoprostheses, screws, bars, plates, wires, nails,
CC rods, artificial joints, breast implants, artificial cranial plates,
CC false teeth, tooth fillings or tooth bridges, as it improves the
CC integration of transplants or implants in the body. The protein is also
CC useful in clarifying ED-B-specific adhesion mechanisms and receptor
CC molecule interactions involved in angiogenesis. The present sequence is a
CC protein of the invention
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 79; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VDITDSSIGLRWTP 15
DB 11 VDITDSSIGLRWTP 25

RESULT 7
ABP74705
ID ABP74705 standard; protein; 91 AA.
XX
AC ABP74705;
XX
DT 03-FEB-2003 (first entry)
XX
DE Human ED-B domain of fibronectin SEQ ID NO:589.
XX
KW Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
KW T cell.
XX
OS Homo sapiens.
XX
PN WO200281646-A2.
XX
PD 17-OCT-2002.
XX
PF 04-APR-2002; 2002WO-US01101.
XX
PR 06-APR-2001; 2001US-028221P.
PR 07-NOV-2001; 2001US-033701P.
PR 07-MAR-2002; 2002US-0363210P.
XX
XX
PA (CTL1-) CTL IMMUNOTHERAPIES CORP.
XX
PI Simard JTL, Diamond DC, Liu L, Xie Z;
XX
XX WPI; 2003-067518/06.
XX
XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid
XX encoding the peptides, that are useful epitopes of target-associated
XX antigens.
XX
XX Claim 1; Page 26; 352pp; English.
XX
XX The present invention describes an isolated epitope (I) and an epitope

CC cluster. Also described is a vaccine or immunotherapeutic composition
CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
CC treating an animal, by administering to an animal the vaccine or
CC immunotherapeutic composition. VC is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic composition, by
CC administering VC to an HLA-transgenic animal and evaluating
CC immunogenicity based on a characteristic of the animal, or by in vitro
CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
CC useful for determining specific T cell frequency, by contacting T cells
CC with a MHC-peptide complex, and further comprising ELISPOT analysis,
CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
CC ABP74713 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 79; DB 6; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VDITDSSIGLRWTP 15
DB 11 VDITDSSIGLRWTP 25

RESULT 8
ADC09564
ID ADC09564 standard; peptide; 91 AA.
XX
AC ADC09564;
XX
DT 18-DEC-2003 (first entry)
XX
DE Epitope with high affinity for MHC class I #SEQ ID 589.
XX
KW Epitope; immunological; vaccine;
KW major histocompatibility complex class I; MHC class I; cancer;
KW immunisation.
XX
OS Unidentified.
XX
PN WO2003008537-A2.
XX
PD 30-JAN-2003.
XX
PF 29-MAR-2002; 2002WO-US010189.
XX
PR 06-APR-2001; 2001US-028221P.
PR 07-NOV-2001; 2001US-033701P.
PR 07-MAR-2002; 2002US-0363210P.
XX
XX
PA (CTL1-) CTL IMMUNOTHERAPIES CORP.
XX
PI Simard JTL, Diamond DC, Liu L, Xie Z;
XX
XX WPI; 2003-248010/24.
XX
XX Epitope having high affinity for major histocompatibility complex class I
XX therapeutic composition and for diagnosing a disease.
XX
XX Claim 1; SEQ ID NO 589; 239pp; English.
XX
XX The invention relates to an isolated epitope polypeptide that has high
XX affinity for major histocompatibility complex (MHC) class I, and an
XX epitope cluster comprising the polypeptide. Also disclosed is a vaccine
XX or immunotherapeutic composition containing an epitope of the invention.
XX Compositions of the invention may be used in the treatment of cancer. The
XX method can be combined with a radiation therapy, chemotherapy,
XX biochemotherapy or surgery. The composition is also useful for evaluating
XX immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
XX peptide complexes of the invention are useful for determining specific T

XX ABP74706;
XX
XX 03-FEB-2003 (first entry)
XX
XX

Human ED-B domain of fibronectin SEQ ID NO:590.

XX Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
XX T cell.
XX

XX Homo sapiens.
XX

XX WO200281646-A2.
XX

XX 17-OCT-2002.
XX

XX 04-APR-2002; 2002WO-US011101.
XX

XX 06-APR-2001; 2001US-0282211P.
XX

XX 07-NOV-2001; 2001US-0337017P.
XX

XX 07-MAR-2002; 2002US-0363210P.
XX

XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX

XX Simard JUL, Diamond DC, Liu L, Xie Z;
XX

XX WPI; 2003-067518/06.
XX

XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid
XX encoding the peptides, that are useful epitopes of target-associated
XX antigens.
XX

XX Claim 1; Page 26; 352pp; English.
XX

XX The present invention describes an isolated epitope (I) and an epitope
XX cluster. Also described is a vaccine or immunotherapeutic composition
XX (VC) comprising (I). (I) has cytostatic activity. VC is useful for
XX treating an animal, by administering to an animal the vaccine or
XX immunotherapeutic composition. VC is also useful for evaluating
XX immunogenicity of a vaccine or immunotherapeutic composition, by
XX administering VC to an HLA-transgenic animal and evaluating
XX immunogenicity based on a characteristic of the animal, or by in vitro
XX primary stimulation of a T cell and evaluating immunogenicity. (I) is
XX useful for determining specific T cell frequency, by contacting T cells
XX with a MHC-peptide complex, and further comprises ELISPOT analysis,
XX limiting dilution analysis, flow cytometry, in situ hybridisation and/or
XX polymerase chain reaction (PCR). A983843 to A983858 and ABP74128 to
XX ABP74413 represent sequences used in the exemplification of the present
XX invention
XX

XX Sequence 147 AA;
XX

XX Query Match 100.0%; Score 79; DB 6; Length 147;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDIRSSIGLRWTP 15
DB 45 VDIRSSIGLRWTP 59

RESULT 12

XX AAR60019 standard; protein; 1336 AA.
XX

XX AAR60019;
XX

XX 25-MAR-2003 (revised)
XX

XX 23-FEB-1995 (first entry)
XX

XX Tissue-binding hybrid protein.
XX

XX Tissue binding; tissue sealing; wound healing; vulnery;

KW tissue-binding domain; TBD; crosslinking domain; fibronectin;
KW fibrinogen-alpha; heparin-binding domain; collagen-binding domain;
KW cell-binding domain; hybrid protein.
XX
XX
XX Homo sapiens.
XX

XX Key Location/Qualifiers
XX

XX Domain 2..1336
XX /label= tissue-binding_domain
XX

XX Domain 2..926
XX /label= tissue-binding_domain
XX

XX Domain 928..1336
XX /label= tissue-binding_domain
XX

XX WO9416085-A2.
XX

XX 21-JUL-1994.
XX

XX 30-DEC-1993; 93WO-US012687.
XX

XX 30-DEC-1992; 92US-00998271.
XX

XX (ZYMO) ZYMOGENETICS INC.
XX

XX Irani MH;
XX

XX WPI; 1994-249231/30.
XX

XX N-PSDB; AAQ70007.
XX

XX New hybrid proteins for use in tissue sealing and wound healing -
XX comprising a tissue-binding domain from a protein covalently linked to a
XX crosslinking domain of another protein.
XX

XX Disclosure; Page 63-69; 87pp; English.
XX

XX Hybrid proteins have a tissue-binding domain (TBD) from 1 protein linked
XX to a crosslinking domain from another protein. The TBD comprises: aa 2-
XX 926, 928-1338 and especially 2-1336 of the sequence given in AAR60019;
XX the heparin-binding domain (aa 1812-2171 of AAR60021) of fibronectin; the
XX collagen-binding domain (aa 282-608 of AAR60021) of fibronectin; or the
XX cell-binding domain (aa 1357-1903 or 1532-1631 of AAR60020) of
XX fibronectin. DNA encoding a fibronectin-fibrinogen hybrid is given in
XX CC AAQ70007, and sequences for fibronectin and fibrinogen-alpha in AAQ70008
XX and AAQ70009, respectively. (Updated on 25-MAR-2003 to correct PN field.)
XX

XX Sequence 1336 AA;
XX

XX Query Match 100.0%; Score 79; DB 2; Length 1336;
XX Best Local Similarity 100.0%; Pred. No. 6.3e-05;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDIRSSIGLRWTP 15
DB 239 VDIRSSIGLRWTP 313

RESULT 13

XX ABO01289 standard; protein; 2220 AA.
XX

XX ABO01289;
XX

XX 06-AUG-2003 (first entry)
XX

XX Human protein NOV1b.
XX

XX Human; NOVX; cardiomyopathy; atherosclerosis; hypertension;
XX congenital heart defect; prostate cancer; diabetes; metabolic disorder;
XX neoplasm; graft versus host disease; AIDS; bronchial asthma;
XX Crohn's disease; multiple sclerosis; infectious disease; anorexia;
XX cancer-associated cachexia; neurodegenerative disorder;
XX Alzheimer's disease; Parkinson's disease; immune disorder;
XX haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy;
XX

SNP, single nucleotide polymorphism.

Homo sapiens.

Key Location/Qualifiers
 Misc-difference 639 /note= "May be Phe as the result of a single nucleotide polymorphism"

WO2003023008-A2.

20-MAR-2003.

09-SEP-2002; 2002WO-US028596.

07-SEP-2001; 2001US-0318130P.
 10-SEP-2001; 2001US-0318430P.
 12-SEP-2001; 2001US-0318765P.
 17-SEP-2001; 2001US-0322781P.
 19-SEP-2001; 2001US-0322816P.
 20-SEP-2001; 2001US-0323519P.
 20-SEP-2001; 2001US-0323631P.
 25-SEP-2001; 2001US-0324969P.
 25-SEP-2001; 2001US-0325091P.
 26-SEP-2001; 2001US-0324990P.
 15-FEB-2002; 2002US-0357303P.
 28-FEB-2002; 2002US-0360973P.
 20-MAR-2002; 2002US-0366131P.
 25-MAR-2002; 2002US-0367753P.
 02-APR-2002; 2002US-0369479P.
 10-MAY-2002; 2002US-0379532P.
 17-MAY-2002; 2002US-0381664P.
 17-MAY-2002; 2002US-0381672P.
 28-MAY-2002; 2002US-0383651P.
 29-MAY-2002; 2002US-0384012P.
 19-JUN-2002; 2002US-0390155P.
 06-SEP-2002; 2002US-0390155P.

(CURA-) CURAGEN CORP.

Zhong M, Li L, Gorman L, Spyrek KA, Kekuda R, Taupier RJ; Anderson DW, Vernet CAM, Catterton E, Miller CE, Shenoy SG; Patyanchan N, Pena CE, Tcherev VI, Padigaru M, Guev VY; Malayanar UM, Burgess CE, Gerlach VL, Casman SU, Rieger DK; Grose WM, Smithson G, Peyman JA, Starling G, Rothenberg ME; Larocelle WJ, Shinkets RA, Crabtree J, Rastelli L, Voss EZ; Bolig FL, Edinger SR, Millet I, MacDougall JR, Ellerman K; Chapoval A;

WPI: 2003-312246/30.
 N-PSDB; ACD06170.

New polypeptides and polynucleotides having properties related to stimulation of biochemical or physiological responses in a cell or tissue, useful for diagnosing or preventing e.g. atherosclerosis, hypertension, prostate cancer.

Claim 2; Page 110-111; 849pp; English.

The invention relates to an isolated polypeptide comprising one of 127 sequences (appearing as ABO1288-ABO1414) designated as NOVX, a mature form of NOVX, an amino acid sequence which is at least 95% identical to NOVX or an amino acid sequence comprising one or more conservative substitutions in NOVX. Also included are nucleic acids encoding NOVX proteins, determining the presence or amount of NOVX or NOVX DNA in a sample (by introducing the sample to an antibody that binds immunospecifically to the polypeptide, and determining the presence or amount of antibody bound to the polypeptide), determining the presence of or predisposition to a disease associated with altered levels of expression of NOVX or NOVX DNA in a first mammalian subject, identifying an agent that binds to NOVX, identifying a potential therapeutic agent

for treatment of a pathology related to aberrant expression or aberrant physiological interactions of NOVX, screening for a modulator of activity of or of latency or predisposition to a pathology associated with NOVX, a vector comprising NOVX DNA, a cell comprising the vector (used to produce NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides are useful as a marker for cell or tissue type, and in diagnosing and treating pathologies, diseases, conditions or disorders associated with NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, prostate cancer, diabetes, metabolic disorders, neoplasm, graft versus host disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis, infectious diseases, anorexia, cancer-associated cachexia, neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), immune disorders, haematopoietic disorders, dyslipidaemias, and wasting disorders associated with chronic diseases. These may also be used to screen for molecules which inhibit or enhance NOVX activity or function, and for detecting specific cell types. These may also be used in chromosome mapping, gene therapy, tissue typing, and in forensic biology. The present sequence represents a NOVX protein

Sequence 2220 AA;

Query Match 100.0%; Score 79; DB 6; Length 2220;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDIIDSSIGLRWTP 15
 1276 VDIIDSSIGLRWTP 1290

RESULT 14
 AAR60021 standard; protein; 2446 AA.

AC AAR60021;
 DT 25-MAR-2003 (revised)
 DT 23-FEB-1995 (first entry)

DE Fibrinogen-alpha.

XX Tissue binding; tissue sealing; wound healing; vunerary;
 XX tissue-binding domain; TSD; crosslinking domain; fibronectin;
 KW fibrinogen-alpha; heparin-binding domain; collagen-binding domain;
 XX cell-binding domain; hybrid protein.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 282..608
 FT /label= collagen-binding domain
 FT /note= "acts as tissue-binding domain of hybrid protein"
 FT Domain 1812..2171
 FT /label= heparin-binding domain
 FT /note= "acts as tissue-binding domain of hybrid protein"

PN MO9416085-A2.

PD 21-JUL-1994.

XX 30-DEC-1993; 93WO-US012687.
 XX 30-DEC-1992; 92US-00998271.

XX (ZYMO) ZYMOGENETICS INC.

PI Iranl KH;

DR WPI: 1994-249231/30.
 DR N-PSDB; AAQ70009.

XX New hybrid proteins for use in tissue sealing and wound healing -

PT comprising a tissue-binding domain from a protein covalently linked to a
PT crosslinking domain of another protein.

XX
XX
PS Disclosure; Page 37-48; 87pp; English.

XX Hybrid proteins have a tissue-binding domain (TBD) from 1 protein linked
CC to a crosslinking domain from another protein. The TBD comprises: aa 2-
CC 926, 928-1338 and especially 2-1336 of the sequence given in AAR60019;
CC the heparin-binding domain (aa 1812-2171 of AAR60021) of fibronectin; the
CC collagen-binding domain (aa 1357-1903 or 1532-1631 of AAR60020) of
CC cell-binding domain (aa 1357-1903 or 1532-1631 of AAR60020) of
CC fibronectin. DNA encoding a fibronectin-fibrinogen hybrid is given in
CC AAO70007, and sequences for fibronectin and fibrinogen-alpha in AAO70008
CC and AAO70009, respectively. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 2446 AA;

Query Match 100.0%; Score 79; DB 2; Length 2446;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDITDSSIGLRWTP 15

Db 1276 VDITDSSIGLRWTP 1290

RESULT 15

AAB50377

ID AAB50377 standard; protein; 2446 AA.

XX AAB50377;

XX 12-MAR-2001 (first entry)

DE Human fibronectin.

XX Human; FN; fibronectin; prostate cancer; biallelic marker; diagnosis.

XX Homo sapiens.

XX WO200058509-A2.

XX 05-OCT-2000.

XX 28-MAR-2000; 2000WO-IB000431.

XX 29-MAR-1999; 99US-0126780P.

XX (GSEST) GENSET.

XX Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A;

XX WPI; 2000-594647/56.

XX N-PSDB; AAC89889.

XX Fibronectin polynucleotide and polypeptide sequences, useful for
PT determining the predisposition of individuals to cancer, such as prostate
PT cancer.

XX Claim 4; Page 185-190; 208pp; English.

XX The present sequence is given in a specification relating to an isolated
CC or purified recombinant polynucleotide comprising a contiguous span of at
CC least 12 nucleotides of a fibronectin (FN) gene. The methods and
CC sequences are useful for determining the predisposition of individuals to
CC cancer such as prostate cancer and for the prognosis/detection of an
CC eventual treatment response to therapeutic agents acting against prostate
CC cancer. Biallelic markers allow association studies to be performed to
CC identify genes involved in complex traits

XX Sequence 2446 AA;

Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDITDSSIGLRWTP 15

Db 1276 VDITDSSIGLRWTP 1290

Search completed: September 21, 2004, 05:53:29
Job time : 40.2206 secs

Query Match

100.0%; Score 79; DB 3; Length 2446;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:49:08 ; Search time 99.1544 Seconds

(without alignments)
48.581 Million cell updates/sec

Title: US-10-676-049-1

Sequence: 1 VDIRDSIGLRWTP 15

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1342398 seqs, 32133274 residues

Total number of hits satisfying chosen parameters: 1342398

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	15	9	US-09-942-117-1
2	79	100.0	91	9	US-09-942-117-4
3	79	100.0	91	14	US-10-094-699-89
4	79	100.0	91	15	US-10-117-937-589
5	79	100.0	91	16	US-10-450-012-5
6	79	100.0	147	14	US-10-094-699-90
7	79	100.0	147	15	US-10-117-937-580
8	79	100.0	2220	12	US-10-236-392-4
9	69	87.3	13	9	US-09-942-117-9
10	54	68.4	15	9	US-09-942-117-10
11	50	63.3	9	14	US-10-094-699-97
12	50	63.3	9	15	US-10-117-937-284
13	49	62.0	90	14	US-10-029-366-30537
14	49	62.0	92	9	US-09-864-761-35713
15	49	62.0	3063	12	US-09-918-715-257

16	49	62.0	3063	14	US-10-177-293-61	Sequence 61, App1
17	49	62.0	3063	14	US-10-177-293-61	Sequence 63, App1
18	49	62.0	3063	14	US-10-301-822-26	Sequence 26, App1
19	47	59.5	15	9	US-09-942-117-8	Sequence 8, App1
20	46	58.2	8	14	US-10-094-699-96	Sequence 96, App1
21	46	58.2	8	15	US-10-117-937-283	Sequence 283, App
22	46	58.2	88	9	US-09-864-761-36851	Sequence 36851, A
23	46	58.2	1259	16	US-10-741-601-362	Sequence 362, App
24	46	58.2	1259	16	US-10-741-601-362	Sequence 365, App
25	46	58.2	1259	16	US-10-741-601-362	Sequence 368, App
26	46	58.2	1259	16	US-10-741-601-362	Sequence 369, App
27	46	58.2	1259	16	US-10-741-601-362	Sequence 370, App1
28	46	58.2	1259	16	US-10-741-601-362	Sequence 371, App1
29	46	58.2	1259	16	US-10-741-601-362	Sequence 372, App1
30	46	58.2	1259	16	US-10-741-601-362	Sequence 373, App1
31	46	58.2	1259	16	US-10-741-601-362	Sequence 374, App1
32	46	58.2	1259	16	US-10-741-601-362	Sequence 375, App1
33	46	58.2	1259	16	US-10-741-601-362	Sequence 376, App1
34	46	58.2	1259	16	US-10-741-601-362	Sequence 377, App1
35	46	58.2	1259	16	US-10-741-601-362	Sequence 378, App1
36	46	58.2	1259	16	US-10-741-601-362	Sequence 379, App1
37	46	58.2	1259	16	US-10-741-601-362	Sequence 380, App1
38	46	58.2	1259	16	US-10-741-601-362	Sequence 381, App1
39	46	58.2	1259	16	US-10-741-601-362	Sequence 382, App1
40	46	58.2	1259	16	US-10-741-601-362	Sequence 383, App1
41	46	58.2	1259	16	US-10-741-601-362	Sequence 384, App1
42	46	58.2	1259	16	US-10-741-601-362	Sequence 385, App1
43	46	58.2	1259	16	US-10-741-601-362	Sequence 386, App1
44	46	58.2	1259	16	US-10-741-601-362	Sequence 387, App1
45	46	58.2	1259	16	US-10-741-601-362	Sequence 388, App1

ALIGNMENTS

RESULT 1
US-09-942-117-1
; Sequence 1, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAHR, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBROBLAST DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942,117
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-1

Query Match 100.0%; Score 79; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 VDIRDSIGLRWTP 15
Db 1 VDIRDSIGLRWTP 15


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; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: CTILMM.015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-699-90

Query Match      100.0%; Score 79; DB 14; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDTTSSIGLRWTP 15
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         45 VDTTSSIGLRWTP 59

RESULT 8
US-10-236-392-4
; Sequence 4, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Caterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie

US-10-117-937-590
; ORGANISM: Homo sapiens
; TYPE: PRT
; LENGTH: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-590

Query Match      100.0%; Score 79; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDTTSSIGLRWTP 15
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         45 VDTTSSIGLRWTP 59

RESULT 7
US-10-117-937-590
; Sequence 590, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTILMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-590

Query Match      100.0%; Score 79; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDTTSSIGLRWTP 15
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         45 VDTTSSIGLRWTP 59

RESULT 9
US-09-942-117-9
; Sequence 9, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
```

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; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kexuda, Ramesh
; APPLICANT: LaRochelette, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyanekar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 4
; LENGTH: 2220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-4

Query Match      100.0%; Score 79; DB 12; Length 2220;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDTTSSIGLRWTP 15
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         1276 VDTTSSIGLRWTP 1290

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US-09-942-117-9
; Sequence 9, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
```

```
APPLICANT: EGNER, URSULA
APPLICANT: BAHN, INKE
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
FILE REFERENCE: SCH-1832
CURRENT APPLICATION NUMBER: US/09/942,117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-942-117-9
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Db      1 ITDSIGLRWTP 13
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Sequence 10, Application US/09942117
Publication No. US20020197700A1
GENERAL INFORMATION:
APPLICANT: MENRAD, ANDREAS
APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPPLITZ, MARCUS
APPLICANT: EGNER, URSULA
APPLICANT: BAHN, INKE
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
FILE REFERENCE: SCH-1832
CURRENT APPLICATION NUMBER: US/09/942,117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-942-117-10
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Best Local Similarity 100.0%; Pred. No. 0.065;
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QY      6 SIGLRWTP 15
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Db      1 SIGLRWTP 10
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RESULT 11
US-10-094-699-97
Sequence 97, Application US/10094699
Publication No. US20030046714A1
GENERAL INFORMATION:
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APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
FILE REFERENCE: CTIIMM.015A
CURRENT APPLICATION NUMBER: US/10/094,699
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/274,063
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien
US-10-094-699-97
```

```
Query Match      63.3%; Score 50; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      7 SIGLRWTP 15
        |||||
Db      1 SIGLRWTP 9
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```
RESULT 12
US-10-117-937-284
Sequence 284, Application US/10117937
Publication No. US2003020239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPTOPE SEQUENCES
FILE REFERENCE: CTIIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
CURRENT APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 284
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-937-284
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Query Match      63.3%; Score 50; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      7 SIGLRWTP 15
        |||||
Db      1 SIGLRWTP 9
```

```
RESULT 13
US-10-029-386-30537
Sequence 30537, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
```


FILE REFERENCE: AEOmica-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 30537
LENGTH: 90
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL096771.11
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.6
OTHER INFORMATION: SWISSPROT HIT: Q99715, EVALU 4.00e-48
US-10-029-386-30537

Query Match 62.0%; Score 49; DB 14; Length 90;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DITDSSIGLRWT 13
DB 11 DITDTSIGAYWT 22

RESULT 14
US-09-864-761-35713
Sequence 35713, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeo mica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/160,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35713
LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL096771.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN HE1100, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
OTHER INFORMATION: SWISSPROT HIT: Q99715, EVALU 9.00e-49
OTHER INFORMATION: EST_HUMAN HIT: AU137153.1, EVALU 5.00e-07
US-09-864-761-35713

Query Match 62.0%; Score 49; DB 9; Length 92;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DITDSSIGLRWT 13
DB 11 DITDTSIGAYWT 22

RESULT 15
US-09-918-715-257
Sequence 257, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 257
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo sapiens
US-09-918-715-257

Query Match 62.0%; Score 49; DB 12; Length 3063;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DITDSSIGLRWT 13
DB 915 DITDTSIGAYWT 926

Search completed: September 21, 2004, 06:30:29
Job time : 100.154 secs

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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:47:40 ; Search time 8.60294 Seconds

(without alignments)
90.015 Million cell updates/sec

Title: US-10-676-049-1

Perfect score: 79
Sequence: 1 VDIITDSIGIRWTP1 15

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	1336	2	US-08-551-356-6
2	79	100.0	1336	5	PCT-US93-12687-6
3	79	100.0	2446	2	US-08-551-356-2
4	79	100.0	2446	5	PCT-US93-12687-2
5	46	58.2	269	2	US-08-727-311-3
6	46	58.2	2231	1	US-08-153-799-16
7	46	58.2	2324	1	US-08-283-857-1
8	46	58.2	2324	5	PCT-US95-09819-1
9	46	58.2	2327	6	545158-1
10	46	58.2	2386	2	US-09-016-366A-12
11	44	55.7	73	3	US-09-063-950-9
12	44	55.7	331	3	US-09-061-702-4
13	44	55.7	331	4	US-09-069-023-32
14	44	55.7	331	4	US-08-842-760A-2
15	44	55.7	536	1	US-08-354-456A-2
16	44	55.7	536	1	US-07-999-280A-2
17	44	55.7	536	1	US-08-426-279-2
18	44	55.7	536	1	US-08-401-013-2
19	44	55.7	536	1	US-08-426-570-2
20	44	55.7	536	3	US-08-425-876-2
21	44	55.7	536	3	US-08-426-243-2
22	44	55.7	536	3	US-08-401-632-2
23	44	55.7	553	5	PCT-US94-00658-4
24	44	55.7	554	1	US-08-347-254-1
25	44	55.7	554	2	US-08-464-463-1
26	44	55.7	554	5	PCT-US93-08282-2
27	43	54.4	491	1	US-07-804-224-2

28	43	54.4	491	5	PCT-US92-10511-2	Sequence 2, Appl1
29	43	54.4	1241	3	US-09-040-774-2	Sequence 2, Appl1
30	42	53.2	73	4	US-09-252-991A-31055	Sequence 31055, A
31	42	53.2	89	5	US-08-793-273C-10	Sequence 10, Appl1
32	42	53.2	89	5	PCT-US95-11684-10	Sequence 10, Appl1
33	42	53.2	172	4	US-08-793-273C-29	Sequence 29, Appl1
34	42	53.2	1810	4	US-08-793-273C-4	Sequence 4, Appl1
35	42	53.2	1810	5	PCT-US95-11684-4	Sequence 4, Appl1
36	41	51.9	754	4	US-09-198-452A-874	Sequence 874, App
37	41	51.9	852	4	US-09-741-150-2	Sequence 2, Appl1
38	41	51.9	852	4	US-10-160-187-2	Sequence 2, Appl1
39	40	50.6	370	6	5240706-5	Patent No. 5240706
40	40	50.6	555	2	US-08-982-232-7	Sequence 7, Appl1
41	40	50.6	567	2	US-08-841-483-2	Sequence 2, Appl1
42	40	50.6	567	3	US-09-382-911-2	Sequence 2, Appl1
43	39.5	50.0	572	2	US-08-467-963C-4	Sequence 4, Appl1
44	39.5	50.0	572	2	US-08-838-189D-4	Sequence 4, Appl1
45	39.5	50.0	572	3	US-08-852-344D-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-551-356-6
Sequence 6, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Iranil, Neher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,356
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
FILING DATE:
APPLICATION NUMBER: US/07/998,271
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holly, Julie A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-3329
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-356-6
Query Match 100.0%; Score 79; DB 2; Length 1336;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDIITDSIGIRWTP1 15
|||||

Db 299 VDIIDSSIGLRWTP 313

RESULT 2

PCT-US93-12687-6
Sequence 6, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Iran, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-547-8080
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-6

Query Match 100.0%; Score 79; DB 5; Length 1336;

Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 VDIIDSSIGLRWTP 15
Db 299 VDIIDSSIGLRWTP 313

RESULT 3

US-08-551-356-2
Sequence 2, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Iran, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/551,356
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
FILING DATE:
APPLICATION NUMBER: US/07/998,271
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holly, Julie A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-356-2

Query Match 100.0%; Score 79; DB 2; Length 2446;

Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 VDIIDSSIGLRWTP 15
Db 1276 VDIIDSSIGLRWTP 1290

RESULT 4

PCT-US93-12687-2
Sequence 2, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Iran, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-2

Query Match 100.0%; Score 79; DB 5; Length 2446;
 Best Local Similarity 100.0%; Pred. No. 6.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDIIDSSIGLRWTP 15
 DB 1276 VDIIDSSIGLRWTP 1230

RESULT 5

US-08-727-311-3
 ; Sequence 3, Application US/08727311
 ; Patent No. 5928876
 ; GENERAL INFORMATION:
 ; APPLICANT: Masanbu OBARA et al.
 ; TITLE OF INVENTION: PEPTIDE AND COLLAGEN CONTRACTION INHIBITOR
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Menderoth, Lind & Ponack
 ; STREET: 805 Fifteenth Street, N.W., #700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/727,311
 ; FILING DATE: October 8, 1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren M. Cheek, Jr.
 ; REGISTRATION NUMBER: 33,367
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-8850
 ; TELEFAX:
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 269 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY:
 ; LOCATION:
 ; IDENTIFICATION METHOD:
 ; OTHER INFORMATION:
 ; US-08-727-311-3

Query Match 58.2%; Score 46; DB 2; Length 269;
 Best Local Similarity 57.1%; Pred. No. 3;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VDIIDSSIGLRWTP 14
 DB 103 VNETDSTVLRWTP 116

RESULT 6
 US-08-153-799-16
 ; Sequence 16, Application US/08153799
 ; Patent No. 5766883
 ; GENERAL INFORMATION:

APPLICANT: Ballance, David J
 APPLICANT: Godey, Andrew R
 TITLE OF INVENTION: Polypeptides
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: R Hain Swope, BOC Health Care Inc
 STREET: 100 Mountain Avenue
 CITY: Murray Hill
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07974

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/153,799
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/847975
 FILING DATE: 06-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 8909916.2
 FILING DATE: 29-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB90/00650
 FILING DATE: 26-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/775952
 FILING DATE: 29-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Swope, R Hain
 REGISTRATION NUMBER: 24864
 REFERENCE/DOCKET NUMBER: 92H832
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 665 2400
 TELEFAX: (908) 771 6159
 TELEX: 219484
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2231 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..2231
 OTHER INFORMATION: /note="Human fibronectin"
 ; US-08-153-799-16

Query Match 58.2%; Score 46; DB 1; Length 2231;
 Best Local Similarity 57.1%; Pred. No. 33;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VDIIDSSIGLRWTP 14
 DB 975 VNETDSTVLRWTP 988

RESULT 7
 US-08-283-857-1
 ; Sequence 1, Application US/08283857
 ; Patent No. 5792742
 ; GENERAL INFORMATION:
 ; APPLICANT: GOLD, Leslie I.
 ; APPLICANT: ROSTAGNO, Agueda A.
 ; APPLICANT: BARON Martin
 ; APPLICANT: CAMPBELL, Iain D.

Tue Sep 21 07:04:00 2004

us-10-676-049-1.open.rai

Page 4

APPLICANT: WILLIAMS, Michael, J.
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: CODING THEREFOR AND USERS THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,857
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/714,134
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOLD-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2324 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-283-857-1

Query Match 58.2%; Score 46; DB 1; Length 2324;
Best Local Similarity 57.1%; Pred. No. 35;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VDIIDSSIGLRWTP 14
Db 975 VNETDSTVLVRWTP 988

RESULT 8

PCT-US95-09819-1
Sequence 1, Application PC/TUS9509819
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: CODING THEREFOR AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09819
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,857

FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOLD-1A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2324 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-09819-1

Query Match 58.2%; Score 46; DB 5; Length 2324;
Best Local Similarity 57.1%; Pred. No. 35;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VDIIDSSIGLRWTP 14
Db 975 VNETDSTVLVRWTP 988

RESULT 9

5455158-1
Patent No. 5455158
APPLICANT: VOGEL, TIKVA, LEVANO, AVIGDOR, WERBER, MOSHE M.;
GUY, RACHEL, PANET, AMOS
TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND
USERS AND METHODS OF PRODUCING SAME
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/58,241
FILING DATE: 04-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 526,397
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: 345,952
FILING DATE: 28-APR-1985
APPLICATION NUMBER: 291,951
FILING DATE: 29-DEC-1988
SEQ ID NO: 1:
LENGTH: 2327
5455158-1

Query Match 58.2%; Score 46; DB 6; Length 2327;
Best Local Similarity 57.1%; Pred. No. 35;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VDIIDSSIGLRWTP 14
Db 978 VNETDSTVLVRWTP 991

RESULT 10

US-09-016-366A-12
Sequence 12, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA

COUNTRY: U.S.A.
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,366A
 FILING DATE: January 30, 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/037,090
 FILING DATE: 05-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Flumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7093
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2386 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-016-366A-12

Query Match 58.2%; Score 46; DB 2; Length 2386;
 Best Local Similarity 57.1%; Pred. No. 36;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VDTDSIGLRWTP 14
 :|||:||||
 Db 1006 VNEDSTVLVWTP 1019

RESULT 11
 US-09-063-950-9
 Sequence 9, Application US/09063950C
 Patent No. 6225085
 GENERAL INFORMATION:
 APPLICANT: Holtzman, Douglas A.
 TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION: THEREFOR
 FILE REFERENCE: MEI-019
 CURRENT APPLICATION NUMBER: US/09/063,950C
 CURRENT FILING DATE: 1998-04-21
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 9
 LENGTH: 73
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Consensus
 US-09-063-950-9

Query Match 55.7%; Score 44; DB 3; Length 73;
 Best Local Similarity 61.5%; Pred. No. 1.5;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DITDSIGLEWTP 14
 |||:||||
 Db 11 DITPISIVSWTP 23

RESULT 12
 US-09-061-702-4

Sequence 4, Application US/09061702
 Patent No. 6165737
 GENERAL INFORMATION:
 APPLICANT: Wang, Xiaodong
 APPLICANT: Liu, Xuesong
 TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN
 TITLE OF INVENTION: APOPTOSIS
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/061,702
 FILING DATE: Concurrently Herewith
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: McMillian, Nabeela R.
 REGISTRATION NUMBER: P-43,363
 REFERENCE/DOCKET NUMBER: UTSD:546
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512)418-3000
 TELEFAX: (512)474-7577
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 331 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-061-702-4

Query Match 55.7%; Score 44; DB 3; Length 331;
 Best Local Similarity 66.7%; Pred. No. 8.4;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDTDSIGLRW 12
 |||:||||
 Db 113 VDETSGAGLRW 124

RESULT 13
 US-09-069-023-32
 Sequence 32, Application US/09069023A
 Patent No. 6348573
 GENERAL INFORMATION:
 APPLICANT: Nunez, Gabriel
 APPLICANT: Inohara, Naohiro
 APPLICANT: Koseki, Takeyoshi
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
 TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
 FILE REFERENCE: UM-03333
 CURRENT APPLICATION NUMBER: US/09/069,023A
 CURRENT FILING DATE: 1998-04-27
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 32
 LENGTH: 331
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-069-023-32

Query Match 55.7%; Score 44; DB 4; Length 331;
 Best Local Similarity 66.7%; Pred. No. 8.4;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Tue Sep 21 07:04:00 2004

us-10-676-049-1.open.ra1

Page 6

OY 1 VDIITDSIGLRW 12
113 VDETDSGAGLKM 124

RESULT 14
US-08-842-760A-2
Sequence 2, Application US/08842760A
Patent No. 6515118

GENERAL INFORMATION:

APPLICANT: WANG, Xiaodong

TITLE OF INVENTION: TRAF2-Associated Kinase

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/842,760A

FILING DATE: 17-Apr-1997

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: USTD:1268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 331 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-842-760A-2

Query Match 55.7%; Score 44; DB 4; Length 331;
Best Local Similarity 66.7%; Pred. No. 8.4;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VDIITDSIGLRW 12
113 VDETDSGAGLKM 124

RESULT 15
US-08-354-456A-2

Sequence 2, Application US/08354456A

Patent No. 5567611

GENERAL INFORMATION:

APPLICANT: Ralph, Peter

APPLICANT: Martin, George

APPLICANT: Paterek, Michael

APPLICANT: Latrick, James W.

TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding

TITLE OF INVENTION: Therefor

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION

STREET: Intellectual Property - R440, P.O. Box 8097

CITY: Emeryville

STATE: California

COUNTRY: U.S.A.

ZIP: 94662-8097

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/354,456A

FILING DATE: 12-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/995,338

FILING DATE: 21-DEC-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: McGarrigle, Jr., Philip L.

REGISTRATION NUMBER: 31,395

REFERENCE/DOCKET NUMBER: 750,003/32387

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 601-2718

TELEFAX: (510) 655-3542

TELEX: n/a

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 536 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-354-456A-2

Query Match 55.7%; Score 44; DB 1; Length 536;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 DIITDSIGLRWTP 14
275 DIITDSIGLRWTP 287

Search completed: September 21, 2004, 06:15:26
Job time : 11.6029 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53 ; Search time 7.5 Seconds

(without alignments)
192.383 Million cell updates/sec

Title: US-10-676-049-2

Perfect score: 85
Sequence: 1 GYVTGTGLEPGIDYD 15

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	90	2	I46162
2	85	100.0	147	2	S00848
3	85	100.0	1020	2	A29355
4	85	100.0	2477	2	S14428
5	85	100.0	2477	2	A43908
6	57	67.1	2265	1	FNBO
7	57	67.1	2265	1	FNMT
8	57	67.1	2265	1	FNMT
9	57	67.1	2265	1	FNMT
10	48	56.5	26926	1	I38344
11	47	55.3	1356	2	A90255
12	47	55.3	1356	2	A45445
13	47	55.3	2944	2	A54849
14	45	52.9	351	2	S11237
15	45	52.9	588	1	BVEUC
16	45	52.9	588	1	C90960
17	45	52.9	588	1	C90960
18	45	52.9	588	1	C90960
19	43	50.6	321	2	H82573
20	43	50.6	321	2	H82573
21	43	50.6	321	2	H82573
22	43	50.6	321	2	H82573
23	43	50.6	321	2	H82573
24	43	50.6	321	2	H82573
25	43	50.6	321	2	H82573
26	43	50.6	321	2	H82573
27	43	50.6	321	2	H82573
28	43	50.6	321	2	H82573
29	43	50.6	321	2	H82573

30	42	49.4	843	2	A40970	undulin 1 - human
31	42	49.4	933	2	A31930	cytoactin - chick
32	42	49.4	1095	2	PC1114	SKDC25 protein -
33	42	49.4	1353	1	JH0675	restictin precurs
34	42	49.4	1746	1	A31964	tenascin precursor
35	42	49.4	1810	1	A32230	tenascin precursor
36	42	49.4	1897	1	TDBULK	leukocyte antigen-
37	42	49.4	2019	1	J01322	tenascin precursor
38	42	49.4	2201	2	A32160	tenascin-C - human
39	42	49.4	4135	2	T12629	tenascin-X - bovin
40	42	49.4	6805	2	S20901	tenascin - rabbit (fr
41	42	48.2	290	2	G69416	copalamin biosynth
42	42	48.2	356	2	E97010	chorioleptin synthas
43	42	48.2	438	2	T36953	conserved hypothet
44	42	48.2	440	2	T50213	protein-tyrosine-p
45	42	48.2	610	2	A60227	exonuclease ABC c

ALIGNMENTS

```

RESULT 1
146162
Fibronectin ED-B - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
C:Accession: I46162
R: Zhang, D.W.; Burdon-Murster, N.; Lust, G.
J Biol. Chem. 270, 1817-1822, 1995
A:Title: Alternative splicing of ED-A and ED-B sequences of fibronectin pre-mRNA differ
A:Reference number: I46161; MUID:95130563; PMID:7829518
A:Accession: I46162
A>Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: mRNA
A:Residues: 1-90 <ZHA>
A:Cross-references: EMBL:U16208; NID:9562168; PIDN:AAA67749.1; PID:9562169
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II rep

Query Match          100.0%; Score 85; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GYVTGTGLEPGIDYD 15
Db 55 GYVTGTGLEPGIDYD 69

RESULT 2
S00848
fibronectin, transformation-associated splice form - human (fragment)
N:Alternate names: fibronectin ED-B
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jul-2000
C:Accession: S00848; I59102; R28347
R: Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
A:Title: Sequence analysis and in vivo expression show that alternative splicing of ED-
A:Reference number: S00848; MUID:88233940; PMID:3375063
A:Accession: S00848
A:Molecule type: DNA
A:Residues: 1-147 <PAO>
A:Cross-references: EMBL:X07717; NID:931406; PIDN:CAB52437.1; PID:95725425
R: Gutman, A.; Kornblith, A.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7179-7182, 1987
A:Title: Identification of a third region of cell-specific alternative splicing in human
A:Reference number: I59102; MUID:88041070; PMID:3478690
A:Accession: I59102
A>Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 26-134 <GUT>
A:Cross-references: GB:M8179; NID:9182693; PIDN:AAA52461.1; PID:9182695
R: Zardi, L.; Carnemolla, B.; Sili, A.; Petersen, T.E.; Paolella, G.; Sebastio, G.; Bara
EMBO J. 6, 2337-2342, 1987

```

A>Title: Transformed human cells produce a new fibronectin isoform by preferential altered
A:Reference number: A28347; MUID:88029324; PMID:2822387
A:Accession: A28347
A:Molecule type: protein
A:Residues: 3146 <2AR>
C:Genetics:
A:Gene: GDB:FN1
A:Cross-references: GDB:119135; OMIM:135600
A:Map position: 2q34-2q34
A:Insertions: 35/1; 126/1
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat
C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter
F:35-118/Domain: fibronectin type III repeat homology <3FR>
F:35-118/Domain: fibronectin type III repeat homology <3FR>
Query Match 100.0%; Score 85; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 2,3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GYTVTGLPEGIDYD 15
Db 90 GYTVTGLPEGIDYD 104
RESULT 3
A29355
Fibronectin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 12-Feb-1999
C:Accession: A29355
R:Norton, P.A.; Hynes, R.O.
Mol. Cell. Biol. 7, 4297-4307, 1987
A>Title: Alternative splicing of chicken fibronectin in embryos and in normal and trans
A:Reference number: A29355; MUID:88142820; PMID:2830487
A:Accession: A29355
A:Molecule type: mRNA
A:Residues: 1-1020 <NOR>
C:Genetics:
A:Insertions: 176/3
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter
F:186/Domain: fibronectin type III repeat homology <FN3A>
F:192-177/Domain: fibronectin type III repeat homology <FN3A>
F:180-262/Domain: fibronectin type III repeat homology <FN3A>
F:257-259/Region: cell attachment (R-G-D) motif
F:274-356/Domain: fibronectin type III repeat homology <FN3A>
F:364-446/Domain: fibronectin type III repeat homology <FN3A>
F:454-536/Domain: fibronectin type III repeat homology <FN3A>
F:546-628/Domain: fibronectin type III repeat homology <FN3A>
F:636-718/Domain: fibronectin type III repeat homology <FN3A>
F:837-917/Domain: fibronectin type III repeat homology <FN3A>
F:947-979/Domain: fibronectin type I repeat homology <FN10>
F:940-969,967-979,985-1012/Disulfide bonds: #status predicted
Query Match 100.0%; Score 85; DB 2; Length 1020;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GYTVTGLPEGIDYD 15
Db 149 GYTVTGLPEGIDYD 163
RESULT 4
S14428
fibronectin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Aug-1999
C:Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049
R:Hynes, R.O.
submitted to the EMBL Data Library, July 1989
A:Reference number: S14428
A:Accession: S14428
A:Molecule type: mRNA
A:Residues: 1-2477 <HYN>
A:Cross-references: EMBL:X15906; NID:G56163; PIDN:CAA34020.1; PID:G56164
R:Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A>Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
A:Reference number: S12455; MUID:88054951; PMID:2445560
A:Accession: S12455
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 609-1810, 'T', 1812-2283 <SCH>
A:Cross-references: EMBL:X15906
R:Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A>Title: A single rat fibronectin gene generates three different mRNAs by alternative sp
A:Reference number: A22319; MUID:84280897; PMID:6089177
A:Accession: A22319
A:Molecule type: DNA
A:Residues: 2052-2237 <TAM>
R:Falkenberg, C.; Enghild, J.U.; Thøgersen, I.B.; Salvesen, G.; Akervold, B.
Biochem. J. 301, 745-751, 1994
A>Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in
A:Reference number: S46203; MUID:94330948; PMID:7519849
A:Accession: S46203
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1183-1192, 'G', 1270-1271, 'D', 1273, 'CF', 1276, 'PY', 1385-1399 <FAL>
R:Patel, R.S.; Odeh, E.; Schwarzbauer, J.E.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1987
A>Title: Organization of the fibronectin gene provides evidence for exon shuffling durin
A:Reference number: S00459; MUID:88054950; PMID:3119323
A:Accession: S00459
A:Molecule type: DNA
A:Residues: 1-139, 2382-2477 <PAT>
A:Cross-references: EMBL:X05831
A>Note: The authors translated the codon CCG for residues 51 and 94 as Ala
R:Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
Cell 35, 421-431, 1983
A>Title: Three different fibronectin mRNAs arise by alternative splicing within the codi
A:Reference number: A27252; MUID:84082067; PMID:6317187
A:Accession: A27252
A:Molecule type: mRNA
A:Residues: 1586-1720, 'T', 1722, 1813-2477 <SC2>
R:Odeh, E.; Tamkun, J.W.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A>Title: Repeating modular structure of the fibronectin gene: Relationship to protein st
A:Reference number: I59049; MUID:86016741; PMID:3863113
A:Accession: I59049
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1722-1810 <R3S>
A:Cross-references: GB:M11750; NID:G204164; PIDN:AAA41170.1; PID:G554437
C:Genetics:
A:Insertions: 51/1; 94/1, 2416/3; 2454/3
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C:Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; dupli
F:1-33/Domain: signal sequence #status predicted <SIG>
F:33-447/Domain: fibronectin type I repeat homology <1F1>
F:53-88/Domain: fibronectin type I repeat homology <1F2>
F:98-136/Domain: fibronectin type I repeat homology <1F3>
F:142-180/Domain: fibronectin type I repeat homology <1F4>
F:187-226/Domain: fibronectin type I repeat homology <1F5>
F:232-271/Domain: fibronectin type I repeat homology <1F6>
F:308-342/Domain: fibronectin type II repeat homology <2F1>
F:360-401/Domain: fibronectin type II repeat homology <2F2>
F:420-461/Domain: fibronectin type II repeat homology <2F3>
F:470-508/Domain: fibronectin type I repeat homology <1F7>
F:518-555/Domain: fibronectin type I repeat homology <1F8>
F:561-599/Domain: fibronectin type I repeat homology <1F9>
F:609-692/Domain: fibronectin type II repeat homology <FN3A>
F:718-800/Domain: fibronectin type III repeat homology <FN3B>
F:809-890/Domain: fibronectin type III repeat homology <FN3C>
F:905-987/Domain: fibronectin type III repeat homology <FN3D>

F:779-860/Domain: fibronectin type III repeat homology <FN3C>
F:875-957/Domain: fibronectin type III repeat homology <FN3D>
F:965-1046/Domain: fibronectin type III repeat homology <FN3E>
F:1055-1134/Domain: fibronectin type III repeat homology <FN3F>
F:1142-1227/Domain: fibronectin type III repeat homology <FN3G>
F:1235-1318/Domain: fibronectin type III repeat homology <FN3H>
F:1326-1404/Domain: fibronectin type III repeat homology <FN3I>
F:1410-1517/Domain: cell attachment <CAD>
F:1416-1502/Domain: fibronectin type III repeat homology <FN3J>
F:1493-1495/Region: cell attachment (R-G-D) motif
F:1510-1529/Domain: fibronectin type III repeat homology <FN3K>
F:1600-1682/Domain: heparin binding <HB2>
F:1692-1773/Domain: fibronectin type III repeat homology <FN3M>
F:1781-1863/Domain: fibronectin type III repeat homology <FN3N>
F:1970-1972/Region: cell attachment (R-G-D) motif
F:1982-2062/Domain: fibronectin type III repeat homology <FN3O>
F:1985-2206/Domain: fibrin binding <FB2>
F:2085-2124/Domain: fibronectin type I repeat homology <FI10>
F:2130-2167/Domain: fibronectin type I repeat homology <FI11>
F:2174-2209/Domain: fibronectin type I repeat homology <FI12>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status expiring
F:21-47/45-56-66-94-92-104-110-138-136-148-155-184-182-194-200-229-227-239-277-304-302-3
7-2155-2167-2174-2200-2198-2209/disulfide bonds: #status predicted
F:359-497/511-846-976-1213-1987/Binding site: carboxylate (Asn) (covalent) #status expe
F:1205-1692/Binding site: carboxylate (Asn) (covalent) #status absent
F:1943-1944/Binding site: carboxylate (Thr) (covalent) #status experimental
F:246/Disulfide bonds: interchain (to 2250) #status predicted
F:2250/Disulfide bonds: interchain (to 2246) #status predicted
F:2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 67.1%; Score 57; DB 1; Length 2265;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 3 YVTGEGRGIDY 14
Db 1747 YTTGLQPGIDY 1758

RESULT 7
FNUH
Fibronectin precursor [validated] - human
N:Alternate names: fibronectin splice form ED-A
C:Species: Homo sapiens (man)
C:Date: 27-Nov-1985 #sequence_revision 31-Mar-1993 #text_change 08-Dec-2000
C:Accession: A26460; #sequence A26461; A24854; A24476; A91008; A93529; A21011; A90495; A22
R:Dean, D.C.; Bowlin, C.L.; Bourgeois, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A:Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A:Reference number: A26460; MUID:87175578; PMID:3031656
A:Accession: A26460
A:Molecule type: DNA
A:Residues: 1-49 <DEA>
A:Cross-references: GB:M15801; NID:g182686; PIDN:AAA5376.1; PID:g553293
R:Oldberg, A.; Ruoslahti, E.
J. Biol. Chem. 261, 2113-2116, 1986
A:Title: Evolution of the fibronectin gene.
A:Reference number: A26284; MUID:86111901; PMID:3003095
A:Accession: A26284
A:Molecule type: DNA
A:Residues: 1447-1540 <OLD>
A:Cross-references: GB:M12549; NID:g182688
A:Note: the authors translated the codon TTC for residue 1494 as Gln
R:Palotila, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
A:Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B
A:Reference number: S00848; MUID:88233940; PMID:3375063
A:Accession: S03917
A:Molecule type: DNA
A:Residues: 1594-1767; 'V', 1769-1783 <PAO>
A:Cross-references: EMBL:X07716; NID:g31402

A:Note: the authors translated the codon AAC for residue 1631 as Asp
R:Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986
A:Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:
A:Reference number: A24854; MUID:87030929; PMID:3770201
A:Accession: A24854
A:Molecule type: DNA
A:Residues: 1992-2147 <YIB>
A:Cross-references: GB:X04530; NID:g31436
R:Gutman, A.; Yamada, K.M.; Kornblith, A.
FEBS Lett. 207, 145-148, 1986
A:Title: Human fibronectin is synthesized as a pre-propolypeptide.
A:Reference number: A24476; MUID:87030890; PMID:3770189
A:Accession: A24476
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-14; 'Q', 16-38 <GUT>
R:Kornblith, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985
A:Title: Primary structure of human fibronectin: differential splicing may generate at l
A:Reference number: A91008; MUID:85284965; PMID:2992939
A:Accession: A91008
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 32-1344, 1346-2080, 2112-2386 <KOR>
A:Cross-references: GB:X02761
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5868, 1984
A:Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A:Reference number: A93529; MUID:84272258; PMID:6462919
A:Accession: A93529
A:Molecule type: mRNA
A:Residues: 973-2080; 2112-2386 <KO2>
A:Cross-references: GB:X00739
R:Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A:Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a
A:Reference number: A21011; MUID:83290929; PMID:668418
A:Accession: A21011
A:Molecule type: mRNA
A:Residues: 1434-1537 <OL2>
A:Cross-references: GB:X00055; NID:g182680; PIDN:AAA52459.1; PID:g182683
R:Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A:Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra
A:Reference number: A90495; MUID:85280409; PMID:2992573
A:Accession: A90495
A:Molecule type: mRNA
A:Residues: 1594-2386 <EBR>
A:Cross-references: GB:M10905; NID:g182696; PIDN:AAA52462.1; PID:g182697
R:Umezawa, K.; Kornblith, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A:Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A:Reference number: A22245; MUID:85231203; PMID:2989004
A:Accession: A22245
A:Molecule type: mRNA
A:Residues: 1948-2067 <DME>
A:Cross-references: GB:M27589; NID:g182705; PIDN:AAA52465.1; PID:g182706
A:Accession: B22245
A:Molecule type: mRNA
A:Residues: 1975-1991, 2017-2039 <DM2>
A:Cross-references: GB:M27590
R:Sekiguchi, K.; Kios, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4938-4941, 1986
A:Title: Human liver fibronectin complementary DNAs: identification of two different mes
A:Reference number: 152394; MUID:87026578; PMID:3021206
A:Accession: 165273
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 <SEK>
A:Cross-references: GB:M14060; NID:g182701; PIDN:AAA52464.1; PID:g182704
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983

A>Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A/Reference number: A21165; MUID:83221567; PMID:6304699
A/Accession: A21165
A/Molecule type: mRNA
A/Residues: 2291-2386 <K03>
A/Cross-references: GB:K00799; NID:9182681; PIDN:AA52460.1; PID:9182684
R/Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 258, 12670-12674, 1983
A/Title: Primary structure of human plasma fibronectin.
A/Reference number: A92398; MUID:84032463; PMID:6630202
A/Accession: A92398
A/Molecule type: protein
A/Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>
R/Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993.
A/Title: Further characterization of the binding of fibronectin to gelatin reveals the F
A/Reference number: S34791; MUID:93312001; PMID:8323285
A/Accession: S34791
A/Molecule type: protein
A/Residues: 291-300/551-560 <GAR2>
R/Giffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A/Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A/Reference number: A60904; MUID:87029725; PMID:3532418
A/Accession: A60904
A/Molecule type: protein
A/Residues: 293-301 <GR1>
R/Calaycay, J.; Pandé, H.; Lee, T.; Borsi, L.; Sirt, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A/Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pl
A/Reference number: A23901; MUID:86008277; PMID:3390070
A/Accession: A23901
A/Molecule type: protein
A/Residues: 616-677, 'Q', 679-703, 'PT', <CAL>
R/Pieterschacher, M.D.; Rucslahli, E.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A/Title: The cell attachment domain of fibronectin. Determination of the primary structu
A/Reference number: A92386; MUID:82256604; PMID:7050098
A/Accession: A92386
A/Molecule type: protein
A/Residues: 1441-1548 <PRE>
A/Note: residues 1524-1527 are responsible for the cell-binding activity
R/Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A/Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dom
A/Reference number: A32517; MUID:87241275; PMID:3593230
A/Accession: A32517
A/Molecule type: protein
A/Residues: 1589-1630, 'T', 1722-2058 <GAR3>
R/Tessell, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pand
Biochem. J. 274, 731-738, 1991
A/Title: Human plasma fibronectin. Demonstration of structural differences between the A
A/Reference number: S14357; MUID:91190085; PMID:2012601
A/Accession: S14357
A/Molecule type: protein
A/Residues: 1614-1630, 'T', 1722-2081, 2113-2244 <TRE>
R/Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A/Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dal
A/Reference number: A23891; MUID:85261459; PMID:4019516
A/Accession: A23891
A/Molecule type: protein
A/Residues: 2071-2080/2112-2356 <GAR4>
C/Comment: The extra domain and connecting strand 3 are subject to developmental and tis
C/Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
action, and transformation.
C/Genetics:
A/Gene: GDB:FNI
A/Cross-references: GDB:119135; OMIM:135600
A/Map position: 2q34-q34
A/Intons: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C/Superfamily: fibronectin, fibronectin type I repeat homology, fibronectin type II rep
C/Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicated

F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-31/Domain: propeptide #status predicted <PRO>
F:32-2386/Product: fibronectin #status experimental <MNT>
F:52-272/Domain: fibrin and heparin binding <FHB>
F:52-87/Domain: fibronectin type I repeat homology <1F1>
F:57-135/Domain: fibronectin type I repeat homology <1F2>
F:141-179/Domain: fibronectin type I repeat homology <1F3>
F:186-225/Domain: fibronectin type I repeat homology <1F4>
F:231-270/Domain: fibronectin type I repeat homology <1F5>
F:308-608/Domain: collagen binding <CBR>
F:308-347/Domain: fibronectin type I repeat homology <1F6>
F:320-401/Domain: fibronectin type II repeat homology <2F1>
F:420-461/Domain: fibronectin type II repeat homology <2F2>
F:470-508/Domain: fibronectin type I repeat homology <1F7>
F:518-555/Domain: fibronectin type I repeat homology <1F8>
F:561-599/Domain: fibronectin type I repeat homology <1F9>
F:609-692/Domain: fibronectin type III repeat homology <3FA>
F:616-706/Domain: heparin binding <HPB>
F:719-801/Domain: fibronectin type III repeat homology <3FB>
F:810-891/Domain: fibronectin type III repeat homology <3FC>
F:906-988/Domain: fibronectin type III repeat homology <3FD>
F:996-1077/Domain: fibronectin type III repeat homology <3FE>
F:1086-1164/Domain: fibronectin type III repeat homology <3FF>
F:1173-1258/Domain: fibronectin type III repeat homology <3FG>
F:1266-1349/Domain: fibronectin type III repeat homology <3FH>

Query Match 67.1%; Score 57; DB 1; Length 2386;
Best Local Similarity 75.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVGSLPGIDY 14
Db 1868 YTTGLPGIDY 1879

RESULT 8
A28512
C/Species: gallus gallus (chicken)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Aug-1999
C/Accession: A28512
R/Kubomura, S.; Obara, M.; Karasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi,
Biochim. Biophys. Acta 910, 171-181, 1987
A/Title: Genetic analysis of the cell binding domain region of the chicken fibronectin
A/Reference number: A28512; MUID:88050550; PMID:2823899
A/Accession: A28512
A/Molecule type: DNA
A/Residues: 1-273 <KUN>
A/Cross-references: GB:X06533; NID:963393; PIDN:CA29781.1; PID:9295716
A/Note: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 24
C/Genetics:
A/Intons: 90/1; 129/1; 184/1; 236/1
C/Superfamily: fibronectin, fibronectin type I repeat homology, fibronectin type II rep
C/Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; hete
F:1-82/Domain: fibronectin type III repeat homology (fragment) <FN31>
F:90-172/Domain: fibronectin type III repeat homology <FN3J>
F:167-169/Region: cell attachment (R-G-D) motif
F:184-266/Domain: fibronectin type III repeat homology <FN3K>

Query Match 62.4%; Score 53; DB 2; Length 273;
Best Local Similarity 72.7%; Pred. No. 0.62;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 TWTGSLPGIDY 14
Db 147 TITGLPGIDY 157

RESULT 9
I38344
C/Intin: cardiac muscle [validated] - human
N/Alternate names: connectin
N/contains: serine/threonine-specific protein kinase (EC 2.7.1.-)

C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text change 15-Sep-2000
C:Accession: 18344; 138345; S20898; S20897; S20899; S63665; S37393
R:Label: S.; Kolmerer, B.
Science 270, 293-296, 1995
A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330; PMID:7569978
A:Accession: 138344
A:Status: nucleic acid sequence not shown; translated from GB/EMBL
A:Molecule type: mRNA
A:Residues: 1-26926 <LMB1>
A:Cross-references: EMBL:X90568; NID:61017424; PID:61017425
R:Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
A:Title: Dissecting titin into its structural motifs: identification of an alpha-helix
A:Reference number: 138345; MUID:95119041; PMID:7819245
A:Accession: 138345
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1977-2014 <MCS>
A:Cross-references: EMBL:X62270; NID:6602579; PIDN:CAA58243.1; PID:6602580
A:Note: Correspondence and properties are reported for a synthetic peptide corresponding to
R:Label: S.; Gauteil, M.; Lahey, A.; Trinch, J.
EMBO J. 11, 1711-1716, 1992
A:Title: Towards a molecular understanding of titin.
A:Reference number: S20897; MUID:92258380; PMID:1582406
A:Accession: S20898
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 13597-14200, 'I', 14202-14696 <IAB>
A:Cross-references: EMBL:X64698; NID:937192; PIDN:CAA45939.1; PID:937193
A:Accession: S20897
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: tRNA
A:Residues: 16330-16382, 'S', 16384-16756, 'F', 16758-16860 <IAB>
A:Cross-references: EMBL:X64699; NID:937190; PIDN:CAA45940.1; PID:937191
A:Accession: S20899
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 'P', 22431, 'R', 22433-22448, 'G', 22450-22453, 'O', 22455-22480, 'TR', 22483-22484
A:Cross-references: EMBL:X64697; NID:937190; PIDN:CAA45938.1; PID:937195
R:Kolmerer, B.; Olivieri, N.; Wilt, C.C.; Herrmann, B.G.; Labelle, S.
J. Mol. Biol. 256, 556-563, 1996
A:Title: Genomic organization of M line titin and its tissue-specific expression in two
A:Reference number: S63665; MUID:9617761; PMID:8604138
A:Accession: S63665
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 26729-26825 <KOL>
A:Cross-references: EMBL:X92412; NID:61236761
R:Gauteil, M.; Leonard, K.; Labelle, S.
EMBO J. 12, 3827-3834, 1993
A:Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differentiating
A:Reference number: S37393; MUID:94008990; PMID:8404852
A:Accession: S37393
A:Molecule type: mRNA
A:Residues: 26831-26926 <GAU>
R:Improta, S.; Politou, A.S.; Pastore, A.
Submitted to the Brookhaven Protein Data Bank, February 1996
A:Reference number: A66736; PDB:1RTT
A:Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
R:Pfuhl, M.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66201; PDB:1NET
A:Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
C:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q32
C:Function:
A:Description: structural protein forming filaments in striated muscle
A:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; pqq
A:Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glyced

structural protein
F:24752-25008/Domain: protein kinase homology <Kin>
F:84,177,905,2276,2378,2459,2481,5563,2659,2763,2896,3086,3179,3384,3432,3628,3772,4068,
98,11066,11488,11515,11535,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,1
catus Predicted
F:16780,16976,17579,17602,17667,17681,17845,17899,18121,18188,18209,18336,18670,18680,18
21900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,248
F:26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status: experimental

Query Match 56.5%; Score 48; DB 1; Length 26926;
Best Local Similarity 69.2%; Pred. No. 5.3e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDYD 15
|||||
Db 21416 YTVTGLSPGDHYE 21428

RESULT 10
A90255
hypochemical protein SSO1033 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #ext_change 24-May-2001
C:Accession: A90255
R:Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A9139
A:Accession: A90255
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-725 <KUR>
A:Cross-references: GB:AE006641; NID:g13814216; PIDN:AAK1296.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO1033

Query Match 55.3%; Score 47; DB 2; Length 725;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
|||||
Db 374 YTVTGLKDGITY 385

RESULT 11
A45445
janusin precursor, long form - rat
N:Alternate names: neural recognition glycoprotein J1-160/180, long form
N:Contains: neural recognition glycoprotein J1-160/180, short form
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #ext_change 20-Aug-1999
C:Accession: A45445; B45445; G32023
R:Fusus, B.; Wintergerst, E.S.; Bartsch, U.; Schachner, M.
U: Cell Biol. 120, 1237-1249, 1993
A:Title: Molecular characterization and in situ mRNA localization of the neural recogni-
A:Reference number: A45445; MVID:93171267; PMID:7679676
A:Accession: A45445
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1356 <FUS>
A:Cross-references: GB:218630; NID:g57961; PIDN:CAA79229.1; PID:g57962
A:Accession: B45445
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-772,863-1356 <FU2>
A:Cross-references: GB:218630
R:Fusus, B.; Wintergerst, E.; Bartsch, U.; Schachner, M.
submitted to the EMBL Data Library, November 1992
A:Description: Molecular characterization and in situ mRNA localization of the neural re-
A:Reference number: S32023

A/Accession: S32023
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-1356 <FN2>
A/Cross-references: EMBL:Z18630; NID:G57961; PIDN:CAA79229.1; PID:G57962
C/Keywords: alternative splicing; EGF homology; fibronogen beta/gamma homology; fibronectin type
C/Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; oligo
F:1-1356/Product: jansin, long form #status experimental <ALT>
F:1-772,865-1356/Product: jansin, short form #status experimental <ALT>
F:204-230/Domain: EGF homology <EG1>
F:235-261/Domain: EGF homology <EG2>
F:266-292/Domain: EGF homology <EG3>
F:297-323/Domain: EGF homology <EG4>
F:335-405/Domain: fibronectin type III repeat homology <FN1>
F:413-494/Domain: fibronectin type III repeat homology <FN2>
F:502-584/Domain: fibronectin type III repeat homology <FN3>
F:592-676/Domain: fibronectin type III repeat homology <FN4>
F:664-764/Domain: fibronectin type III repeat homology <FN5>
F:772-854/Domain: fibronectin type III repeat homology <FN6>
F:1038-1118/Domain: fibronectin type III repeat homology <FN7>
F:1133-1341/Domain: fibronogen beta/gamma homology <FG>

Query Match 55.3%; Score 47; DB 2; Length 1356;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 738 YTTGDEPGVGY 749

RESULT 12
A54849
collagen alpha 1(VII) chain precursor - human
N/Alternate names: procollagen alpha 1(VII) chain
C/Species: Homo sapiens (man)
C/Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text change 15-Sep-2003
C/Accession: A54849; PH0844; S16316; I56328; A30296; I84686
J./Christiano, A.M.; Greenspan, D.S.; Lee, S.; Vitto, J.
R. Biol. Chem. 269, 20256-20262, 1994
A/Title: Cloning of human type VII collagen. Complete primary sequence of the alpha1(VII)
A/Reference number: A54849; MUID:94327588; PMID:8051117
A/Accession: A54849
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-2944 <CHR>
A/Cross-references: GB:102870; NID:G987124; PIDN:AA75438.1; PID:G987125
R./Tanaka, T.; Takahashi, K.; Furukawa, F.; Imanura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A/Title: Molecular cloning and characterization of type VII collagen cDNA.
A/Reference number: PH0844; MUID:92231902; PMID:1567409
A/Accession: PH0844
A/Molecule type: mRNA
A/Residues: 'EPR', 340-475, 'RALSASHSTLCWATRMRHPCNRGSHWTRACCEPNRPAHARAG', 524-528, 'C',
A/Cross-references: DDBJ:D1152; DDBJ:D13694; NID:G453698; PIDN:BA02853.1; PID:G453699
A/Experimental source: keratinocyte
A/Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R./Patene, M.G.; Chung, L.C.; Rymaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A/Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A/Reference number: S16316; MUID:91333380; PMID:1871109
A/Accession: S16316
A/Molecule type: mRNA
A/Residues: 815-892, 'E', 894-1439 <PAR>
A/Cross-references: GB:M6518; GB:S49017; NID:G180914; PIDN:AA96439.1; PID:G180915
A/Experimental source: keratinocyte
R./Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Pritsyant, P.S.; Cook, M.E.; Wright, J.
J. Invest. Dermatol. 99, 691-696, 1992
A/Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion pro
A/Reference number: I56328; MUID:93107742; PMID:1469284
A/Accession: I56328
A/Status: translated from GB/EMBL/DDBJ
A/Molecule type: mRNA

A/Residues: 'EPR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A/Cross-references: GB:S51236; NID:G262308; PIDN:AB24637.1; PID:G262309
R./Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgess, R.E
J. Biol. Chem. 264, 3822-3826, 1989
A/Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagen
A/Reference number: A30296; MUID:89139437; PMID:2537292
A/Accession: A30296
A/Molecule type: protein
A/Residues: 'A', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E', 12032, 'C', 2034-2041;
A/Note: two reported peptides cannot be reliably located
R./Greenspan, D.S.
Hum. Mol. Genet. 2, 273-278, 1993
A/Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A/Reference number: I48103; MUID:93271985; PMID:8499916
A/Accession: I48103
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 2395-2871, 'S', 2873-2944 <RE2>
A/Cross-references: GB:L06862; NID:G388713; PIDN:AA89196.1; PID:G388714
R./Christiano, A.M.; Rymaenen, M.; Vitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A/Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser sub
A/Reference number: A55255; MUID:94224777; PMID:8170945
A/Contents: annotation
A/Comments: prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C/Genetics:
A/Genes: GDB:COL7A1; EBRL; EBD1; EB
A/Cross-references: GDB:128750; OMIM:120120
A/Map position: 3p21.3-3p21.3
A/Note: defects in this gene can result in dominant and recessive dystrophic epidermol
A/Note: there are 118 introns
C/Complex: type VII collagen is probably a homotrimer
C/Function:
A/Description: structural component of extracellular polymer associated with anchoring
C/Keywords: collodion; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol
F:1-17/Domain: signal sequence #status predicted <SIG>
F:17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
F:17-1253/Domain: amino-terminal nonhelical #status predicted <NCT>
F:166-201/Domain: von Willebrand factor type A repeat homology <VWA1>
F:231-318/Domain: fibronectin type III repeat homology <FN1>
F:327-413/Domain: fibronectin type III repeat homology <FN2>
F:414-502/Domain: fibronectin type III repeat homology <FN3>
F:508-593/Domain: fibronectin type III repeat homology <FN4>
F:598-683/Domain: fibronectin type III repeat homology <FN5>
F:686-771/Domain: fibronectin type III repeat homology <FN6>
F:776-862/Domain: fibronectin type III repeat homology <FN7>
F:864-952/Domain: fibronectin type III repeat homology <FN8>
F:954-1045/Domain: fibronectin type III repeat homology <FN9>
F:1052-1219/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1170-1172/Region: cell attachment (R-G-D) motif
F:1189-1253/Region: cysteine/proline-rich
F:1254-2783/Region: interrupted helical
F:1334-1336/Region: cell attachment (R-G-D) motif
F:2008-2010/Region: cell attachment (R-G-D) motif
F:2553-2555/Region: cell attachment (R-G-D) motif
F:2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NCT2>
F:2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:337,786,1109/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:3167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #status expe
F:2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F:2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
F:2634,2802,2804/Disulfide bonds: interchain #status predicted

Query Match 55.3%; Score 47; DB 2; Length 2944;
Best Local Similarity 80.0%; Pred. No. 7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1015 YTTGDEPGVGY 1024

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:37 ; Search time 4.30:47 Seconds

(without alignments)
181.578 Million cell updates/sec

Title: US-10-676-049-2

Perfect score: 85
Sequence: 1 GYVTGTLRPGIDVD 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	1256	1 FINC_CHICK	P11722 gallus gall
2	85	100.0	2477	1 FINC_MOUSE	P11276 mus musculu
3	85	100.0	2477	1 FINC_RAT	P04937 rattus norv
4	75	88.2	1328	1 FINC_PLEMA	Q91289 pleurodeles
5	71	83.5	2481	1 FINC_XENLA	Q91740 xenopus lae
6	57	67.1	522	1 FINC_CANFA	Q28275 canis fami
7	57	67.1	522	1 FINC_HORSE	Q28377 equus cabal
8	57	67.1	2265	1 FINC_BOVIN	P07589 bos taurus
9	57	67.1	2366	1 FINC_HUMAN	P02751 homo sapien
10	47	55.3	725	1 VA33_SUISO	Q97257 suifolobus
11	47	55.3	1560	1 TENN_MOUSE	Q80271 mus musculu
12	47	55.3	2944	1 CAL7_HUMAN	Q02368 homo sapien
13	45	52.9	610	1 UVRC_ECOLI	Q9P034 xylella fas
14	45	52.9	621	1 UVRC_XYLEFA	Q9P034 xylella fas
15	45	52.9	621	1 UVRC_XYLEFA	Q9P034 xylella fas
16	45	52.9	746	1 PPK_STRCO	Q9K276 streptomyces
17	45	52.9	1294	1 TENN_HUMAN	Q9UGD3 homo sapien
18	44	51.8	216	1 CARE_HUMAN	Q90479 brachydanio
19	43	50.6	1004	1 CARE_HUMAN	Q90479 brachydanio
20	42	49.4	340	1 YCEG_ECOLI	Q95X16 homo sapien
21	42	49.4	441	1 YC14_PYRHO	P28306 escherichia
22	42	49.4	1095	1 CC25_SACKL	O58969 pyrococcus
23	42	49.4	1746	1 TENA_PIG	Q02342 saccharomyc
24	42	49.4	1808	1 TENA_PIG	Q29116 sus scrofa
25	42	49.4	1897	1 PTFP_CHICK	P10039 gallus gall
26	42	49.4	2201	1 TENA_HUMAN	P10366 homo sapien
27	41	48.2	290	1 COBD_ARCFU	P24821 homo sapien
28	41	48.2	610	1 UVRC_YERPE	O28933 archaeglob
29	41	48.2	668	1 F13B_MOUSE	O28552 yerina pe
30	41	48.2	872	1 GUXA_MOUSE	Q07968 mus musculu
31	40.5	47.6	819	1 PK61_DROME	P50401 cellulomona
32	40	47.1	334	1 ILVC_STRMU	Q95011 drosophila
33	40	47.1	468	1 LACG_STRMU	Q95916 staphylococ
					P50978 streptococc

ALIGNMENTS

RESULT	ID	FINC_CHICK	STANDARD	PRT	1256 AA
AC	P11722	Q90921			
DT	01-OCT-1988	(Rel. 12, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-MAR-2004	(Rel. 43, Last annotation update)			
DE	Fibronectin (FN) (Fragments)				
GN	FN1				
OS	Gallus gallus (Chicken)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus				
OX	NCBI_TaxID=90311				
RN	[1]				
RP	SEQUENCE OF 1-50 FROM N.A.				
RX	MEDLINE=83117850; PubMed=6572007;				
RA	Hirano H., Yamada Y., Sullivan M., de Crombrughe B., Paetan I.,				
RA	Yamada K.M.,				
RT	"Isolation of genomic DNA clones spanning the entire fibronectin				
RT	gene."				
RL	Proc. Natl. Acad. Sci. U.S.A. 80:46-50(1983).				
RN	[2]				
RP	SEQUENCE OF 51-1256 FROM N.A.				
RC	STRAIN=White leghorn;				
RA	Norton P.A.,				
RN	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.				
RP	SEQUENCE OF 227-415 FROM N.A.				
RX	MEDLINE=96183658; PubMed=8603103;				
RA	Gehris A.L., Brandt D.W., Lewis S.D., Bennett V.D.;				
RT	"The exon encoding the fibronectin type III-9 repeat is				
RT	constitutively included in the mRNA from chick limb mesenchyme and				
RT	cartilage."				
RL	Biochim. Biophys. Acta 1311:5-12(1996).				
RN	[4]				
RP	SEQUENCE OF 327-599 FROM N.A.				
RX	MEDLINE=88050950; PubMed=2823699;				
RA	Kubomura S., Obara M., Karasaki Y., Taniguchi H., Gotcho S.,				
RA	Tsuda T., Higashi K., Onato K., Hiarto H.;				
RT	"Genetic analysis of the cell binding domain region of the chicken				
RT	fibronectin gene."				
RL	Biochim. Biophys. Acta 910:171-181(1987).				
RN	[5]				
RP	SEQUENCE OF 413-1256 FROM N.A.				
RX	MEDLINE=88142820; PubMed=2830487;				
RA	Norton P.A., Hynes R.O.;				
RT	"Alternative splicing of chicken fibronectin in embryos and in normal				
RT	and transformed cells."				
RL	Mol. Cell. Biol. 7:4297-4307(1987).				
CC	- FUNCTION: Fibronectins bind cell surfaces and various compounds				
CC	including collagen, fibrin, heparin, DNA, and actin. Fibronectins				
CC	are involved in cell adhesion, cell motility, opsonization, wound				
CC	healing, and maintenance of cell shape.				
CC	- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED				
CC	VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;				

34	40	47.1	482	1	GLCA_CLOPE	O8XPA1 clostridium
35	40	47.1	547	1	ILVG_MYCTU	O50613 mycobacteri
36	40	47.1	610	1	UVRC_SALTI	O82513 salmoneilla
37	40	47.1	610	1	UVRC_SALTY	O66041 salmoneilla
38	40	47.1	679	1	WHIT_CERCA	O17320 cercaritis c
39	40	47.1	880	1	GUNA_THERFU	P26521 thermomons
40	40	47.1	972	1	POIS_TIPYNY	P22495 infectious
41	40	47.1	1329	1	KP10_HUMAN	O92618 homo sapien
42	40	47.1	1447	1	DDC_HUMAN	P43146 homo sapien
43	40	47.1	1447	1	DDC_MOUSE	P70211 mus musculu
44	40	47.1	4289	1	TENX_HUMAN	P22105 homo sapien
45	39	45.9	287	1	HTPX_VIBCH	O9KEY9 vibrio chol

CC TO A LESSER EXTEND HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Comment=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced. Each of the "extra
 CC domain" and the connecting strand 3 are present in some forms of
 CC fibronectin and absent in others;
 CC Name=1;
 CC Icdid=P11722-1; Sequence=Displayed;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 CC forms), made by fibroblasts, epithelial and other cell types, is
 CC deposited as fibrils in the extracellular matrix.
 CC -1- PMW: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains at least 8 fibronectin type III domains.
 CC -1- SIMILARITY: Contains at least 8 fibronectin type III domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: V00432; CA23714.1; -;
 CC EMBL: U21327; AAA73566.1; -;
 CC EMBL: X06533; CA429781.1; -;
 CC EMBL: M26186; AAA48772.1; ALT_SEQ.
 CC EMBL: U20386; AAB01062.1; -;
 CC PIR: A28512; A28512.
 CC PIR: A29355; A29355.
 CC PIR: S71465; S71465.
 CC HSSP: P02751; 1FNH.
 CC InterPro: IPR000083; Fibronctn1.
 CC InterPro: IPR008957; FN-III-like.
 CC InterPro: IPR003961; FN-III.
 CC InterPro: IPR000562; FN_Type_II.
 CC InterPro: IPR003962; FNIII_subd.
 CC PRINTS: PR00014; FNTPHIII.
 CC SMART: SM00058; FN1; 3.
 CC SMART: SM00060; FN3; 9.
 CC PROSITE: PS00023; FIBRONECTIN_2; PARTIAL.
 CC PROSITE: PS01253; FIBRONECTIN_1; 2.
 CC GlycoProfile: Plasma; Heparin-binding; Acute phase; Cell adhesion;
 CC Repeat; Sulfation; Alternative splicing.
 CC KW NON_TER 1 51
 CC FT NON_TER 1 51
 CC FT DOMAIN 236 509
 CC FT DOMAIN 690 961
 CC FT DOMAIN 1153 1226
 CC FT DOMAIN 327 415
 CC FT DOMAIN 416 509
 CC FT DOMAIN 510 599
 CC FT DOMAIN 600 689
 CC FT DOMAIN 690 781
 CC FT DOMAIN 782 871
 CC FT DOMAIN 872 961
 CC FT DOMAIN 962 1082
 CC FT DOMAIN 1083 1152
 CC FT DOMAIN 1174 1218
 CC FT DOMAIN 1219 >1256
 CC SITE 493 495
 CC FT DISULFID 1176 1205
 CC FT DISULFID 1203 1215
 CC FT DISULFID 1221 1248
 CC FT CARBOHYD 122 122
 CC FT CARBOHYD 1078 1078
 CC FT CARBOHYD 1034 1034
 CC FT CARBOHYD 1035 1035
 CC FT CARBOHYD 516 516
 CC FT CONFLICT 569 572
 CC FT NON_TER 1256 1256

SQL SEQUENCE 1256 AA; 137435 MW; 345A4CA0E4D71D9B CRC64;
 Query Match 100.0%; Score 85; DB 1; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 1,4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GYTVTGHPGIDYD 15
 DB 199 GYTVTGHPGIDYD 213
 RESULT 2
 ID FINE MOUSE STANDARD; PRT; 2477 AA.
 AC P11276; O61567; O61569; O64233; Q80U14;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin precursor (FN).
 GN FN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE OF 1-920 FROM N.A.
 RC STRAIN=FVB/N-3; TISSUE=Breast tumor;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheafer C.F., Bhat N.K.,
 RA Hopkins S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marulanda K., Farmer A.A., Rubin G.M., Hong L.,
 RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Stadleton M.J., Ustin T.B., Toshlycki S., Carninci P., Prange C.,
 RA Brownstein M.J., Ustin T.B., Toshlycki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalobos D.K., Nuzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Matra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RA human and mouse cDNA sequences.";
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL (2)
 RN SEQUENCE OF 1-28 FROM N.A.
 RP TISSUE=Liver;
 RC MEDLINE=9413113; PubMed=8299972;
 RX POLLY P., Nicholson R.C.;
 RA "Sequence of the mouse fibronectin-encoding gene promoter region.";
 RL Gene 137:353-354(1993).
 RN (3)
 RP SEQUENCE OF 562-834 FROM N.A.
 RC STRAIN=MARI;
 RX MEDLINE=95403556; PubMed=7673336;
 RA Tates J.F., Welier A., Timpi R., Ekblom M., Ekblom P.;
 RL "Regulation of mesenchymal extracellular matrix protein synthesis by
 RL transforming growth factor-beta and glucocorticoids in tumor
 RL stroma.";
 RL J. Cell Sci. 108:2153-2162(1995).
 RN (4)
 RP SEQUENCE OF 859-2376 FROM N.A.
 RC Gozdek G., Aros M., Notron P.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RC MEDLINE=88124987; PubMed=3124113;
 RL Blatti S.P., Foster D.N., Ranganathan G., Moses H.L., Getz M.J.;
 RA "Induction of fibronectin gene transcription and mRNA is a primary

RT response to growth-factor stimulation of AKR-2B cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).
 RN [6]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93011702; Pubmed=1327855;
 RA Khandjian E.W., Salomon C., Leonard N., Tremblay S., Turler H.;
 RT "Fibronectin gene expression in proliferating, quiescent, and SV40-
 infected mouse kidney cells";
 RL Exp. Cell Res. 202:464-470(1992).
 RN [7]
 RP STRUCTURE BY NMR OF 1447-1630.
 RX MEDLINE=98202578; Pubmed=9533887;
 RA Cople V., Tomita Y., Akiyama S.K., Aota S., Yamada K.M., Venable R.M.,
 R Pastor R.W., Krueger S., Torchia D.A.;
 RT "solution structure and dynamics of linked cell attachment modules of
 mouse fibronectin containing the RGD and synergy regions: comparison
 with the human fibronectin crystal structure.";
 RL J. Mol. Biol. 277:663-682(1998).
 RN [8]
 RP DOWN-REGULATION BY GLUCOCORTICOIDS.
 RX MEDLINE=2160963; Pubmed=11737251;
 RA Gu Y.-C., Tals J.F., Guilberg D., Timpl R., Ekblom M.;
 RT "Glucocorticoids down-regulate the extracellular matrix proteins
 fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
 RL Eur. J. Haematol. 67:176-184(2001).
 CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
 including collagen, fibrin, heparin, DNA, and actin. Fibronectins
 are involved in cell adhesion, cell motility, opsonization, wound
 healing, and maintenance of cell shape.
 CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
 variants, connected by 2 disulfide bonds near the carboxyl ends;
 to a lesser extend homodimers. Interacts with FHLN1 (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=1;
 Comment=A number of isoforms are produced. Each of the "extra
 domain" and the connecting strand 3 are present in some forms of
 fibronectin and absent in others;
 CC Name=1;
 CC -1- ISOLCD=P11276-1; Sequence=Displayed;
 CC TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 forms), made by fibroblasts, epithelial and other cell types, is
 deposited as fibrils in the extracellular matrix.
 CC -1- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
 synthesis.
 CC -1- PTM: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: BC051082; AAHS1082.1; -
 DR EMBL: 222729; CAAB0422.1; -
 DR EMBL: X82402; CAAS7796.1; -
 DR EMBL: X93167; CAAG3654.1; -
 DR EMBL: X18194; AAAG7636.1; -
 DR EMBL: S45680; AAB23491.1; -
 DR PIR: A49173; A49173.
 DR PIR: I48349; I48349.
 DR PDB: 1MFN; 29-APR-98.
 DR PDB: 2MFN; 29-APR-98.
 DR MCD: MGI:95566; Fnl.
 DR GO: GO:0007155; P:cell adhesion, IDA.

DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR000083; Fibinectn.
 DR InterPro; IPR008957; FN-III-like.
 DR InterPro; IPR003961; FN-III.
 DR InterPro; IPR000562; FN type II.
 DR InterPro; IPR003962; FnlII subd.
 DR InterPro; IPR008924; MCR_alpha_beta_C.
 DR PRINTS: PR00014; FNTYPEII.
 DR SMART; SMC0058; FNI; 4.
 DR SMART; SMC0060; FN3; 12.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
 KW Sulfation; Cell adhesion; Repeat; Alternative splicing; Signal;
 KW 3d-structure.
 FT SIGNAL 1 32
 FT CHAIN 33 2477 BY SIMILARITY.
 FT DOMAIN 53 273 FIBRONECTIN.
 FT DOMAIN 308 608 FIBRIN- AND HEPARIN-BINDING 1.
 FT DNA_BIND 906 1171 COLLAGEIN-BINDING.
 FT DOMAIN 1357 1630
 FT DOMAIN 1811 2081 CELL-ATTACHMENT.
 FT DOMAIN 2296 2427 FIBRIN-BINDING 2.
 FT DOMAIN 51 96 FIBRONECTIN TYPE-1 1.
 FT DOMAIN 96 140 FIBRONECTIN TYPE-1 2.
 FT DOMAIN 140 185 FIBRONECTIN TYPE-1 3.
 FT DOMAIN 185 230 FIBRONECTIN TYPE-1 4.
 FT DOMAIN 230 272 FIBRONECTIN TYPE-1 5.
 FT DOMAIN 306 343 FIBRONECTIN TYPE-1 6.
 FT DOMAIN 345 404 FIBRONECTIN TYPE-1 7.
 FT DOMAIN 405 469 FIBRONECTIN TYPE-1 8.
 FT DOMAIN 468 516 FIBRONECTIN TYPE-1 9.
 FT DOMAIN 516 559 FIBRONECTIN TYPE-1 10.
 FT DOMAIN 559 602 FIBRONECTIN TYPE-1 11.
 FT DOMAIN 609 706 FIBRONECTIN TYPE-1 12.
 FT DOMAIN 707 808 FIBRONECTIN TYPE-1 13.
 FT DOMAIN 809 904 FIBRONECTIN TYPE-1 14.
 FT DOMAIN 904 993 FIBRONECTIN TYPE-1 15.
 FT DOMAIN 995 1084 FIBRONECTIN TYPE-1 16.
 FT DOMAIN 1085 1172 FIBRONECTIN TYPE-1 17.
 FT DOMAIN 1173 1264 FIBRONECTIN TYPE-1 18.
 FT DOMAIN 1265 1355 FIBRONECTIN TYPE-1 19.
 FT DOMAIN 1356 1446 FIBRONECTIN TYPE-1 20.
 FT DOMAIN 1447 1536 FIBRONECTIN TYPE-1 21.
 FT DOMAIN 1537 1630 FIBRONECTIN TYPE-1 22.
 FT DOMAIN 1631 1720 FIBRONECTIN TYPE-1 23.
 FT DOMAIN 1721 1810 FIBRONECTIN TYPE-1 24.
 FT DOMAIN 1811 1902 FIBRONECTIN TYPE-1 25.
 FT DOMAIN 1903 1991 FIBRONECTIN TYPE-1 26.
 FT DOMAIN 1992 2081 FIBRONECTIN TYPE-1 27.
 FT DOMAIN 2082 2201 FIBRONECTIN TYPE-1 28.
 FT DOMAIN 2202 2283 FIBRONECTIN TYPE-1 29.
 FT DOMAIN 2284 2338 FIBRONECTIN TYPE-1 30.
 FT DOMAIN 2339 2381 FIBRONECTIN TYPE-1 31.
 FT DOMAIN 2383 2426 FIBRONECTIN TYPE-1 32.
 FT SITE 1614 1616 CELL ATTACHMENT SITE.
 FT SITE 2181 2183 CELL ATTACHMENT SITE.
 FT DISULFID 53 78 BY SIMILARITY.
 FT DISULFID 77 89 BY SIMILARITY.
 FT DISULFID 98 126 BY SIMILARITY.
 FT DISULFID 124 136 BY SIMILARITY.
 FT DISULFID 142 170 BY SIMILARITY.
 FT DISULFID 168 180 BY SIMILARITY.
 FT DISULFID 187 216 BY SIMILARITY.
 FT DISULFID 214 226 BY SIMILARITY.
 FT DISULFID 232-261 BY SIMILARITY.
 Query Match 100.0%; Score 85; DB 1; Length 2477;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GYTVTGHPGIDYD 15

Db 1320 GYTTVTGLEPIDYD 1334

RESULT 3
FIND_RAT STANDARD; PRT; 2477 AA.
AC P04937;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin precursor (FN).
CN FN1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer; TISSUE=Liver;
RX MEDLINE=88054951; PubMed=2445560;
RA Schwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;
RT "Multiple sites of alternative splicing of the rat fibronectin gene transcript."
RT EMBL J. 6:2573-2580(1987).
RN [2]
RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.
RC STRAIN=Fischer; TISSUE=Liver;
RX MEDLINE=88054950; PubMed=311323;
RA Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.;
RT "Organization of the fibronectin gene provides evidence for exon shuffling during evolution."
RT EMBL J. 6:2565-2572(1987).
RN [3]
RP SEQUENCE OF 1586-2477 FROM N.A.
RX MEDLINE=84082067; PubMed=6317187;
RA Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.;
RT "Three different fibronectin mRNAs arise by alternative splicing within the coding region."
RT Cell 35:421-431(1983).
RN [4]
RP FUNCTION: Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS. CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS; NO A LESSER EXTEND HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Each of the "extra domain" and the connecting strand 3 are present in some forms of fibronectin and absent in others;
CC Name=1;
CC IsoId=P04937-1; Sequence=Displayed;
CC Name=2; Synonyms=FNIII-13-1a88;
CC IsoId=P04937-2; Sequence=VSP_003258;
CC Name=3; Synonyms=Lambda-RLFA-5;
CC IsoId=P04937-3; Sequence=VSP_003259;
CC Name=4; Synonyms=Lambda-RLFA-6;
CC IsoId=P04937-4; Sequence=VSP_003260;
CC TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted by hepatocytes. Cellular FN (dimeric or cross-linked multimeric forms), made by fibroblasts, epithelial and other cell types, is deposited as fibrils in the extracellular matrix.
CC -1- PM: Sulfated (By similarity).
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
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CC or send an email to license@isb.ch).
CC
CC -----
CC EMBL; X15906; CAA34020.1; -
CC DR EMBL; L29191; AAA41166.1; -
CC DR EMBL; L00191; AAA41166.1; JOINED.
CC DR EMBL; L29191; AAA41167.1; -
CC DR EMBL; L00191; AAA41167.1; JOINED.
CC DR EMBL; L29191; AAA41168.1; -
CC DR EMBL; L00191; AAA41168.1; JOINED.
CC DR EMBL; X05831; CAA29278.1; -
CC DR EMBL; X05832; CAA29279.1; -
CC DR EMBL; X05833; CAA29280.1; -
CC DR EMBL; X05834; CAA29281.1; -
CC PIR; S14428; S14428.
CC HSSP; P02751; IFBR.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR000083; Fibronctn1.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR000562; FN_Type_II.
CC InterPro; IPR003962; FNIII_stud.
CC Pfam; PF00039; fn1; 12.
CC Pfam; PF00040; fn2; 2.
CC Pfam; PF00041; fn3; 17.
CC PRINTS; PR00013; ENTPEIII.
CC PRINTS; PR00014; ENTPEIII.
CC PRODOM; PD000995; FN_Type_II; 2.
CC SMART; SMO0058; FN1; 12.
CC SMART; SMO0059; FN2; 2.
CC SMART; SMO0060; FN3; 13.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS00023; FIBRONECTIN_1; 2.
CC PROSITE; PS01253; FIBRONECTIN_1; 12.
CC Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
CC Sulfation; Cell adhesion; Repeat; Alternative splicing; Signal.
CC SIGNAL 1 32
CC CHAIN 33 2477
CC FT DOMAIN 53 273
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CC FT DNA_BIND 906 1171
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CC FIBRONECTIN.
CC FIBRIN- AND HEPARIN-BINDING 1.
CC COLLAGEN-BINDING.
CC CELL-ATTACHMENT.
CC HEPARIN-BINDING 2.
CC FIBRIN-BINDING 2.
CC FIBRONECTIN TYPE-I 1.
CC FIBRONECTIN TYPE-I 2.
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CC FIBRONECTIN TYPE

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DE  Fibronectin (FN) (Fragment).
OC  Plurodeles waltl:ii (Iberian ribbed newt).
OC  Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;
OC  Plurodeles.
XX  NCBI_TaxId=8319;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  MEDLINE=94363379; PubMed=8081872;
RX  Cavalier L., Rich U., Desimone D.W.;
RI  "Amphibian Plurodeles waltl fibronectin: cDNA cloning and
RL  developmental expression of spliced variants.";
RL  Cell Adhes. Commun. 1:83-91(1993).
CC  -I- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC  including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC  are involved in cell adhesion, cell motility, opsonization, wound
CC  healing, and maintenance of cell shape. (By similarity)
CC  -I- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
CC  CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
CC  SIMILARITY).
CC  -I- SIMILARITY: Contains at least 3 fibronectin type I domains.
CC  -I- SIMILARITY: Contains at least 10 fibronectin type III domains.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb.ch/announce/
CC  or send an email to license@isb.sib.ch).
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DR  EMBL; X66813; CAA47292.1; -.
DR  HSPD; P02751; IFNH.
DR  InterPro; IPR006209; EGF_like.
DR  InterPro; IPR000083; Fibrinctnl.
DR  InterPro; IPR008957; FN_III-like.
DR  InterPro; IPR003961; FN_III.
DR  InterPro; IPR003962; FNIII_subd.
DR  Pfam; PF00039; fnl; 3.
DR  Pfam; PF00041; fn3; 11.
DR  PRINTS; PR00014; FNTYPEIII.
DR  SMART; SM00058; FN1; 3.
DR  SMART; SM00060; FN3; 9.
DR  PROSITE; PS00023; EGF_1; 1.
DR  PROSITE; PS01253; FIBRONECTIN_1; 1.
KM  Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
KM  Repeat.
FT  NON_TER 1
FT  DANA_BIND <1 13
FT  DOMAIN 203 477 CELL-ATTACHMENT.
FT  DOMAIN 658 929 HEPARIN-BINDING 2 (BY SIMILARITY).
FT  DOMAIN 1157 1288 FIBRIN-BINDING 2 (BY SIMILARITY).
FT  DOMAIN <1 14 FIBRONECTIN TYPE-III.
FT  DOMAIN 15 110 FIBRONECTIN TYPE-III.
FT  DOMAIN 111 201 FIBRONECTIN TYPE-III (EXTRA DOMAIN).
FT  DOMAIN 202 292 FIBRONECTIN TYPE-III.
FT  DOMAIN 293 383 FIBRONECTIN TYPE-III.
FT  DOMAIN 384 477 FIBRONECTIN TYPE-III.
FT  DOMAIN 478 567 FIBRONECTIN TYPE-III.
FT  DOMAIN 568 657 FIBRONECTIN TYPE-III (EXTRA DOMAIN).
FT  DOMAIN 658 743 FIBRONECTIN TYPE-III.
FT  DOMAIN 749 838 FIBRONECTIN TYPE-III.
FT  DOMAIN 839 929 FIBRONECTIN TYPE-III.
FT  DOMAIN 930 1064 CONNECTING STRAND 3 (CS-3) (V REGION).
FT  DOMAIN 1065 1143 FIBRONECTIN TYPE-I.
FT  DOMAIN 1155 1199 FIBRONECTIN TYPE-I.
FT  DOMAIN 1200 1243 FIBRONECTIN TYPE-I.
FT  DOMAIN 1245 1287 FIBRONECTIN TYPE-I.
FT  DISULFID 1157 1186 BY SIMILARITY.
FT  DISULFID 1184 1196 BY SIMILARITY.
FT  DISULFID 1202 1229 BY SIMILARITY.
FT  DISULFID 1227 1240 BY SIMILARITY.
FT  DISULFID 1247 1270 BY SIMILARITY.

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CC major: transcript in articular cartilage, but it is absent from
CC
CC -1- PFM: Sulfated (By similarity).
CC -1- SIMILARITY: Contains at least 4 fibronectin type III domains.
CC -1- SIMILARITY: Contains at least 3 fibronectin type I domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U52106; AAC48612.1; -.
CC DR EMBL; U52105; AAC48611.1; -.
CC DR HSPSP; P02751; FNH.
CC DR InterPro; IPR000083; Fibnrcn1.
CC DR InterPro; IPR008957; FN_III-like.
CC DR InterPro; IPR003961; FN_III.
CC DR InterPro; IPR003962; FcIII_subd.
CC DR Pfam; PF00039; fn1; 3.
CC DR Pfam; PF00041; fn3; 3.
CC DR PRINTS; PR00014; FNNTYPE11.
CC DR SMART; SM00058; FN1; 2.
CC DR SMART; SM00060; FN3; 3.
CC DR PROSITE; PS01253; FIBRONECTIN_1; 2.
CC KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
CC Repeat; Sulfation; Alternative splicing.
CC
CC FT DOMAIN 1 1 204 1 HEPARIN-BINDING 2 (BY SIMILARITY).
CC FT DOMAIN 325 >522 FIBRIN-BINDING 2 (BY SIMILARITY).
CC FT DOMAIN <1 25 FIBRONECTIN TYPE-III 13.
CC FT DOMAIN 26 114 FIBRONECTIN TYPE-III 14.
CC FT DOMAIN 115 204 FIBRONECTIN TYPE-III 15.
CC FT DOMAIN 205 315 CONNECTING STRAND 3 (CS-3) (V REGION).
CC FT DOMAIN 316 395 FIBRONECTIN TYPE-III 16.
CC FT DOMAIN 417 461 FIBRONECTIN TYPE-I 10.
CC FT DOMAIN 462 504 FIBRONECTIN TYPE-I 11.
CC FT DOMAIN >522 FIBRONECTIN TYPE-I 12.
CC FT SITE 304 306 CELL ATTACHMENT SITE (POTENTIAL).
CC FT DISULFID 419 448 BY SIMILARITY.
CC FT DISULFID 446 458 BY SIMILARITY.
CC FT DISULFID 464 491 BY SIMILARITY.
CC FT DISULFID 489 501 BY SIMILARITY.
CC FT DISULFID 508 >522 BY SIMILARITY.
CC FT MOD_RES 509 509 SULFATION (POTENTIAL).
CC FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
CC FT CARBOHYD 277 277 O-LINKED (GALNAC. . .) (BY SIMILARITY).
CC FT CARBOHYD 278 278 O-LINKED (GALNAC. . .) (BY SIMILARITY).
CC FT VARSPIC 205 205 D->E (in isoform 2).
CC FT /FTid=VSP_003251.
CC FT /Missing (in isoform 2).
CC FT /FTid=VSP_003252.
CC FT VARSPIC 206 462
CC
CC FT NON_TER 522 522
CC SQ SEQUENCE 522 AA; 57700 MW; DB1D9A54C2BDAE26 CRC64;
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CC Query Match 67.1%; Score 57; DB 1; Length 522;
CC Best Local Similarity 75.0%; Pred. No. 0.17;
CC Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC
CC Oy 3 YTVTGLPGAGDY 14
CC ||:||||:|
CC Db 81 YTVTGLPGAGDY 92
CC
CC RESULT 7
CC FING_HORSE STANDARD; PRT; 522 AA.
CC AC 028377; 028378;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-MAR-2004 (Rel. 43, Last annotation update)

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DE Fibronectin (FN) (Fragment).
 GN FN1.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Liver.
 RX MEDLINE=66324983; PubMed=8702559;
 RA MacLeod J.N., Burton-Murster N., Gu D.N., Lust G.;
 RT "Fibronectin mRNA splice variant in articular cartilage lacks bases
 encoding the V, III-15, and I-10 protein segments.";
 RL J. Biol. Chem. 271:18954-18960(1996).
 CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
 including collagen, fibrin, heparin, DNA, and actin. Fibronectins
 are involved in cell adhesion, cell motility, opsonization, wound
 healing, and maintenance of cell shape.
 CC -1- FUNCTION: Isoform 2 is probably involved in matrix organization of
 cartilage.
 CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
 VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
 TO A LESSER EXTEND HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist. Each of the "extra
 domain" and the connecting strand 3 are present in some forms of
 fibronectin and absent in others;
 CC Name=1;
 CC IsoId=Q28377-1; Sequence=Displayed;
 CC Name=2; Synonyms=(V+C)-;
 CC IsoId=Q28377-2; Sequence=VSP_003253; VSP_003254;
 CC Note=Lacks repeat 15 of fibronectin type-III, repeat 10 of
 CC fibronectin type-I, and the connecting strand 3;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 CC forms), made by fibroblasts, epithelial and other cell types, is
 CC deposited as fibrils in the extracellular matrix. Isoform 2 is the
 CC major transcript in articular cartilage; very low levels in lymph
 CC node, bone, aorta, and skin; absent from liver, spleen, placenta,
 CC cardiac muscle, skeletal muscle, stomach, small intestine, and
 CC kidney.
 CC -1- Ptm: Sulfated (by similarity).
 CC -1- SIMILARITY: Contains at least 3 fibronectin type III domains.
 CC -1- SIMILARITY: Contains at least 4 fibronectin type I domains.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U52107; AAC48613.1; -;
 DR EMBL: U52108; AAC48614.1; -;
 DR HSSP: P02751; 1FNH.
 DR InterPro: IPR000083; Fibnrcn1.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003962; FnIII_subd.
 DR Pfam: PF00039; fn1; 3.
 DR Pfam: PF00041; fn1; 3.
 DR PRINTS: PR00014; ENTPEIII.
 DR SMART: SMO0058; FN1; 2.
 DR SMART: SMO0060; FN1; 3.
 DR PROSITE: PS01253; FIBRONECTIN_1; 2.
 KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
 KW Repeat; Sulfation; Alternative splicing.
 FT NON TER 1 204
 FT DOMAIN 1 204 HEPARIN-BINDING 2 (BY SIMILARITY).
 FT 325 >522 FIBRIN-BINDING 2 (BY SIMILARITY).

FT DOMAIN 1 25
 FT NON TER 26 114 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 115 204 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 205 315 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 316 395 CONNECTING STRAND 3 (CS-3) (V REGION).
 FT DOMAIN 417 461 FIBRONECTIN TYPE-III 16.
 FT DOMAIN 462 504 FIBRONECTIN TYPE-I 10.
 FT DOMAIN 506 >522 FIBRONECTIN TYPE-I 11.
 FT SITE 304 306 FIBRONECTIN TYPE-I 12.
 FT SITE 419 448 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFD 446 458 BY SIMILARITY.
 FT DISULFD 464 491 BY SIMILARITY.
 FT DISULFD 489 501 BY SIMILARITY.
 FT MOD RES 515 515 SULFATION (POTENTIAL).
 FT CARBOHD 321 321 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHD 277 277 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT CARBOHD 278 278 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT VASPLIC 205 205 D -> E (in isoform 2).
 FT VASPLIC 206 462 /FTId=VSP_003253.
 FT VASPLIC 462 462 /FTId=VSP_003254.
 FT NON TER 522 522
 FT SEQUENCE 522 AA; 5757 MW; 893B8AC895864D41 CRC64;
 SQ
 Query Match 67.1%; Score 57; DB 1; Length 522;
 Best Local Similarity 75.0%; Pred. No. 0.17;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 3 YVTGTLEPGIDY 14
 Db 81 YTTTGLPGIDY 92
 RESULT 8
 FNC BOVIN STANDARD; PRT; 2265 AA.
 ID FNC BOVIN
 AC P07589;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin (FN).
 GN FN1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87054047; PubMed=3780752;
 RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
 RT "Complete primary structure of bovine plasma fibronectin.";
 RL Eur. J. Biochem. 161:441-453(1986).
 RN [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=83117805; PubMed=6218503;
 RA Petersen T.E., Thorstensen H.C., Skorstengaard K., Vibe-Pedersen K.,
 RA Sahl P., Sottirup-Jensens L., Magnusson S.;
 RT "Partial primary structure of bovine plasma fibronectin: three types
 of internal homology.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
 RN [3]
 RP SEQUENCE OF 2170-2265 FROM N.A.
 RX MEDLINE=83221567; PubMed=6304699;
 RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
 RT "Isolation and characterization of cDNA clones for human and bovine
 fibronectins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3228-3222(1983).
 CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
 including collagen, fibrin, heparin, DNA, and actin. Fibronectins
 are involved in cell adhesion, cell motility, opsonization, wound
 healing, and maintenance of cell shape.
 CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED

CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS: Secreted; extracellular matrix.
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC IsoId=P07589-1; Sequence=Displayed;
CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
CC forms), made by fibroblasts, epithelial and other cell types, is
CC deposited as fibrils in the extracellular matrix.
CC -1- PTM: Sulfated (By similarity).
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC -1- SIMILARITY: Contains 15 fibronectin type III domains.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, X00800; AAA30521.2; -
CC PIR, A26452; FN2.
CC HSSP, P02751; FN2.
CC InterPro, IPR006209; EGF-like.
CC InterPro, IPR000083; Fibnctn1.
CC InterPro, IPR008957; FN-III-like.
CC InterPro, IPR003961; FN-III.
CC InterPro, IPR000562; FN Type II.
CC InterPro, IPR003962; FnIII_subd.
CC Pfam, PF000039; fn1; 12.
CC Pfam, PF000040; fn2; 2.
CC Pfam, PF00041; fn3; 15.
CC PRINTS, PR00013; FN Type II.
CC PRINTS, PR00014; FN Type II.
CC ProDom, PD000995; FN Type II; 2.
CC SMART, SM00059; FN1; 12.
CC SMART, SM00059; FN2; 2.
CC SMART, SM00060; FN3; 14.
CC PROSITE, PS00022; EGF_1; 2.
CC PROSITE, PS00023; FIBRONECTIN_2; 2.
CC PROSITE, PS01253; FIBRONECTIN_1; 12.
CC Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
CC Sulfation; Cell adhesion; Repeat; Alternative splicing;
CC Pyridoxine carboxylic acid.
CC MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
CC MOD RES 21 241 FIBRIN- AND HEPARIN-BINDING 1.
CC MOD RES 277 577 COLLAGEN-BINDING.
CC MOD RES 876 1141 CELL-ATTACHMENT.
CC MOD RES 1236 1509 HEPARIN-BINDING 2.
CC MOD RES 1600 1870 FIBRIN-BINDING 2.
CC MOD RES 1991 2216 FIBRONECTIN TYPE-1 1.
CC MOD RES 19 59 FIBRONECTIN TYPE-1 2.
CC MOD RES 64 107 FIBRONECTIN TYPE-1 3.
CC MOD RES 108 151 FIBRONECTIN TYPE-1 4.
CC MOD RES 153 197 FIBRONECTIN TYPE-1 5.
CC MOD RES 198 242 FIBRONECTIN TYPE-1 6.
CC MOD RES 275 314 FIBRONECTIN TYPE-1 7.
CC MOD RES 314 373 FIBRONECTIN TYPE-1 8.
CC MOD RES 373 438 FIBRONECTIN TYPE-1 9.
CC MOD RES 437 480 FIBRONECTIN TYPE-1 10.
CC MOD RES 485 527 FIBRONECTIN TYPE-1 11.
CC MOD RES 527 571 FIBRONECTIN TYPE-1 12.
CC MOD RES 571 669 FIBRONECTIN TYPE-1 13.
CC MOD RES 669 778 FIBRONECTIN TYPE-1 14.
CC MOD RES 778 874 FIBRONECTIN TYPE-1 15.
CC MOD RES 874 964 FIBRONECTIN TYPE-1 16.
CC MOD RES 964 1054 FIBRONECTIN TYPE-1 17.

FT DOMAIN 965 1054 FIBRONECTIN TYPE-III 5.
FT DOMAIN 1055 1141 FIBRONECTIN TYPE-III 6.
FT DOMAIN 1142 1234 FIBRONECTIN TYPE-III 7.
FT DOMAIN 1235 1325 FIBRONECTIN TYPE-III 8.
FT DOMAIN 1326 1415 FIBRONECTIN TYPE-III 9.
FT DOMAIN 1416 1509 FIBRONECTIN TYPE-III 10. (EXTRA DOMAIN).
FT DOMAIN 1510 1599 FIBRONECTIN TYPE-III 11.
FT DOMAIN 1600 1691 FIBRONECTIN TYPE-III 12.
FT DOMAIN 1692 1780 FIBRONECTIN TYPE-III 13.
FT DOMAIN 1781 1870 FIBRONECTIN TYPE-III 14.
FT DOMAIN 1871 1990 FIBRONECTIN TYPE-III 15.
FT DOMAIN 1982 2061 FIBRONECTIN TYPE-III 16.
FT DOMAIN 2062 2127 FIBRONECTIN TYPE-III 17.
FT DOMAIN 2128 2170 FIBRONECTIN TYPE-III 18.
FT DOMAIN 2172 2215 FIBRONECTIN TYPE-III 19.
FT SITE 1493 1495 CELL ATTACHMENT SITE.
FT DISULFID 21 47
FT DISULFID 45 56
FT DISULFID 66 94
FT DISULFID 92 104
FT DISULFID 110 138
FT DISULFID 136 148
FT DISULFID 155 184
FT DISULFID 182 194
FT DISULFID 200 229
FT DISULFID 227 239
FT DISULFID 277 304
FT DISULFID 302 311
FT DISULFID 329 355
FT DISULFID 343 370
FT DISULFID 389 415
FT DISULFID 403 430
FT DISULFID 439 467
FT DISULFID 465 477
FT DISULFID 487 514
FT DISULFID 512 524
FT DISULFID 530 558
FT DISULFID 556 568
FT DISULFID 2085 2114
FT DISULFID 2112 2124
FT DISULFID 2130 2157
FT DISULFID 2155 2167
FT DISULFID 2174 2200
FT DISULFID 2198 2209
FT DISULFID 2246 2246
FT DISULFID 2250 2250
FT MOD RES 845 845
FT MOD RES 850 850
FT MOD RES 850 850
FT MOD RES 399 399
FT CARBOHYD 497 497
FT CARBOHYD 511 511
FT CARBOHYD 846 846
FT CARBOHYD 976 976
FT CARBOHYD 1213 1213
FT CARBOHYD 1987 1987
FT CARBOHYD 1943 1943
FT CARBOHYD 1944 1944
FT MOD RES 2263 2263
SQ SEQUENCE 2265 AA; 249557 MW; C2D21D486F49B5C CRC64;
Query Match Score 57; DB 1; Length 2265;
Best Local Similarity 75.0%; Pred. No. 0.76;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 YTVTGLRGIDY 14
Db 1747 YTTGLQPGTDY 1758
RESULT 9
PINC HUMAN STANDARD: PRT; 2386 AA.
AC P02751; G95609; G95610; Q14312; Q14325; Q14326; Q86127; Q81V18;

AC Q96KP7; Q96KP8; Q9HIB8; Q9HAP3; Q9UMK2;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).
GN FN1 OR FN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=21600194; PubMed=11737888;
RA Schor S.L., Schor A.M.;
RT "Phenotypic and genetic alterations in mammary stroma: implications
for tumour progression.";
RL Breast Cancer Res. 3:373-379(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 3; 7 AND 10).
RC TISSUE=Cervix;
RA Alsorge W., Krieger S., Regiert T., Rittmuller C., Schwager B.,
RA Mewes H.W., Weil B., Amd C., Osanger A., Fobo G., Han M.,
RA Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-38 FROM N.A.
RX MEDLINE=87030890; PubMed=3770189;
RA Gutman A., Yamada K.M., Kornblith A.R.;
RT "Human fibronectin is synthesized as a pre-propolypeptide.";
RL FEBS Lett. 207:145-148(1986).
RN [4]
RP SEQUENCE OF 1-49 FROM N.A.
RX MEDLINE=87175578; PubMed=3031656;
RA Dean D.C., Bowles C.L., Bourgeois S.;
RT "Cloning and analysis of the promoter region of the human fibronectin
gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).
RN [5]
RP SEQUENCE OF 28-2386 FROM N.A. (ISOFORM 3).
RX MEDLINE=85284965; PubMed=2992939;
RA Kornblith A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;
RT "Primary structure of human fibronectin: differential splicing may
generate at least 10 polypeptides from a single gene.";
RL EMBO J. 4:1755-1759(1985).
RN [6]
RP SEQUENCE OF 103-481 AND 2228-2386 FROM N.A. (ISOFORMS 1; 3; 8 AND 9).
RC TISSUE=Perithelial blood T-cell, and Umbilical vein endothelial cells;
RA Godfrey H.P., Ebrahim A.A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 973-2386 FROM N.A. (ISOFORM 3).
RX MEDLINE=84272258; PubMed=6462919;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Human fibronectin: cell specific alternative mRNA splicing generates
polypeptide chains differing in the number of internal repeats.";
RL Nucleic Acids Res. 12:5853-5861(1984).
RN [8]
RP SEQUENCE OF 1232-1782 FROM N.A. (ISOFORM 7).
RX MEDLINE=88233940; PubMed=3375063;
RA Paolella G., Henchcliffe C., Sebastio G., Baralle F.E.;
RT "Sequence analysis and in vivo expression show that alternative
splicing of ED-B and ED-A regions of the human fibronectin gene are
independent events.";
RL Nucleic Acids Res. 16:3545-3557(1988).
RN [9]
RP SEQUENCE OF 1257-1365 FROM N.A. (ISOFORM 11).
RX MEDLINE=88041070; PubMed=3478690;
RA Gutman A., Kornblith A.R.;
RT "Identification of a third region of cell-specific alternative
splicing in human fibronectin mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7179-7182(1987).
RN [10]
RP SEQUENCE OF 1441-1548.
RX MEDLINE=82265604; PubMed=7050098;
RA Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
RT "The cell attachment domain of fibronectin. Determination of the
primary structure.";
RL J. Biol. Chem. 257:9593-9597(1982).
RN [11]
RP SEQUENCE OF 1448-1540 FROM N.A.
RX MEDLINE=83290925; PubMed=6688418;
RA Oldberg A., Linney E., Ruoslahti E.;
RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for
the cell attachment domain in human fibronectin.";
RL J. Biol. Chem. 258:10193-10196(1983).
RN [12]
RP SEQUENCE OF 1448-1540 FROM N.A.
RX MEDLINE=8611901; PubMed=3003095;
RA Oldberg A., Ruoslahti E.;
RT "Evolution of the fibronectin gene. Exon structure of cell attachment
domain.";
RL J. Biol. Chem. 261:2113-2116(1986).
RN [13]
RP SEQUENCE OF 1594-2386 FROM N.A. (ISOFORM 1).
RX MEDLINE=85280409; PubMed=2925573;
RA Bernard M.P., Kolbe M., Weil D., Chu M.-L.;
RT "Human cellular fibronectin: comparison of the carboxyl-terminal
portion with rat identifies primary structural domains separated by
hypervariable regions.";
RL Biochemistry 24:2698-2704(1985).
RN [14]
RP SEQUENCE OF 1712-1739 FROM N.A.
RX MEDLINE=87026578; PubMed=3021206;
RA Sekiguchi K., Rios A.M., Kurachi K., Yoshitake S., Hakomori S.;
RT "Human liver fibronectin complementary DNAs: identification of two
different messenger RNAs possibly encoding the alpha and beta
subunits of plasma fibronectin.";
RL Biochemistry 25:4936-4941(1986).
RN [15]
RP SEQUENCE OF 1788-2386 FROM N.A. (ISOFORMS 4; 5 AND 6).
RC TISSUE=Cartilage;
RX MEDLINE=22126815; PubMed=12127832;
RA Parker A.E., Bottell J., Carr A., Maciewicz R.A.;
RT "Novel cartilage-specific splice variants of fibronectin.";
RL Osteoarthritis Cartilage 10:528-534(2002).
RN [16]
RP SEQUENCE OF 32-290.
RX MEDLINE=84032463; PubMed=6630202;
RA Garcia-Pardo A., Pearlstein E., Frangione B.;
RT "Primary structure of human plasma fibronectin. The 29,000-dalton
NH2-terminal domain.";
RL J. Biol. Chem. 258:12670-12674(1983).
RN [17]
RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
RX MEDLINE=87080265; PubMed=3024962;
RA Owens R.J., Baralle F.E.;
RT "Mapping the collagen-binding site of human fibronectin by expression
in Escherichia coli.";
RL EMBO J. 5:2825-2830(1986).
RN [18]
RP SULFATION.
RX MEDLINE=86042625; PubMed=2414772;
RA Liu M.C., Yu S., Sy J., Redman C.M., Lippmann F.;
RT "Tyrosine sulfation of proteins from the human hepatoma cell line
HepG2.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
RN [19]
RP O-GLYCOSYLATION OF THR-2064.
RX MEDLINE=91190085; PubMed=2012601;
RA Tresselt T., McCarthy J.B., Calaycay J., Lee T.D., Legesse K.,
RA Shively J.E., Pande H., Calaycay J., Lee T.D., Legesse K.,
RT "Human plasma fibronectin. Demonstration of structural differences
between the A- and B-chains in the III CS region.";
RL Biochem. J. 274:731-738(1991).
RN [20]
RP FN1N1-BINDING SITE.

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RX MEDLINE=93015879; PubMed=1400330;
RA Balbona K., Iran H., Godyna S., Ingham K.C., Strickland D.K.,
RA Argaves W.S.;
RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding
RT region of fibronectin."
RL J. Biol. Chem. 267:20120-20125(1992).
RN [21]
RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
RX MEDLINE=95081153; PubMed=7969369;
RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.T.;
RT "Further characterization of the NH2-terminal fibrin-binding site on
RT fibronectin."
RL J. Biol. Chem. 269:31938-31945(1994).
RN [22]
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=92162710; PubMed=1311202;
RA Baron M., Main A.L., Discoll P.C., Mardon H.J., Boyd J.,
RA Campbell I.D.;
RT "H NMR assignment and secondary structure of the cell adhesion type
RT III module of fibronectin."
RL Biochemistry 31:2068-2073(1992).
RN [23]
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=93046665; PubMed=1423622;
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;
RT "The three-dimensional structure of the tenth type III module of
RT fibronectin: an insight into RGD-mediated interactions."
RL Cell 71:671-678(1992).
RN [24]
RP STRUCTURE BY NMR OF 182-275.
RX MEDLINE=9411923; PubMed=8308992;
RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.T.,
RA Campbell I.D.;
RT "Solution structure of a pair of fibronectin type I modules with
RT fibrin binding activity."
RL J. Mol. Biol. 235:1302-1311(1994).
RN [25]
RP STRUCTURE BY NMR OF 32-92.
RX MEDLINE=96069779; PubMed=7583666;
RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;
RT "High-resolution structural studies of the factor XIIIa crosslinking
RT site and the first type I module of fibronectin."
RL Nat. Struct. Biol. 2:946-950(1995).
RN [26]
RP STRUCTURE BY NMR OF 406-464.
RX MEDLINE=98179558; PubMed=9514732;
RA Steicht H., Pickford A.R., Potts J.R., Campbell I.D.;
RT "Solution structure of the glycosylated second type 2 module of
RT fibronectin."
RL J. Mol. Biol. 276:177-187(1998).
RN [27]
RP STRUCTURE BY NMR OF EXTRA ED-B DOMAIN FROM ISOFORM 7.
RN [27]
Query Match 67.1%; Score 57; DB 1; Length 2386;
Best Local Similarity 75.0%; Pred. No. 0.8;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 YVTGLEGPDY 14
Db 1868 YTIRGLQPGDY 1879

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OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A. / DSM 1617 / P2;
RC STRAIN=ATCC 35092;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aweez M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erasmo G., Fletcher C., Gordon P.M.K.,
RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Th-Ngoc H.P., Redder P., Schenk W.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC -1- SIMILARITY: Contains 3 fibronectin type III domains.
CC -1- SIMILARITY: Contains 6 kelch repeats.
CC CC
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CC CC
CC EMBL; AE006722; AAK41296.1; -.
CC PIR; A90255; A90255.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR006552; Kelch_rep.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF0344; Kelch; 5.
CC SMART; SM00060; FN3; 3.
CC HYPOTHETICAL protein; Kelch repeat; Repeat; Signal; Complete proteome.
FT SIGNAL 1 28
FT CHAIN 29 725
FT REPEAT 59 100
FT REPEAT 101 145
FT REPEAT 146 199
FT REPEAT 201 248
FT REPEAT 250 297
FT REPEAT 299 342
FT DOMAIN 323 398
FT DOMAIN 412 490
FT DOMAIN 585 652
FT DOMAIN 78465 MW; F8BFI20D013BAB6 CRC64;
SQ SEQUENCE 725 AA; 78465 MW; F8BFI20D013BAB6 CRC64;
Query Match 55.3%; Score 47; DB 1; Length 725;
Best Local Similarity 75.0%; Pred. No. 9.2;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 YVTGLEGPDY 14
Db 374 YVTGLKDGIDY 385

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RESULT 11
ID TENN_MOUSE STANDARD; PRT; 1560 AA.
AC Q80271;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tenascin N precursor.
GN TNN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, ALTERNATIVE SPLICING, TISSUE
RP SPECIFICITY, AND DEVELOPMENTAL STAGE.

```

RC STRAIN=C57BL/6;
 RX MEDLINE=22697596; PubMed=12812753;
 RA Weidhauf J., Fein S., Kutsche W., Loehler J., Schachner M.;
 RT "tenascin-N: characterization of a novel member of the tenascin family
 RL that mediates neurite repulsion from hippocampal explants.";
 RT Mol. Cell. Neurosci. 23:193-209(2003).
 CC -1- FUNCTION: Isoform 2 inhibits neurite outgrowth and cell migration
 CC in hippocampal explants while isoform 1 does not have this
 CC effect.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced;
 CC Name=1;
 CC -1- Isoform 1: Sequence=Displayed;
 CC -1- TISSUE SPECIFICITY: Highest expression in kidney followed by
 CC spleen and brain. In brain, highest expression is found in
 CC hippocampus, cerebellum and olfactory bulb.
 CC -1- DEVELOPMENTAL STAGE: Hardly detectable at embryonic day 14, then
 CC increases until post-natal day 17 and remains detectable in the
 CC adult.
 CC -1- SIMILARITY: Contains 3 EGF-like domains.
 CC -1- SIMILARITY: Contains 12 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 fibronectin C-terminal domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF455756; AAC63807.1; -;
 DR MGD: MGI:2665790; Tm.
 DR GO: GO:0016049; P:cell growth; IDA.
 DR GO: GO:0016477; P:cell migration; IDA.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR002181; Fibronectin_C.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR006210; IEGF.
 DR Pfam: PF00008; EGF_3.
 DR Pfam: PF00147; fibronectin_C_1.
 DR Pfam: PF00041; fn3_12.
 DR SMART: SM00181; EGF_3.
 DR SMART: SM00186; FBG_1.
 DR SMART: SM00060; FN3_12.
 DR PROSITE: PS00022; EGF_1; 3.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS00514; FIBRIN AG C DOMAIN; 1.
 DR Repeat; EGF-like domain; Signal; Alternative splicing.
 KW Repeat; EGF-like domain; Signal; Alternative splicing.
 FT STGNAL 26
 FT CHAIN 1
 FT DOMAIN 1560
 FT DOMAIN 167
 FT DOMAIN 198
 FT DOMAIN 199
 FT DOMAIN 229
 FT DOMAIN 230
 FT DOMAIN 260
 FT DOMAIN 262
 FT DOMAIN 340
 FT DOMAIN 351
 FT DOMAIN 443
 FT DOMAIN 520
 FT DOMAIN 531
 FT DOMAIN 608
 FT DOMAIN 619
 FT DOMAIN 707
 FT DOMAIN 784
 FT DOMAIN 795
 FT DOMAIN 883
 FT DOMAIN 960
 FT DOMAIN 971
 FT DOMAIN 1048
 FT DOMAIN 1059
 FT DOMAIN 1136
 FT DOMAIN 1147
 FT DOMAIN 1224
 FT DOMAIN 1235
 FT DOMAIN 1312
 FT DOMAIN 1328
 FT DISULFID 171
 FT DISULFID 175
 FT DISULFID 188
 FT DISULFID 197
 FT DISULFID 202
 FT DISULFID 212

FT DISULFID 206 217 POTENTIAL.
 FT DISULFID 219 228 POTENTIAL.
 FT DISULFID 233 243 POTENTIAL.
 FT DISULFID 237 248 POTENTIAL.
 FT DISULFID 250 259 POTENTIAL.
 SQ SEQUENCE 1560 AA; 173115 MW; D6C4F46C086D3A7F CRC64;
 Query Match 55.3%; Score 47; DB 1; Length 1560;
 Best Local Similarity 58.3%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Oy 3 YTVGTEPGIDY 14
 Db 408 YDITGLPGCTEY 419
 RESULT 12
 ID CA17 HUMAN STANDARD; PRT; 2944 AA.
 AC Q023B9; Q14054; Q16507;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1(VII) chain precursor (Long-chain collagen) (LC
 DE collagen).
 GN COL7A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94327588; PubMed=8051117;
 RA Christiano A.M., Greenspan D.S., Lee S., Uitto J.;
 RT "Cloning of human type VII collagen. Complete primary sequence of the
 RT alpha 1(VII) chain and identification of intragenic polymorphisms.";
 RL J. Biol. Chem. 269:20256-20262(1994).
 RN [2]
 RP SEQUENCE OF 128-1493 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=9338437; PubMed=1307247;
 RA Christiano A.M., Rosenbaum L.M., Chung-Honet L.C., Parente M.G.,
 RA Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Burgess R.E.,
 RA Uitto J.;
 RT "The large non-collagenous domain (NC-1) of type VII collagen is
 RT amino-terminal and chimeric. Homology to cartilage matrix protein,
 RT the type III domains of fibronectin and the A domains of von
 RT Willebrand factor.";
 RL Hum. Mol. Genet. 1:475-481(1992).
 RN [3]
 RP SEQUENCE OF 815-1439 FROM N.A.
 RX MEDLINE=91334380; PubMed=1871109;
 RA Parente M.G., Chung L.C., Ryyanen J., Woodley D.T., Wynn K.W.,
 RA Bauer E.A., Mattei M.-G., Chu M.-L., Uitto J.;
 RT "Human type VII collagen: cDNA cloning and chromosomal mapping of the
 RT gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:6931-6935(1991).
 RN [4]
 RP SEQUENCE OF 369-1255 FROM N.A.
 RX MEDLINE=93107742; PubMed=1469284;
 RA Gannon W.R., Abernethy M.L., Padilla K.M., Pitsayanh P.S.,
 RA Cook M.E., Wright J., Brigaman R.A., Hunt S.W. III;
 RT "Noncollagenous (NC1) domain of collagen VII resembles multidomain
 RT adhesion proteins involved in tissue-specific organization of
 RT extracellular matrix.";
 RL J. Invest. Dermatol. 99:691-696(1992).
 RN [5]
 RP SEQUENCE OF 340-675 FROM N.A.
 RX MEDLINE=92231902; PubMed=1567409;
 RA Tanaka T., Takahashi K., Furukawa F., Imamura S.;
 RT "Molecular cloning and characterization of type VII collagen cDNA.";
 RL Biochem. Biophys. Res. Commun. 183:958-963(1992).
 RN [6]

RP SEQUENCE OF 2395-2944 FROM N.A.
RX MEDLINE=93271995; PubMed=8499916;
RA Greenspan D.S.;
RT "The carboxyl-terminal half of type VII collagen, including the non-
RT collagenous NC-2 domain and intron/exon organization of the
RT corresponding region of the COL7A1 gene.";
RL Hum. Mol. Genet. 2:273-278(1993).
RN [17]
RP SEQUENCE OF 1-87 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94375010; PubMed=8088784;
RA Christiano A.M., Hoffman G.G., Chung-Honet L.C., Lee S., Cheng W.,
RA Ultio J., Greenspan D.S.;
RT "Structural organization of the human type VII collagen gene (COL7A1),
RT composed of more exons than any previously characterized gene.";
RL Genomics 21:169-179(1994).
RN [18]
RP VARIANT EBDSC ARG-2034.
RX MEDLINE=89227237; PubMed=2653224;
RA Fine J.D., Johnson L., Wright T.;
RT "Epidermolysis bullosa simplex superficialis. A new variant of
RT epidermolysis bullosa characterized by subcorneal skin cleavage
RT mimicking peeling skin syndrome.";
RL Arch. Dermatol. 125:633-638(1989).
RN [19]
RP REVIEW ON DEB VARIANTS.
RX MEDLINE=96041696; PubMed=9375848;
RA Jaervikallio A., Pulkkinen L., Ultio J.;
RT "Molecular basis of dystrophic epidermolysis bullosa: mutations in
RT the type VII collagen gene (COL7A1).";
RL Hum. Mutat. 10:338-347(1997).
RN [10]
RP VARIANT DEB LYS-2798.
RX MEDLINE=93291877; PubMed=8513326;
RA Christiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y.,
RA Lin A.N., Dietz H.C., Hovnanian A., Ultio J.;
RT "A missense mutation in type VII collagen in two affected siblings
RT with recessive dystrophic epidermolysis bullosa.";
RL Nat. Genet. 4:62-66(1993).
RN [11]
RP VARIANT DEB SER-2040.
RX MEDLINE=94224777; PubMed=8170945;
RA Christiano A.M., Ryyanen M., Ultio J.;
RT "Dominant dystrophic epidermolysis bullosa: identification of a
RT Gly-→Ser substitution in the triple-helical domain of type VII
RT collagen.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3549-3553(1994).
RN [12]
RP VARIANT DEB CYS-2623.
RX MEDLINE=96081220; PubMed=8541842;
RA Christiano A.M., Lee J.Y.-Y., Chen W.J., Laforgia S., Ultio J.;
RT "Pretibial epidermolysis bullosa: genetic linkage to COL7A1 and
RT identification of a glycine-to-cysteine substitution in the triple-
RT helical domain of type VII collagen.";
RL Hum. Mol. Genet. 4:1579-1583(1995).
RN [13]
RP VARIANT DEB ARG-2043.
RX MEDLINE=95164985; PubMed=7861014;
RA Christiano A.M., Morricone A., Paradisi M., Angelo C., Mazzanti C.,
RA Cavallieri R., Ultio J.;
RT "A glycine-to-arginine substitution in the triple-helical domain of
RT type VII collagen in a family with dominant dystrophic epidermolysis
RT bullosa.";
RL J. Invest. Dermatol. 104:438-440(1995).
RN [14]
RP VARIANTS DEB.
RX MEDLINE=96220218; PubMed=8644729;
RA Christiano A.M., McGrath J.A., Tan K.C., Ultio J.;
RT "Glycine substitutions in the triple-helical region of type VII
RT collagen result in a spectrum of dystrophic epidermolysis bullosa
RT phenotypes and patterns of inheritance.";
RL Am. J. Hum. Genet. 58:671-681(1996).
RN [15]

RP VARIANT DEB ARG-2575.
RX MEDLINE=96154068; PubMed=8592061;
RA Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., Ultio J.;
RT "Molecular basis of recessive dystrophic epidermolysis bullosa:
RT genotype/phenotype correlation in a case of moderate clinical
RT severity.";
RL J. Invest. Dermatol. 106:119-124(1996).
RN [16]
RP VARIANT DEB ARG-1782.
RX MEDLINE=96183562; PubMed=8618018;
RA Christiano A.M., McGrath J.A., Ultio J.;
RT "Influence of the second COL7A1 mutation in determining the
RT phenotypic severity of recessive dystrophic epidermolysis bullosa.";
RL J. Invest. Dermatol. 106:766-770(1996).
RN [17]
RP VARIANT DEB ASP-2073.
RX MEDLINE=96310789; PubMed=8757758;
RA Dunnill M.G.S., McGrath J.A., Richards A.J., Christiano A.M.,
RA Ultio J., Pope F.M., Bady R.A.J.;
RT "Clinicopathological correlations of compound heterozygous COL7A1
RT mutations in recessive dystrophic epidermolysis bullosa.";
RL J. Invest. Dermatol. 107:171-177(1996).
RN [18]
RP VARIANTS DEB TRP-1982; GLY-2008; ALA-2025; GLU-2049; TRP-2063 AND
RP ARG-2575.
RX MEDLINE=97465605; PubMed=9326325;
RA Hovnanian A., Roehat A., Bodemer C., Petit E., Rivers C.A., Prost C.,
RA Fratag S., Christiano A.M., Ultio J., Lathrop M., Barrandon Y.,
RA de Prost Y.;
RT "Characterization of 18 new mutations in COL7A1 in recessive
RT dystrophic epidermolysis bullosa provides evidence for distinct
RT molecular mechanisms underlying defective anchoring fibril
RT formation.";
RL Am. J. Hum. Genet. 61:559-610(1997).
RN [19]
RP VARIANT DEB ARG-1652.
RX MEDLINE=98106792; PubMed=9444387;
RA Cserhalmi-Friedman P.B., Karpali S., Horvath A., Christiano A.M.;
RT "Identification of a glycine substitution and a splice site mutation
RT in the type VII collagen gene in a proband with mild recessive
RT dystrophic epidermolysis bullosa.";
RL Arch. Dermatol. Res. 289:640-645(1997).
RN [20]
RP VARIANTS DEB ARG-2009 AND ARG-2043.
RX MEDLINE=97358588; PubMed=9215684;
RA Winberg J.-O., Hammami-Hausali N., Nilsson O., Anton-Lamprecht I.,
RA Naylor S.L., Kerpacher K., Zimmermann M., Krajci P.,
RA Gedde-Dahl T. Jr., Bruckner-Tuderman L.;
RT "Modulation of disease severity of dystrophic epidermolysis bullosa by
RT a splice site mutation in combination with a missense mutation in the
RT COL7A1 gene.";
RL Hum. Mol. Genet. 6:1125-1135(1997).
RN [21]
RP VARIANTS DEB ASP-1519; ASP-2006; GLU-2015 AND ARG-2034.
RX MEDLINE=98334662; PubMed=9668111;
RA Hammami-Hausali N., Schumann H., Ragunath M., Kilgus O., Luetch U.,
RA Luger T., Bruckner-Tuderman L.;
RT "Some, but not all, glycine substitution mutations in COL7A1 result in
RT intracellular accumulation of collagen VII, loss of anchoring
RT fibrils, and skin blistering.";
RL J. Biol. Chem. 273:19228-19234(1998).
RN [22]
RP VARIANTS DEB CYS-2008; ARG-2207 AND SER-2775.
RX MEDLINE=98410969; PubMed=9740253;
RA Kon A., Pulkkinen L., Ishida-Yamamoto A., Hashimoto I., Ultio J.;
RT "Novel COL7A1 mutations in dystrophic forms of epidermolysis
RT bullosa.";
RL J. Invest. Dermatol. 111:534-537(1998).
RN [23]
RP VARIANT DEB ARG-1347.
RX MEDLINE=99019477; PubMed=9804332;
RA Terracina M., Postoraro P., Schubert M., Sonego G., Atzori F.,

Query Match 55.3%; Score 47; DB 1; Length 2944;
Best Local Similarity 80.0%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Dy 5 VTGLEPGIDY 14
Db 1015 VTGLEPGVSY 1024

RESULT 13

UVRC_ECOLI STANDARD; PRT; 610 AA.
AC P07028; P76311; Q8XBDS;
DT 01-APR-1988 (Rel. 07, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE UVrABC system protein C (uvrc protein) (Excinuclease ABC subunit C).
GN UVRC OR B1913 OR C2326 OR Z3001 OR EC52651.
OS Escherichia coli O6, and
OS Escherichia coli O6, and
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562, 217992, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66176730; PubMed=3515318;
RA Sharma S., Stark T.F., Beattie W.G., Moses R.E.;
RT "Multiple control elements for the uvrc gene unit of Escherichia coli";
RL Nucleic Acids Res. 14:2301-2318(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84247323; PubMed=6330676;
RA Sancar G.B., Sancar A., Rupp W.D.;
RT "Sequences of the E. coli uvrc gene and protein";
RL Nucleic Acids Res. 12:4593-4608(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=92785003;
RA Blatner F.R., Plunkett G., Ili, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map";
RL DNA Res. 3:319-392(1996).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22386234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G., Ili, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Ison S.-R., Boutin N., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S.-R., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donenberg M.S., Blatner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [6]
RP SEQUENCE FROM N.A.

RC STRAIN=0157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G., Ili, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin N., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimandha E.T., Potanous K.,
RA Apodaca J., Anantharaman T.S., Ili J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [7]
RP SEQUENCE FROM N.A.
RX STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kubura S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).
RN [8]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=87231005; PubMed=3295776;
RA Moolenaar G.F., van Sluis C.A., Backendorf C., van de Putte P.;
RT "Regulation of the Escherichia coli excision repair gene uvrc.
Overlapping between the uvrc structural gene and the region coding for a
24 kD protein";
RL Nucleic Acids Res. 15:4273-4289(1987).
RN [9]
RP SEQUENCE OF 604-610 FROM N.A.
RX MEDLINE=8611778; PubMed=3003065;
RA Gopalakrishnan A.S., Chen Y.C., Temkin M., Dowhan W.;
RT "Structure and expression of the gene locus encoding the
phosphatidylylglycerophosphate synthase of Escherichia coli";
RL J. Biol. Chem. 261:1329-1338(1986).
RN [10]
RP FUNCTION, AND MUTAGENESIS OF ASP-399; ASP-438; ASP-466 AND HIS-538.
RX STRAIN=K12;
MEDLINE=92388118; PubMed=1387639;
RA Lin J.-J., Sancar A.;
RT "Active site of (A)BC excinuclease. I. Evidence for 5' incision by
uvrc through a catalytic site involving Asp399, Asp438, Asp466, and
His538 residues";
RL J. Biol. Chem. 267:17688-17692(1992).
RN [11]
RP FUNCTION, AND MUTAGENESIS OF ARG-42.
RX MEDLINE=20138260; PubMed=10671556;
RA Verhoeven E.E., van Kesteren M., Moolenaar G.F., Visse R., Goosen N.;
RT "Catalytic sites for 3' and 5' incision of Escherichia coli nucleotide
excision repair are both located in uvrc";
RL J. Biol. Chem. 275:5120-5123(2000).
RN [12]
RP FUNCTION: The UVrABC repair system catalyzes the recognition and
processing of DNA lesions. UVRC both incises the 5' and 3' sides
of the lesion. The N-terminal half is responsible for the 5'
incision and the C-terminal half is responsible for the 3'
incision.
CC -1- SUBUNIT: Interacts with uvrb in an incision complex.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the uvrc family.
CC -1- SIMILARITY: Contains 1 Uvr domain.
CC -----
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DR EMBL: X03691; CAA27329.1; ALT INT.
DR EMBL: AE000284; AAC74980.1; ALT INIT.
DR EMBL: D00023; E016732.1

RA Coutinho A.P., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Falcinetti A.P., Ferreira A.U.S., Ferreira V.C.A., Fétro L.R.,
 RA Fraga U.S., França S.C., Franco M.C., Frohme M., Furian J.A.,
 RA Gantier L.G., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohisel J.D., Junqueira M.L., Kemper E.L., Kiteajina J.P.,
 RA Krieger U.E., Kurumae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.V., Medeiros A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.B.S.,
 RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,
 RA Ouaguo R.E., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terezini M.F., Trufi D., Tsai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Seubal J.C.;
 RA "The genome sequence of the plant pathogen *Xylella fastidiosa*,"
 RT Nature 406:151-159(2000).
 CC -1- FUNCTION: The UvrAC repair system catalyzes the recognition and
 CC processing of DNA lesions. UvrC both incises the 5' and 3' sides
 CC of the lesion. The N-terminal half is responsible for the 5'
 CC incision and the C-terminal half is responsible for the 5'
 CC incision (By similarity).
 CC -1- SUBUNIT: Interacts with UvrB in an incision complex (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the uvrC family.
 CC -1- SIMILARITY: Contains 1 Uvr domain.
 CC
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 DR EMBL, AE004042, AA085110.1, ALT_INT.
 DR PIR, H62573, H62573.
 DR HAMAP, MF_00203, -1.
 DR InterPro, IPR0004455, HNH.
 DR InterPro, IPR003583, HNH 1.
 DR InterPro, IPR001943, UvrB/C.
 DR InterPro, IPR004791, UvrC.
 DR InterPro, IPR001162, UvrC.C.
 DR InterPro, IPR003035, UvrC_N.
 DR Pfam, PF01541, Excl_endo_N, 1.
 DR Pfam, PF00633, HHH, 2.
 DR Pfam, PF02151, UVR, 1.
 DR ProDom, PD005870, UvrC_C, 1.
 DR SMART, SM00465, Glyc, 1.
 DR SMART, SM00278, HHH, 2.
 DR TIGRFAMs, TIGR00194, UvrC, 1.
 DR PROSITE, PSS0151, UVR, 1.
 DR PROSITE, PSS0164, UVR_C, 1.
 DR PROSITE, PSS0165, UVR_C_2, 1.
 DR SOS response, Excision nucleases, DNA repair, DNA recombination,
 KM DNA excision, Complete proteome.
 FT DQAIN 207 242 UVR.
 ST
 SQ SEQUENCE 621 AA; 68935 MW; 3571B5E12C058A7 CRC64;
 Query March 52.9%; Score 45; DB 1; Length 621;
 Best Local Similarity 58.3%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 3 YVTGTGEPGIDY 14
 :|::|
 428 YNIGIRPGDDY 439

Matches	7;	Conservative	2;	Mismatches	3;	Indels	0;	Gaps	0;
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QY 3 YTVTGLEPGIDY 14
 DB 428 YNIGTIRPGDDY 439

Search completed: September 21, 2004, 05:47:30
 Job time : 6.30147 secs

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RESULT 15
UVR_C_XYLEFT STANDARD; PRT; 621 AA.
AC 087BX2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE UVRABC system protein C (UvrC protein) (Exonuclease ABC subunit C).
GN UVR_C OR PD1325
OS Xylella fastidiosa (strain Temecula / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=183190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2421331; Pubmed=1253478;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA Miyaki C.Y., Furlan L.R., Canaipo L.E.A., da Silva A.C.R., Moon D.H.,
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harkava R., Kuramae E.E.,
RA Martino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Bata G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leon S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of Xylella
RT fastidiosa."
RL J. Bacteriol. 185:1018-1026(2003).
CC -1- FUNCTION: The UvrABC repair system catalyzes the recognition and
CC processing of DNA lesions. UvrC both incises the 5' and 3'
CC sides of the lesion. The N-terminal half is responsible for the 5'
CC incision and the C-terminal half is responsible for the 5'
CC incision (By similarity).
CC -1- SUBUNIT: Interacts with UvrB in an incision complex (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the uvrC family.
CC -1- SIMILARITY: Contains 1 UVR domain.
CC -----
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CC -----
CC EMBL, AEO12558; AAC29173.1; -
CC HAMAP, MF_00203; -; 1.
CC InterPro: IPR000445; HNH.
CC InterPro: IPR001943; UVRB/C.
CC InterPro: IPR001162; UVR_C.
CC InterPro: IPR000305; UVR_C_N.
CC Pfam: PF01541; Exc1_endo_N; 1.
CC Pfam: PF00633; HNH; 2.
CC Pfam: PF02151; UVR; 1.
CC PROSITE, PSS0151; UVR; 1.
CC PROSITE, PSS0164; UVR_C_1; 1.
CC PROSITE, PSS0165; UVR_C_2; 1.
CC SOS response; Excision nuclease; DNA repair; DNA recombination;
CC DNA excision; Complete proteome.
CC DOMAIN 207 242 UVR.
CC SEQUENCE 621 AA; 68928 MW; 4016AEFP90DD0F12 CRC64;
  
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QY 1 GYTTVTGLEPGIDYD 15
|||
DQ 55 GYTTVTGLEPGIDYD 69

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RESULT 2
ID Q9WZ32 PRELIMINARY; PRT; 134 AA.
AC Q9WZ32;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibronectin ED-B+ region (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA De Candia L.M., Rodgers R.J.;
RT "Characterization of the expression of the alternative splicing of ED-
RT A, ED-B and V regions of fibronectin mRNA in bovine ovarian follicles
RT and corpora lutea.";
RL Reprod. Fertil. Dev. 0:0-0(2000).
DR EMBL; AF260304; AAF91380.1; -.
DR HSSP; P02751; 1FNF.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
FT NON_TER 1
FT NON_TER 134
SQ SEQUENCE 134 AA; 14408 MW; 820971B2619A48A5 CRC64;

Query Match 100.0%; Score 85; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTVTGLPGLDIDY 15
DB 84 GYTVTGLPGLDIDY 98

RESULT 3
ID Q93406 PRELIMINARY; PRT; 2478 AA.
AC Q93406;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibronectin.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao Q., Colloidi P.;
RT "Characterization and expression of zebrafish fibronectin.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081128; AAC31947.1; -.
DR HSSP; P02751; 1FBR.
DR ZFIN; ZDB-GENE-000426-1; fn1.
DR GO; GO:0005576; C:extracellular; ISA.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR000083; Fibnctnl.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00013; FNTYPEII.

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DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 14.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 11.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
SQ SEQUENCE 2478 AA; 271652 MW; A03475C55A385750 CRC64;

Query Match 87.1%; Score 74; DB 13; Length 2478;
Best Local Similarity 86.7%; Pred. No. 0.0061;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYTVTGLPGLDIDY 15
DB 1319 GYTVHGLPGLDIDY 1333

RESULT 4
ID Q7TOK8 PRELIMINARY; PRT; 215 AA.
AC Q7TOK8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibronectin (Fragment).
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
RN [1]
RP SEQUENCE FROM N.A.
RA Safi R., Bertrand S., De Luze A., Vanacker J.M., Marchand O.,
RA Carregil A., Demenex B., Laudet V.;
RT "Tyroid Hormone Response in A Neotenic Amphibian, The Axolotl
RT (Ambystoma mexicanum).";
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139973; AAN37600.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 215 AA; 23438 MW; 5207871B67C64C3 CRC64;

Query Match 67.1%; Score 57; DB 13; Length 215;
Best Local Similarity 75.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLPGLDIDY 14
DB 196 YTVTGLPGLDIDY 207

RESULT 5
ID Q9SKV4 PRELIMINARY; PRT; 320 AA.
AC Q9SKV4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibronectin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RA Parker A.B., Boutell J., Carr A., Maciewicz R.A.;
RT "Novel Cartilage-Specific Splice Variants of Fibronectin.";
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ320529; CAC86917.1; -.

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DR GO:0005576; C:extracellular; IEA.
DR InterPro: IPR000083; Fibrinctn1.
DR InterPro: IPR003962; FNIII subd.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00039; FN1; 3.
DR Pfam: PF00041; FN3; 2.
DR PRINTS: PR00012; FNTPER1.
DR PRINTS: PR00014; FNTPER1I.
DR SMART: SM00058; FN1; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS01253; FIBRONECTIN_1; 2.
KW Repeat.
FT NON_TER 1
FT SEQUENCE 320 AA; 35485 MW; 93E2F4AF2ACF2F0E CRC64;

Query Match
Best Local Similarity 75.0%; Pred. No. 0.4; Length 320;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
Db 81 YTVTGLEPGIDY 92

RESULT 6
Q95KV5 PRELIMINARY; PRT; 347 AA.
ID Q95KV5;
AC Q95KV5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibronectin (Fragment).
GN FN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Parker A.E., Boutell J., Carr A., Maciewicz R.A.;
RT "Novel Cartilage-Specific Splice Variants of Fibronectin.";
RL Submitted (JUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ120528; C:extracellular; IEA.
DR GO:0005576; C:extracellular; IEA.
DR InterPro: IPR000083; Fibrinctn1.
DR InterPro: IPR003962; FNIII subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00039; FN1; 2.
DR Pfam: PF00041; FN3; 3.
DR PRINTS: PR00012; FNTPER1.
DR PRINTS: PR00014; FNTPER1I.
DR SMART: SM00058; FN1; 1.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01253; FIBRONECTIN_1; 1.
KW Repeat.
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 347 AA; 38344 MW; 3DCA85910BEA461 CRC64;

Query Match
Best Local Similarity 75.0%; Pred. No. 0.44; Length 347;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
Db 81 YTVTGLEPGIDY 92

RESULT 7
Q9UOS6
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ID Q9UOS6 PRELIMINARY; PRT; 354 AA.
AC Q9UOS6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibronectin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=bone marrow;
RA Dutt P., Yoder M.C.;
RT "Alternative splicing of fibronectin in human bone marrow stromal
cells.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U60068; AAD10853.1; -.
DR HSSP: P02751; IENH.
DR InterPro: IPR003962; FNIII subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00041; FN3; 3.
DR PRINTS: PR00014; FNTPER1I.
DR SMART: SM00060; FN3; 2.
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 354 AA; 38656 MW; 596107AF3078F9P9 CRC64;

Query Match
Best Local Similarity 75.0%; Pred. No. 0.45; Length 354;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
Db 161 YTVTGLEPGIDY 172

RESULT 8
Q95617 PRELIMINARY; PRT; 379 AA.
ID Q95617;
AC Q95617;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibronectin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=bone marrow;
RA Dutt P., Yoder M.C.;
RT "Alternative splicing of fibronectin in human bone marrow stromal
cells.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U60067; AAD1500.1; -.
DR HSSP: P02751; IENH.
DR InterPro: IPR003962; FNIII subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00041; FN3; 3.
DR PRINTS: PR00014; FNTPER1I.
DR SMART: SM00060; FN3; 2.
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 379 AA; 41370 MW; 7E1CA4B9428AC7C2 CRC64;

Query Match
Best Local Similarity 75.0%; Pred. No. 0.49; Length 379;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 3 YTVTGLEPGIDY 14
 ||:|||||
 Db 161 YTTTGLQPGTDY 172

RESULT 9

Q8R3F3 PRELIMINARY; PRT; 810 AA.

AC Q8R3F3; 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN FN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025521; AAH25521.1; -
 DR MGD; MGI:95566; Fn1.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR000083; Fibrinctn1.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR Pfam; PF00039; fn1; 3.
 DR Pfam; PF00041; fn3; 6.
 DR SMART; SM00058; FN1; 3.
 DR SMART; SM00060; FN3; 6.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 3.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 810 AA; 85228 MW; 9A7A4DD0ED3437F CRC64;

Query Match 67.1%; Score 57; DB 11; Length 810;
 Best Local Similarity 75.0%; Pred. No. 1.2;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
 ||:|||||
 Db 316 YTTTGLQPGTDY 327

RESULT 10
 Q9B091 PRELIMINARY; PRT; 496 AA.

AC Q9B091; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gp30.
 GN 30.
 OS Mycobacteriophage Bxb1.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 NCBI_TaxID=148603;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20572070; PubMed=11123671;
 RA Medavilla J., Jain S., Kriakov J., Ford M.E., Duda R.L., Jacobs W.R.,
 Hendrix R.W., Hatfull G.F.;
 RT "Genome organization and characterization of mycobacteriophage bxb1";
 RL MOL. Microbiol. 38:955-970(2000).
 DR EMBL; AF271693; AAG59735.1; -
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR008957; FN_III-like.
 DR Pfam; PF00144; beta-lactamase; 1.
 SQ SEQUENCE 496 AA; 54891 MW; 37564FA32F260B5F CRC64;
 RX

Query Match 58.8%; Score 50; DB 9; Length 496;
 Best Local Similarity 64.3%; Pred. No. 9.9;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYTVTGLEPGIDY 14
 ||:|||||
 Db 26 GSVTTTGLTPGTDY 39

RESULT 11

O93405 PRELIMINARY; PRT; 922 AA.

AC O93405; 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fibronectin.
 GN FN1 OR FN2.
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhao Q., Colloidi P.;
 RT "Characterization and expression of zebrafish fibronectin";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF061127; AAC1941.1; -
 DR HSSP; P02751; IFBR.
 DR ZFIN; ZDB-GENE-000426-1; fn1.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR InterPro; IPR000083; Fibrinctn1.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR000562; FN_III-like.
 DR Pfam; PF00039; fn1; 9.
 DR Pfam; PF00040; fn2; 2.
 DR Pfam; PF00041; fn3; 3.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRODOM; PD000995; FN_Type_II; 2.
 DR SMART; SM00058; FN1; 9.
 DR SMART; SM00059; FN2; 2.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PS01253; FIBRONECTIN_1; 9.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 SQ SEQUENCE 922 AA; 101814 MW; BF83E4CABBD00B0 CRC64;

Query Match 58.8%; Score 50; DB 13; Length 922;
 Best Local Similarity 53.8%; Pred. No. 20;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 15
 ||:|||||
 Db 663 YTTTGLKPGVYE 675

RESULT 12

O97566 PRELIMINARY; PRT; 1253 AA.

AC O97566; 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Alpha-1 type VII collagen non-collagenous domain (Fragment).
 GN COL7A1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=99002915; PubMed=9784596;
 RX

RA Xu L., Chen M., Peng J., O'Toole E.A., Woodley D.T., Chan L.S.;
 RT "Molecular cloning and characterization of a cDNA encoding canine type
 RT VII collagen non-collagenous (NC1) domain, the target antigen of
 RT autoimmune disease epidermolysis bullosa acquisita (EBA).";
 RL Biochim. Biophys. Acta 1408:25-34(1998).
 DR EMBL: AF042093; AAC72024.1; -.
 DR HSSP: P02751; IFA.

DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF00041; fn3; 9.
 DR Pfam: PF00092; vwa; 2.
 DR PRINTS: PR00453; VWFADOMAIN.
 DR SMART: SMO0360; FN3; 9.
 DR SMART: SMO0327; VWA; 2.
 DR PROSITE: PS50234; VWFPA; 2.
 DR Collagen.
 FT NON TER 1253
 FT SEQUENCE 1253 AA; 133696 MW; 7FF2B50DE4B8CA89 CRC64;

Query Match 58.8%; Score 50; DB 6; Length 1253;
 Best Local Similarity 71.4%; Pred. No. 28;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYVTGTGLPGIDY 14
 DB 1011 GSGQVITGLPGTGY 1024

RESULT 13
 O95608 PRELIMINARY; PRT; 120 AA.
 ID O95608
 AC O95608;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fibronectin (Fragment).
 DE GN FN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Godfrey H.P., Edrahim A.A.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U41724; AAD00013.1; -.
 DR HSSP: P02751; IFA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SMO0060; FN3; 1.
 FT NON TER 1
 FT SEQUENCE 120 AA; 13341 MW; 05E5C3277046ED2F CRC64;

Query Match 57.6%; Score 49; DB 4; Length 120;
 Best Local Similarity 72.7%; Pred. No. 2.9;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 TVTGLPGIDY 14
 DB 41 TITGLPGTGY 51

RESULT 14
 O8CG36 PRELIMINARY; PRT; 189 AA.
 ID O8CG36
 AC O8CG36;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fibronectin (Fragment).
 OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10095;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96262744; PubMed=8691328;
 RA Bergijk E.C., Baelde H.C., Koolstra C.J., De Heer E., Killen P.D.,
 RA Bruijn J.A.;
 RT "Cloning of the mouse fibronectin V-region and variation of its
 RT splicing pattern in experimental immune complex glomerulonephritis";
 RL J. Pathol. 178:462-468(1996).
 DR EMBL: S82292; AAB6743.1; -.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR Pfam: PF00041; fn3; 1.
 FT NON TER 1
 FT NON TER 189
 FT SEQUENCE 189 AA; 20763 MW; BDF6B16ECC274662 CRC64;

Query Match 57.6%; Score 49; DB 11; Length 189;
 Best Local Similarity 72.7%; Pred. No. 4.8;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 TVTGLPGIDY 14
 DB 21 TITGLPGTGY 31

RESULT 15
 O63870 PRELIMINARY; PRT; 2944 AA.
 ID O63870
 AC O63870;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Type VII collagen.
 DE GN COL7A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93315168; PubMed=8325648;
 RA Li K., Christiano A.M., Copeland N.G., Gilbert D.J., Chu M.L.,
 RA Jenkins N.A., Utto J.;
 RT "cDNA cloning and chromosomal mapping of the mouse type VII collagen
 RT gene (Col7a1): evidence for rapid evolutionary divergence of the
 RT gene.";
 RL Genomics 16:733-739(1993).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96275720; PubMed=8752674;
 RA Kivirikko S., Li K., Christiano A.M., Utto J.;
 RT "Cloning of mouse type VII collagen reveals evolutionary conservation
 RT of functional protein domains and genomic organization";
 RL J. Invest. Dermatol. 106:1300-1306(1996).
 RN (3)

RP SEQUENCE FROM N.A.
 RA Kivirikko S., Li K., Christiano A.M., Utto J.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U32107; AAB66593.1; -.
 DR EMBL: S63654; AAB27492.1; -.
 DR PIR: A45748; A45748.
 DR HSSP: P12111; 2KXT.
 DR MGD: MGI:88463; Col7a1.
 DR GO: GO:0004867; F:serine protease inhibitor activity; IFA.
 DR InterPro: IPR008161; C1g_helix.
 DR InterPro: IPR008160; Collagen.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR002223; Kunitz_BPTI.

DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01391; Collagen_24.
DR Pfam; PF00041; Fn3_9.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00092; Vwa; 2.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00453; VWFADOMAIN.
DR ProDom; PD000007; Clg_helix; 6.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SW00060; FN3_9.
DR SMART; SW00327; VWA_2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0234; VWFA; 2.
KW Collagen; Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 2944 AA; 29516 MW; 596FA507BC6C02C2 CRC64;

Query Match 57.6%; Score 49; DB 11; Length 2944;

Best Local Similarity 75.0%; Pred. No. 1.1e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 YVTGLEPGIDY 14
: |||||
Db 1014 HRYTGLEPGISY 1025

Search completed: September 21, 2004, 05:57:06
Job time : 25.6029 secs

OM protein - protein search, using SW model

Run on: September 21, 2004, 05:46:53 ; Search time 30.2206 Seconds
(without alignments)
140.243 Million cell updates/sec

Title: US-10-676-045-2

Perfect score: 85

Sequence: 1 GYTTVGLPEPIDVD 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	AA017876	AA017876 EDB fibro
2	85	100.0	91	AA025405	AA025405 ED-B, 1/1
3	85	100.0	91	AA023838	AA023838 Tpe ED2 d
4	85	100.0	91	ABG98132	ABG98132 Anti-neov
5	85	100.0	91	AA017876	AA017876 EDB fibro
6	85	100.0	91	ABP74705	ABP74705 Human ED-
7	85	100.0	91	ADCO9564	ADCO9564 Epitope w
8	85	100.0	146	ABG98133	ABG98133 Human fib
9	85	100.0	147	ABP74706	ABP74706 Human fib
10	85	100.0	147	ABP74706	ABP74706 Human fib
11	85	100.0	1336	AA060019	AA060019 Tissue-bi
12	85	100.0	2220	AB001289	AB001289 Human pro
13	85	100.0	2446	AA060021	AA060021 Fibrinoge
14	85	100.0	2446	AA050377	AA050377 Human fib
15	85	100.0	2477	AA095959	AA095959 Human fib
16	85	100.0	2477	AD063323	AD063323 Rat Prote
17	72	84.7	15	AA040093	AA040093 Antigenic
18	72	84.7	15	AA088821	AA088821 ED-B anti
19	57	67.1	25	AA066673	AA066673 Peptide d
20	57	67.1	89	AA051357	AA051357 Metastasi
21	57	67.1	89	ABR39962	ABR39962 Fibronect
22	57	67.1	89	ABR39962	ABR39962 Fibronect
23	57	67.1	270	AA078414	AA078414 Human fib
24	57	67.1	271	AA082247	AA082247 Heparin-I
25	57	67.1	271	AA021669	AA021669 Heparin-I

26	57	67.1	271	2	AAW33336	AAW33336 Human fib
27	57	67.1	271	2	AAW13570	AAW13570 Mouse fib
28	57	67.1	271	2	AAW13567	AAW13567 Human fib
29	57	67.1	271	2	AAW13568	AAW13568 Human fib
30	57	67.1	271	6	ABP59433	ABP59433 Human fib
31	57	67.1	271	6	ABP59433	ABP59433 Human fib
32	57	67.1	276	6	ABP59443	ABP59443 Human fib
33	57	67.1	276	7	ABP59443	ABP59443 Human fib
34	57	67.1	296	2	AA098815	AA098815 Cell adhe
35	57	67.1	296	2	AAW13571	AAW13571
36	57	67.1	296	2	AAW13571	AAW13571
37	57	67.1	296	6	AAW13571	AAW13571
38	57	67.1	296	6	ABP59434	ABP59434 Human fib
39	57	67.1	367	2	ADD49013	ADD49013 Fibronect
40	57	67.1	367	2	AA051359	AA051359 Metastasi
41	57	67.1	367	2	AA060352	AA060352 Chimeric
42	57	67.1	367	6	ABP59438	ABP59438 Human fib
43	57	67.1	367	7	ADD49017	ADD49017 Fibronect
44	57	67.1	446	1	AA090823	AA090823 Amino ter
45	57	67.1	457	2	AA051360	AA051360 Metastasi
45	57	67.1	457	2	AA060353	AA060353 Chimeric

ALIGNMENTS

RESULT 1	AA017876	standard; peptide; 15 AA.
ID	AA017876	
XX	AA017876;	
AC	XX	
DT	20-AUG-2002	(first entry)
XX	XX	
DE	EDB fibronectin domain binding peptide #2.	
XX	XX	
KW	EDB fibronectin domain; EDBFD; angiogenesis; gene therapy; transplant;	
KM	implant; receptor molecule interaction.	
XX	XX	
OS	Unidentified.	
XX	XX	
PN	WO200220563-A2.	
XX	XX	
PD	14-MAR-2002.	
XX	XX	
PF	30-AUG-2001; 2001WO-EP010016.	
XX	XX	
PR	07-SEP-2000; 2000DE-01045803.	
XX	XX	
PR	02-MAY-2001; 2001DE-01023133.	
XX	XX	
PA	(SCHD) SCHERING AG.	
PA	(REPL) REPLITZ A.	
PA	(KOPF) KOPFITZ M.	
PA	(EGNE) EGNER U.	
PA	(BAER) BAER I.	
XX	(MENR) MENRAD A.	
XX	XX	
PI	Menrad A;	
XX	XX	
DR	WPI; 2002-479458/51.	
XX	XX	
PT	New proteins binding specifically to the ED-b fibronectin domain, are	
XX	cell adhesion and proliferation mediators useful e.g. in screening tests.	
XX	XX	
PS	Claim 2; Page 41; 66pp; German.	
XX	XX	
CC	The present invention relates to a new protein which binds specifically	
CC	to the EDB fibronectin domain (EDBFD), is specifically expressed or	
CC	activated in endothelial cells, stromal cells of a tumour and tumour	
CC	cells, and has an apparent molecular weight of 120-130 kDa for the light	
CC	chain and 150-160 kDa for the heavy chain. The protein can be used to	
CC	screen compounds which bind to EDBFD or its receptor for coating	
CC	surfaces to which endothelial cells bind, in cell cultures, in	
CC	combination with transplants or in combination with implants	

CC (specifically lung implants, artificial heart pacemakers or valves,
 CC vascular implants, endoprostheses, screws, bars, plates, wires, nails,
 CC rods, artificial joints, breast implants, artificial cranial plates,
 CC false teeth, tooth fillings or tooth bridges, as it improves the
 CC integration of transplants or implants in the body. The protein is also
 CC useful in clarifying ED-B-specific adhesion mechanisms and receptor
 CC molecule interactions involved in angiogenesis. The present sequence is a
 CC protein of the invention

XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 85; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e-07; Mismatches 0; Gaps 0;
 Matches 15; Conservative 0; Indels 0;

OY 1 GYTTVTGLEPGIDYD 15
 |||||
 Db 1 GYTTVTGLEPGIDYD 15

RESULT 2
 AAR25405
 ID AAR25405 standard; protein; 91 AA.

XX AAR25405;

XX 18-JAN-1993 (first entry)

DE ED-B.

XX Fibronectin; antibody; cancer.

XX Homo sapiens.

XX JP04169195-A.

XX 17-JUN-1992.

XX 31-OCT-1990; 90JP-00295820.

XX 31-OCT-1990; 90JP-00295820.

XX (HOJII/) HOJIN G.

XX (GAKU/) GAKUEN F.

XX (SAKA) OHSUKA PHARM CO LTD.

XX WPI; 1992-253398/31.

XX Monoclonal antibody to fragment ED-B of fibronectin - for determining
 PT fibronectin in cancerous tissue.
 XX Claim 1; Page 1; 17pp; Japanese.

XX The sequence given is ED-B which is isolated from fibronectin. This
 CC peptide was used in the production of an anti-ED-B monoclonal antibody.
 CC This antibody is reactive against fibronectin, particularly in cancerous
 CC tissue. The antibody recognises ED-B specifically and has reaction
 CC specificity to cancerous fibronectin. This antibody is useful as a tracer
 CC in determination of immunogen and cancerous fibronectin

XX Sequence 91 AA;

Query Match 100.0%; Score 85; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYTTVTGLEPGIDYD 15
 |||||
 Db 56 GYTTVTGLEPGIDYD 70

RESULT 3

ID AAR23838 standard; protein; 91 AA.

XX AAR23838;

AC 05-NOV-1992 (first entry)

XX The ED2 domain of fibronectin.

XX FN; toxemia; pregnancy; type III.

XX Homo sapiens.

XX US5108898-A.

XX 28-APR-1992.

XX 18-JAN-1989; 89US-00298622.

XX 18-JAN-1989; 89US-00298622.

XX (PETER/) PETERS J H.

XX Peters JH, Lockwood CJ;

XX WPI; 1992-166519/20.

XX Predicting toxemia in pregnancy - by detecting elevated levels of
 PT fibronectin having variably included type III repeat region in body fluid
 PT sample.

XX Disclosure; Fig 2; 9pp; English.

XX The human fibronectin Type III repeat sequence ED2 contains a region
 CC which has little sequence homology with other Type III repeats. Peptides
 CC were synthesised, having a sequence based on the ED2 sequence, which were
 CC used to raise antibodies which will immunoreact with ED2 but not with a
 CC plasma fibronectin monomer. The antibodies can be used for detecting
 CC fibronectin contg. Variably included Type III repeats in a sample, thus
 CC determining patients destined to develop toxemia, partic. preclampsia,
 CC prior to the onset of maternal signs and symptoms of the disease,
 CC allowing for early therapeutic intervention and monitoring. See also
 CC AAR23837-42

XX Sequence 91 AA;

Query Match 100.0%; Score 85; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYTTVTGLEPGIDYD 15
 |||||
 Db 56 GYTTVTGLEPGIDYD 70

RESULT 4
 ABG98132
 ID ABG98132 standard; protein; 91 AA.

XX ABG98132;

XX 08-JAN-2003 (first entry)

DE Anti-neovascular preparation associated epitope #87.

XX Cell-mediated immunity; cellular immune response; CTL response;
 KW tumour neovasculture; anti-angiogenesis.

XX Homo sapiens.

XX WO200269907-A2.

XX 12-SEP-2002.

PF 07-MAR-2002; 2002WO-US007204.
XX
XX 07-MAR-2001; 2001US-0274063P.
XX
XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
XX Simard JTL, Diamond DC;
XX
XX WPI; 2002-750433/81.
XX
XX Evaluating cell-mediated immunity, in particular cytotoxic T lymphocyte
PT responses, by implanting vascular cells, useful for treatment and
PT research models for directly targeting tumor neovasculature.
XX
XX Example 5; Page 25; 73pp; English.
XX
XX The invention describes a method of evaluating cell-mediated immunity
CC comprising implanting vascular cells into an immunodeficient mammal,
CC establishing an immune response in the mammal, and assaying a
CC characteristic to determine cell-mediated immunity in the mammal. The
CC methods and compositions of the present invention are useful for the
CC generation of a cellular immune response, in particular a CTL response,
CC for treatment directly against a tumour neovasculature. They can also be
CC used for making research models targeting tumour neovasculature. The
CC present invention using the anti-angiogenesis approach takes advantage of
CC the need of tumours to recruit a blood supply to support their continued
CC growth. This approach aims to disrupt a tumour's supply of nutrients to
CC cause it to die or at least limit its growth. This is the amino acid
CC sequence of a peptide associated with the neo-vasculature preparation
CC for treatment of cancer described in the invention
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 85; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTVTGLSPGIDYD 15
|||
DB 56 GYVTVTGLSPGIDYD 70

RESULT 5
AA017878
ID AA017878 standard; protein; 91 AA.
XX
XX AA017878;
AC
XX
XX 20-AUG-2002 (first entry)
DT
XX
XX EDB fibronectin domain binding protein.
DE
XX EDB fibronectin domain; EDBFD; angiogenesis; gene therapy; transplant;
KM implant; receptor molecule interaction.
XX
XX Unidentified.
OS
XX
XX WO200220563-A2.
PN
XX
XX 14-MAR-2002.
PD
XX
XX 30-AUG-2001; 2001WO-EP010016.
PF
XX
XX 07-SEP-2000; 2000DE-01045803.
PR
XX 02-MAY-2001; 2001DE-01023133.
XX
XX (SGHD) SCHERING AG.
PA (REDL) REDLITZ A.
PA (KOPF) KOPFITZ M.
PA (EGNE) EGNER U.
PA (BAHR) BAHR I.
PA (MENR) MENRAD A.
XX

PI Menrad A;
XX
XX WPI; 2002-479458/51.
XX
XX New proteins binding specifically to the ED-b fibronectin domain, are
PT cell adhesion and proliferation mediators useful e.g. in screening tests.
XX
XX Claim 18; Page 41-42; 66pp; German.
XX
XX The present invention relates to a new protein which binds specifically
CC to the EDB fibronectin domain (EDBFD), is specifically expressed or
CC activated in endothelial cells, stromal cells of a tumour and tumour
CC cells, and has an apparent molecular weight of 120-130 kDa for the light
CC chain and 150-160 kDa for the heavy chain. The protein can be used to
CC screen compounds which bind to EDBFD or its receptor, for coating
CC surfaces to which endothelial cells bind, in cell cultures, in
CC combination with transplants or in combination with implants
CC (specifically lung implants, artificial heart pacemakers or valves,
CC vascular implants, endoprotheses, screws, bars, plates, wires, nails,
CC rods, artificial joints, breast implants, artificial cranial plates,
CC false teeth, tooth fillings or tooth bridges, as it improves the
CC integration of transplants or implants in the body. The protein is also
CC useful in clarifying EDB-specific adhesion mechanisms and receptor
CC molecule interactions involved in angiogenesis. The present sequence is a
CC protein of the invention
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 85; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTVTGLSPGIDYD 15
|||
DB 56 GYVTVTGLSPGIDYD 70

RESULT 6
ABP74705
ID ABP74705 standard; protein; 91 AA.
XX
XX ABP74705;
AC
XX
XX 03-FEB-2003 (first entry)
DT
XX
XX Human ED-B domain of fibronectin SEQ ID NO:589.
DE
XX Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
KM T cell.
XX
XX Homo sapiens.
OS
XX
XX WO200281646-A2.
PN
XX
XX 17-OCT-2002.
PD
XX
XX 04-APR-2002; 2002WO-US011101.
PF
XX
XX 06-APR-2001; 2001US-0282211P.
PR
XX 07-NOV-2001; 2001US-0337017P.
PR
XX 07-MAR-2002; 2002US-0363210P.
XX
XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
PA
XX
XX Simard JTL, Diamond DC, Liu L, Xie Z;
XX
XX WPI; 2003-067518/06.
XX
XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid
PT encoding the peptides, that are useful epitopes of target-associated
PT antigens.
XX
PS Claim 1; Page 26; 35pp; English.

XX The present invention describes an isolated epitope (I) and an epitope
CC cluster. Also described is a vaccine or immunotherapeutic composition
CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
CC treating an animal, by administering to an animal the vaccine or
CC immunotherapeutic composition. VC is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic composition, by
CC administering VC to an HLA-transgenic animal and evaluating
CC immunogenicity based on a characteristic of the animal, or by in vitro
CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
CC useful for determining specific T cell frequency, by contacting T cells
CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
CC ABP74713 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 85; DB 6; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTVTGLEPGIDYD 15
|||
56 GYTVTGLEPGIDYD 70

RESULT 7
ID ADC09564 standard; peptide: 91 AA.

AC ADC09564;
DT 18-DEC-2003 (first entry)

DE Epitope with high affinity for MHC class I #SEQ ID 589.

XX Epitope; immunological; vaccine;
KM major histocompatibility complex class I; MHC class I; cancer;
KW immunisation.

XX Unidentified.

OS WO2003008537-A2.

XX 30-JAN-2003.

PF 29-MAR-2002; 2002WO-US010189.

PR 06-APR-2001; 2001US-0282211P.

PR 07-NOV-2001; 2001US-0337017P.

PR 07-MAR-2002; 2002US-0363210P.

PA (CTL1-) CTL IMMUNOTHERAPIES CORP.

PI Simard JTL, Diamond DC, Liu L, Xie Z;

DR WPI; 2003-248010/24.

XX Epitope having high affinity for major histocompatibility complex class I

PT useful for treating an animal, evaluating immunogenicity of a vaccine or

PT therapeutic composition and for diagnosing a disease.

XX Claim 1; SEQ ID NO 589; 239pp; English.

CC The invention relates to an isolated epitope polypeptide that has high

CC affinity for major histocompatibility complex (MHC) class I, and an

CC epitope cluster comprising the polypeptide. Also disclosed is a vaccine

CC or immunotherapeutic composition containing an epitope of the invention.

CC Compositions of the invention may be used in the treatment of cancer. The

CC method can be combined with a radiation therapy, chemotherapy,

CC biocompatibility or surgery. The composition is also useful for evaluating

CC immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
CC-peptide complexes of the invention are useful for determining specific T
CC cell frequency. This method is useful for evaluating immunological
CC response by performing the method prior to and subsequent to an
CC immunisation step. Compositions of the invention are useful for
CC diagnosing a disease. The current sequence represents an epitope of the
CC invention with high affinity for MHC class I.
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 85; DB 7; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTVTGLEPGIDYD 15
|||
56 GYTVTGLEPGIDYD 70

RESULT 8
ID ADC09565 standard; peptide: 146 AA.

AC ADC09565;

DT 18-DEC-2003 (first entry)

DE Epitope with high affinity for MHC class I #SEQ ID 590.

XX Epitope; immunological; vaccine;
KM major histocompatibility complex class I; MHC class I; cancer;
KW immunisation.

XX Unidentified.

OS WO2003008537-A2.

XX 30-JAN-2003.

PF 29-MAR-2002; 2002WO-US010189.

PR 06-APR-2001; 2001US-0282211P.

PR 07-NOV-2001; 2001US-0337017P.

PR 07-MAR-2002; 2002US-0363210P.

PA (CTL1-) CTL IMMUNOTHERAPIES CORP.

PI Simard JTL, Diamond DC, Liu L, Xie Z;

DR WPI; 2003-248010/24.

XX Epitope having high affinity for major histocompatibility complex class I

PT useful for treating an animal, evaluating immunogenicity of a vaccine or

PT therapeutic composition and for diagnosing a disease.

XX Claim 1; SEQ ID NO 590; 239pp; English.

CC The invention relates to an isolated epitope polypeptide that has high

CC affinity for major histocompatibility complex (MHC) class I, and an

CC epitope cluster comprising the polypeptide. Also disclosed is a vaccine

CC or immunotherapeutic composition containing an epitope of the invention.

CC Compositions of the invention may be used in the treatment of cancer. The

CC method can be combined with a radiation therapy, chemotherapy,

CC biocompatibility or surgery. The composition is also useful for evaluating

CC immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC

CC-peptide complexes of the invention are useful for determining specific T

CC cell frequency. This method is useful for evaluating immunological

CC response, by performing the method prior to and subsequent to an

CC immunisation step. Compositions of the invention are useful for

CC diagnosing a disease. The current sequence represents an epitope of the

CC invention with high affinity for MHC class I.
SQ Sequence 146 AA;

Query Match 100.0%; Score 85; DB 7; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTVTGLEPGIDYD 15
|||
90 GYVTVTGLEPGIDYD 104

Db

RESULT 9
ABG98133
ID ABG98133 standard; protein; 147 AA.
XX
XX
AC ABG98133;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human fibronectin gene ED-B region.
XX
KM Cell-mediated immunity; cellular immune response; CTL response;
KM tumour neovasculation; anti-angiogenesis.
OS Homo sapiens.
XX
XX WO200269907-A2.
XX
XX 12-SEP-2002.
XX
PF 07-MAR-2002; 2002MO-US007204.
XX
PR 07-MAR-2001; 2001US-0274063P.
XX
XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
PI Simard JTL, Diamond DC;
XX
XX WPI; 2002-750433/81.
XX
XX N-PSDB; ABX03678.
XX
XX
XX Evaluating cell-mediated immunity, in particular cytotoxic T lymphocyte
PT responses, by implanting vascular cells, useful for treatment and
PT research models for directly targeting tumor neovasculation.
XX
XX Example 5; Page 29; 73pp; English.
XX
XX The invention describes a method of evaluating cell-mediated immunity
CC comprising implanting vascular cells into an immunodeficient mammal,
CC establishing an immune response in the mammal, and assaying a
CC characteristic to determine cell-mediated immunity in the mammal. The
CC methods and compositions of the present invention are useful for the
CC generation of a cellular immune response, in particular a CTL response,
CC for treatment directly against a tumour neovasculation. They can also be
CC used for making research models targeting tumour neovasculation. The
CC present invention using the anti-angiogenesis approach takes advantage of
CC the need of tumours to recruit a blood supply to support their continued
CC growth. This approach aims to disrupt a tumour's supply of nutrients to
CC cause it to die or at least limit its growth. This is the amino acid
CC sequence of a protein associated with the neo-vascularization preparation
CC for treatment of cancer described in the invention
XX
XX SQ Sequence 147 AA;

Query Match 100.0%; Score 85; DB 5; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTVTGLEPGIDYD 15
|||
90 GYVTVTGLEPGIDYD 104

Db

RESULT 10

ABP74706
ID ABP74706 standard; protein; 147 AA.
XX
XX AC ABP74706;
XX
XX DT 03-FEB-2003 (first entry)
XX
XX DE Human ED-B domain of fibronectin SEQ ID NO:590.
XX
XX KM Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
XX T cell.
OS Homo sapiens.
XX
XX WO200281646-A2.
XX
XX 17-OCT-2002.
XX
XX 04-APR-2002; 2002MO-US011101.
XX
XX PF 06-APR-2001; 2001US-028221P.
XX
XX PR 07-NOV-2001; 2001US-0337017P.
XX
XX PR 07-MAR-2002; 2002US-0363210P.
XX
XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
XX PA
XX
XX PI Simard JTL, Diamond DC, Liu L, Xie Z;
XX
XX WPI; 2003-067518/06.
XX
XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid
PT encoding the peptides, that are useful epitopes of target-associated
PT antigens.
XX
XX Claim 1; Page 26; 352pp; English.
XX
XX The present invention describes an isolated epitope (I) and an epitope
CC cluster. Also described is a vaccine or immunotherapeutic composition
CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
CC treating an animal, by administering to an animal the vaccine or
CC immunotherapeutic composition. VC is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic composition, by
CC administering VC to an HLA-transgenic animal and evaluating
CC immunogenicity based on a characteristic of the animal, or by in vitro
CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
CC useful for determining specific T cell frequency, by contacting T cells
CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
CC limiting dilution analysis, flow cytometry, in situ hybridization and/or
CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
CC ABP74713 represent sequences used in the exemplification of the present
CC invention
XX
XX SQ Sequence 147 AA;

Query Match 100.0%; Score 85; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTVTGLEPGIDYD 15
|||
90 GYVTVTGLEPGIDYD 104

Db

RESULT 11
AAR60019
ID AAR60019 standard; protein; 1336 AA.
XX
XX AC AAR60019;
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 23-FEB-1995 (first entry)
XX
XX Tissue-binding hybrid protein.

XX Tissue binding; tissue sealing; wound healing; vulnerary;
 KW tissue-binding domain; TBD; crosslinking domain; fibronectin;
 KW fibrinogen-alpha; heparin-binding domain; collagen-binding domain;
 KW cell-binding domain; hybrid protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 2..1336
 FT Domain /label= tissue-binding_domain
 FT Domain 2..926
 FT Domain /label= tissue-binding_domain
 FT Domain 928..1336
 FT Domain /label= tissue-binding_domain
 XX
 XX WO9416085-A2.
 XX
 XX 21-JUL-1994.
 XX
 XX 30-DEC-1993; 93MO-US012687.
 XX
 XX 30-DEC-1992; 92US-00998271.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Irani MH;
 XX WPI; 1994-249231/30.
 XX N-PSDB; AAQ70007.
 XX
 XX New hybrid proteins for use in tissue sealing and wound healing -
 PT comprising a tissue-binding domain from a protein covalently linked to a
 PT crosslinking domain of another protein.
 XX
 XX Disclosure; Page 63-69; 87pp; English.
 XX
 XX Hybrid proteins have a tissue-binding domain (TBD) from 1 protein linked
 CC to a crosslinking domain from another protein. The TBD comprises: aa 2-
 CC 926, 928-1336 and especially 2-1336 of the sequence given in AAR60019;
 CC the heparin-binding domain (aa 1812-2171 of AAR60021) of fibronectin; the
 CC collagen-binding domain (aa 282-608 of AAR60021) of fibronectin; or the
 CC cell-binding domain (aa 1357-1903 or 1532-1631 of AAR60020) of
 CC fibronectin. DNA encoding a fibronectin-fibrinogen hybrid is given in
 CC AAQ70007, and sequences for fibronectin and fibrinogen-alpha in AAQ70008
 CC and AAQ70009, respectively. (Updated on 25-MAR-2003 to correct FN field.)
 CC
 XX
 SO Sequence 1336 AA;
 OY
 OY Query Match 100.0%; Score 85; DB 2; Length 1336;
 OY Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 OY Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GYTVTGLERPIDYD 15
 OY 344 GYTVTGLERPIDYD 358
 DB
 DB ABO01289 standard; protein; 2220 AA.
 ID ABO01289
 AC ABO01289;
 AC
 AC 06-AUG-2003 (first entry)
 DT
 DT Human protein NOV1b.
 XX
 XX Human; NOVX; cardiomyopathy; atherosclerosis; hypertension;
 KW congenital heart defect; prostate cancer; diabetes; metabolic disorder;
 KW neoplasm; graft versus host disease; AIDS; bronchial asthma;
 KW Crohn's disease; multiple sclerosis; infectious disease; anorexia;
 KW cancer-associated cachexia; neurodegenerative disorder;

XX Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy;
 KW SNP; single nucleotide polymorphism.
 XX
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 639
 FT /note= "May be Phe as the result of a single nucleotide
 FT polymorphism"
 FT
 XX
 XX WO2003023008-A2.
 XX
 XX 20-MAR-2003.
 XX
 XX 09-SEP-2002; 2002WO-US028596.
 XX
 XX 07-SEP-2001; 2001US-0318120P.
 XX 07-SEP-2001; 2001US-0318130P.
 XX 10-SEP-2001; 2001US-0318430P.
 XX 12-SEP-2001; 2001US-0318765P.
 XX 17-SEP-2001; 2001US-0322781P.
 XX 17-SEP-2001; 2001US-0322816P.
 XX 19-SEP-2001; 2001US-0323519P.
 XX 20-SEP-2001; 2001US-0323611P.
 XX 20-SEP-2001; 2001US-0323636P.
 XX 25-SEP-2001; 2001US-0324969P.
 XX 25-SEP-2001; 2001US-0325091P.
 XX 26-SEP-2001; 2001US-0324990P.
 XX 15-FEB-2002; 2002US-0357303P.
 XX 28-FEB-2002; 2002US-0360973P.
 XX 20-MAR-2002; 2002US-0366131P.
 XX 25-MAR-2002; 2002US-0367753P.
 XX 02-APR-2002; 2002US-0369479P.
 XX 10-MAY-2002; 2002US-0379532P.
 XX 17-MAY-2002; 2002US-0381654P.
 XX 17-MAY-2002; 2002US-0381672P.
 XX 28-MAY-2002; 2002US-0383651P.
 XX 29-MAY-2002; 2002US-0384012P.
 XX 19-JUN-2002; 2002US-0390155P.
 XX 06-SEP-2002; 2002US-00390155.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Zhong M, Li L, Gorman L, Spytek KA, Kekuda R, Taupier RJ;
 PI Anderson DW, Vernet CAM, Catterton E, Miller CE, Shenoy SG;
 PI Patyankar UM, Pena CE, Tchervet VT, Padigaru M, Guev VY;
 PI Patyankar UM, Burgess CE, Gerlach VL, Casman SJ, Rieger DK;
 PI Groesse WM, Smithson G, Peyman JA, Starling G, Rothenberg ME;
 PI Larochelle WJ, Shinkens RA, Crabtree J, Rastelli L, Voss EZ;
 PI Boldog FL, Edinger SR, Millet I, Macdougall JR, Ellerman K;
 PI Chapoval A;
 PI
 PI WPI; 2003-313246/30.
 DR N-PSDB; ACD06170.
 DR
 XX
 XX New polypeptides and polynucleotides having properties related to
 PT stimulation of biochemical or physiological responses in a cell or
 PT tissue, useful for diagnosing or preventing e.g. atherosclerosis,
 PT hypertension, prostate cancer.
 PS
 PS Claim 2; Page 110-111; 849pp; English.
 XX
 XX The invention relates to an isolated polypeptide comprising one of 127
 CC sequences (appearing as ABO1288-ABO1414) designated as NOVX, a mature
 CC form of NOVX, an amino acid sequence comprising one or more conservative
 CC NOVX or an amino acid sequence comprising one or more conservative
 CC substitutions in NOVX. Also included are nucleic acids encoding NOVX
 CC proteins, determining the presence or amount of NOVX or NOVX DNA in a
 CC sample (by introducing the sample to an antibody that binds
 CC immunospecifically to the polypeptide, and determining the presence or
 CC amount of antibody bound to the polypeptide), determining the presence of
 CC or predisposition to a disease associated with altered levels of

expression of NOVX or NOVX DNA in a first mammalian subject, identifying an agent that binds to NOVX, identifying a potential therapeutic agent for treatment of a pathology related to aberrant expression or aberrant physical interactions of NOVX, screening for a modulator of activity of or of latency or predisposition to a pathology associated with NOVX, a vector comprising NOVX DNA, a cell comprising the vector (used to produce NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides are useful as a marker for cell or tissue type, and in diagnosing and treating pathologies, diseases, conditions or disorders associated with NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, prostate cancer, diabetes, metabolic disorders, neoplasm, heart versus host disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis, infectious diseases, anorexia, cancer-associated cachexia, neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), immune disorders, hematopoietic disorders, dyslipidemias, and wasting disorders associated with chronic diseases. These may also be used to screen for molecules which inhibit or enhance NOVX activity or function, and for detecting specific cell types. These may also be used in chromosome mapping, gene therapy, tissue typing, and in forensic biology. The present sequence represents a NOVX protein

Query Match 100.0%; Score 85; DB 6; Length 2220;
Best Local Similarity 100.0%; Pred. No. 4,9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTVTGLRPGIDYD 15
Db 1321 GYTVTGLRPGIDYD 1335

RESULT 13
AAR60021 standard; protein; 2446 AA.
AC AAR60021;
DT 25-MAR-2003 (revised)
DT 23-FEB-1995 (first entry)
DE Fibrinogen-alpha.
XX
XX Tissue binding; tissue sealing; wound healing; vulnery;
KM tissue-binding domain; TSD; crosslinking domain; fibrinectin;
KW fibrinogen-alpha; heparin-binding domain; collagen-binding domain;
KW cell-binding domain; hybrid protein.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Domain 282..608
FT /label=collagen-binding_domain
FT /note="acts as tissue-binding domain of hybrid protein"
FT 1812..2171
FT /label=heparin-binding_domain
FT /note="acts as tissue-binding domain of hybrid protein"
XX
XX WO9416085-A2.
XX
XX 21-JUL-1994.
XX
XX 30-DEC-1993; 93WO-US012687.
XX
XX 30-DEC-1992; 92US-00998271.
XX
XX (Zymo) ZYMOGENETICS INC.
XX
XX Irani MH;
XX
XX WPI; 1994-249231/30.
XX
XX N-PSDB; AAO70009.
DR

XX New hybrid proteins for use in tissue sealing and wound healing -
PT comprising a tissue-binding domain from a protein covalently linked to a
PT crosslinking domain of another protein.
XX
XX Disclosure; Page 37-48; 87pp; English.
XX
XX Hybrid proteins have a tissue-binding domain (TBD) from 1 protein linked
CC to a crosslinking domain from another protein. The TBD comprises: aa 2-
CC 926, 928-1338 and especially 2-1336 of the sequence given in AAR60019;
CC the heparin-binding domain (aa 1812-2171 of AAR60021) of fibrinectin; the
CC collagen-binding domain (aa 282-608 of AAR60021) of fibrinectin; or the
CC cell-binding domain (aa 1357-1503 or 1532-1631 of AAR60020) of
CC fibrinectin. DNA encoding a fibrinectin-fibrinogen hybrid is given in
CC AAO70007, and sequences for fibrinectin and fibrinogen-alpha in AAO70008
CC and AAO70009, respectively. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 2446 AA;
SQ
Query Match 100.0%; Score 85; DB 2; Length 2446;
Best Local Similarity 100.0%; Pred. No. 5,4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYTVTGLRPGIDYD 15
Db 1321 GYTVTGLRPGIDYD 1335

RESULT 14
AAB50377
ID AAB50377 standard; protein; 2446 AA.
XX
XX AAB50377;
DT 12-MAR-2001 (first entry)
DT
DE Human fibrinectin.
XX
XX Human; FN; fibrinectin; prostate cancer; biallelic marker; diagnosis.
OS
OS Homo sapiens.
PN WO200058509-A2.
XX
XX 05-OCT-2000.
PD
PF 28-MAR-2000; 2000WO-1B000431.
XX
XX 29-MAR-1999; 99US-0126780P.
PR
XX (GIST) GENSET.
PA
PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A;
XX
XX WPI; 2000-594647/56.
XX
XX N-PSDB; AAC89889.
DR
PT Fibrinectin polynucleotide and polypeptide sequences, useful for
PT determining the predisposition of individuals to cancer, such as prostate
PT cancer.
XX
XX Claim 4; Page 185-190; 208pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
CC or purified recombinant polynucleotide comprising a contiguous span of at
CC least 12 nucleotides of a fibrinectin (FN) gene. The methods and
CC sequences are useful for determining the predisposition of individuals to
CC cancer such as prostate cancer and for the prognosis/detection of an
CC eventual treatment response to therapeutic agents acting against prostate
CC cancer. Biallelic markers allow association studies to be performed to
CC identify genes involved in complex traits
XX
XX Sequence 2446 AA;
SQ

Query Match 100.0%; Score 85; DB 3; Length 2446;
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYTYVTGLEPGIDYD 15
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 Db 1321 GYTYVTGLEPGIDYD 1335

RESULT 15
 AAW9595
 ID AAW9595 standard; peptide; 2477 AA.

XX AAW9595;

XX 22-JUN-1999 (first entry)

XX Human fibronectin.

XX Human; fibronectin; glycoprotein; extracellular matrix; motif; migration;
 KW stimulation; wound healing; periodontal tissue regeneration; metastasis;
 KW tumour; invasion; angiogenesis; inflammation; connective tissue function.

XX Homo sapiens.

XX WC9902674-A1.

XX 21-JAN-1999.

XX 01-JUL-1998; 98WO-GB001939.

XX 08-JUL-1997; 97GB-00014276.

XX (UYDU-) UNIV DUNDEE.

XX Schor SL;

XX WPI; 1999-120875/10.

XX New peptides which modulate cell migration have the motif IGD - and are
 PT useful to stimulate angiogenesis.

XX Disclosure; Fig 5; 57pp; English.

XX This sequence represents the amino acid sequence of human fibronectin, a
 CC widely distributed glycoprotein present in extracellular matrices. The
 CC protein contains the motifs IGDs (AAW95953) and IGDQ (AAW9594) which can
 CC be used in peptides to stimulate cell migration for wound healing,
 CC periodontal tissue regeneration, angiogenesis, inhibition of tumour
 CC invasion and metastasis, and in relation to inflammation or connective
 CC tissue function

XX SQ Sequence 2477 AA;

Query Match 100.0%; Score 85; DB 2; Length 2477;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYTYVTGLEPGIDYD 15
 |||||
 Db 1321 GYTYVTGLEPGIDYD 1335

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:49:08 ; Search time 99.1544 Seconds
(without alignments)
48.591 Million cell updates/sec

Title: US-10-676-049-2
Perfect score: 85 GYVTVTGLEPGIDYD 15
Sequence: 1 GYVTVTGLEPGIDYD 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1342398 seqs, 321133274 residues

Total number of hits satisfying chosen parameters: 1342398

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubppa/US09C_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubppa/US10C_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	15	9	US-09-942-117-2
2	85	100.0	91	9	US-09-942-117-4
3	85	100.0	91	14	US-10-094-699-89
4	85	100.0	91	15	US-10-117-937-589
5	85	100.0	91	16	US-10-450-012-5
6	85	100.0	147	14	US-10-094-699-90
7	85	100.0	147	15	US-10-117-937-590
8	85	100.0	2220	12	US-10-236-392-4
9	72	84.7	15	10	US-09-300-4258-23
10	72	84.7	15	14	US-10-321-558-2
11	57	67.1	270	16	US-10-240-488-2
12	57	67.1	271	10	US-09-043-981-1
13	57	67.1	271	10	US-09-775-964-1
14	57	67.1	457	10	US-09-775-964-22
15	57	67.1	472	10	US-09-775-964-21

16	57	67.1	545	16	US-10-408-765A-349	Sequence 349, App
17	57	67.1	547	10	US-09-775-964-13	Sequence 13, Appl
18	57	67.1	549	10	US-09-775-964-23	Sequence 22, Appl
19	57	67.1	573	10	US-09-775-964-30	Sequence 30, Appl
20	57	67.1	574	10	US-09-775-964-24	Sequence 24, Appl
21	57	67.1	693	16	US-10-741-601-364	Sequence 34, App
22	57	67.1	793	14	US-10-171-211-62	Sequence 62, Appl
23	57	67.1	826	10	US-09-775-964-14	Sequence 14, Appl
24	57	67.1	847	16	US-10-741-601-365	Sequence 361, App
25	57	67.1	1259	16	US-10-741-601-361	Sequence 361, App
26	57	67.1	1286	16	US-10-741-601-362	Sequence 362, App
27	57	67.1	1315	16	US-10-741-601-358	Sequence 358, App
28	57	67.1	1341	16	US-10-741-601-355	Sequence 355, App
29	57	67.1	1348	16	US-10-741-601-353	Sequence 353, App
30	57	67.1	2296	12	US-10-236-392-2	Sequence 2, Appl
31	57	67.1	2320	14	US-10-279-733-8	Sequence 8, Appl
32	57	67.1	2328	12	US-10-182-936A-98	Sequence 98, Appl
33	57	67.1	2328	14	US-10-171-311-64	Sequence 64, Appl
34	57	67.1	2328	15	US-10-236-031B-70	Sequence 70, Appl
35	57	67.1	2328	15	US-10-374-979-98	Sequence 98, Appl
36	57	67.1	2328	15	US-10-144-194A-104	Sequence 104, App
37	57	67.1	2355	15	US-10-360-101-235	Sequence 235, App
38	57	67.1	2355	15	US-10-447-161-3	Sequence 3, Appl
39	57	67.1	2355	16	US-10-734-564-94	Sequence 94, Appl
40	57	67.1	2355	16	US-10-741-601-357	Sequence 357, App
41	57	67.1	2355	16	US-10-741-601-366	Sequence 366, App
42	57	67.1	2386	16	US-09-961-403-1	Sequence 1, Appl
43	57	67.1	2386	16	US-10-741-601-360	Sequence 360, App
44	57	67.1	2386	16	US-10-741-601-360	Sequence 3, Appl
45	57	67.1	2386	16	US-10-741-601-360	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-942-117-2
; Sequence 2, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPELITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAEH, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT FILING DATE: 2002-06-24
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-942-117-2
Query Match 100.0%; Score 85; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 GYVTVTGLEPGIDYD 15
1 GYVTVTGLEPGIDYD 15

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US-09-942-117-4
; Sequence 4, Application US/09942117
; Publication No. US2002019700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAHR, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942,117
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-942-117-4

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Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTVTGLEPGIDYD 15
DB 56 GYVTVTGLEPGIDYD 70

RESULT 3
US-10-094-699-89
; Sequence 89, Application US/10094699
; Publication No. US2003004671A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: CTILIMM.015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-699-89

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Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTVTGLEPGIDYD 15
DB 56 GYVTVTGLEPGIDYD 70

RESULT 4
US-10-117-937-589
; Sequence 589, Application US/10117937
; Publication No. US20030202039A1
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; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTILIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 589
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-589

Query Match          100.0%; Score 85; DB 15; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTVTGLEPGIDYD 15
DB 56 GYVTVTGLEPGIDYD 70

RESULT 5
US-10-450-012-5
; Sequence 5, Application US/10450012
; Publication No. US20040091973A1
; GENERAL INFORMATION:
; APPLICANT: Giovannoni, Leonardo
; TITLE OF INVENTION: Process for selecting anti-angiogenesis
; TITLE OF INVENTION: antibody fragments, anti-angiogenesis antibody fragments thus
; TITLE OF INVENTION: obtained and their use
; FILE REFERENCE: 0380-P03209US0
; CURRENT APPLICATION NUMBER: US/10/450,012
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/EP01/14330
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: FI2000A000247
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-450-012-5

Query Match          100.0%; Score 85; DB 16; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTVTGLEPGIDYD 15
DB 56 GYVTVTGLEPGIDYD 70

RESULT 6
US-10-094-699-90
; Sequence 90, Application US/10094699
; Publication No. US2003004671A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
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; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: CTILIM.015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-699-90

Query Match      100.0%; Score 85; DB 14; Length 147;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTTVTGLEPGIDYD 15
Db      90 GYTTVTGLEPGIDYD 104

RESULT 7
US-10-117-937-590
; Sequence 590, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITYPE SEQUENCES
; FILE REFERENCE: CTILIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-590

Query Match      100.0%; Score 85; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTTVTGLEPGIDYD 15
Db      90 GYTTVTGLEPGIDYD 104

RESULT 8
US-10-236-392-4
; Sequence 4, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgees, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie

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; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grose, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Larocheille, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rottemberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkels, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 4
; LENGTH: 2220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-4

Query Match      100.0%; Score 85; DB 12; Length 2220;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYTTVTGLEPGIDYD 15
Db      1321 GYTTVTGLEPGIDYD 1335

RESULT 9
US-09-300-425B-23
; Sequence 23, Application US/09300425B
; Publication No. US20030045681A1
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TARLI, Lorenzo
; APPLICANT: VITTI, Francesca

```

APPLICANT: BIRCHER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONTIGUATES
FILE REFERENCE: ANGIOGENESIS
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide formula
US-09-300-425B-23

Query Match 84.7%; Score 72; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YVTGLEPGIDYD 15
Db 1 YVTGLEPGIDYD 13

RESULT 10
US-10-321-558-2
Sequence 2, Application US/10321558
Publication No. US2003017665A1
GENERAL INFORMATION:
APPLICANT: NERI, DARIO
APPLICANT: TARLI, LORENZO
APPLICANT: VITTI, FRANCESCA
APPLICANT: BIRCHER, MANFRED
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
FILE REFERENCE: NOTAR-1 C1
CURRENT APPLICATION NUMBER: US/10/321,558
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: 09/512,082
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-321-558-2

Query Match 84.7%; Score 72; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YVTGLEPGIDYD 15
Db 1 YVTGLEPGIDYD 13

RESULT 11
US-10-240-488-2
Sequence 2, Application US/10240488
Publication No. US2004017537A1
GENERAL INFORMATION: Data 1

APPLICANT: Kaufman, Paul L
TITLE OF INVENTION: Agent and Method for Reducing Intraocular Pressure
FILE REFERENCE: 960296.96951
CURRENT APPLICATION NUMBER: US/10/240,488
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/192942
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 270
TYPE: PRT
ORGANISM: Homo sapiens
US-10-240-488-2

Query Match 67.1%; Score 57; DB 16; Length 270;
Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YVTGLEPGIDY 14
Db 147 YVTGLOPGIDY 158

RESULT 12
US-09-043-981-1
Sequence 1, Application US/09043981
Publication No. US20030039640A1
GENERAL INFORMATION:
APPLICANT: Williams, David A.
TITLE OF INVENTION: METHODS FOR ENHANCED VIRUS MEDIATED DNA TRANSFER USING
TITLE OF INVENTION: MOLECULES WITH VIRUS AND CELL BINDING DOMAINS
FILE REFERENCE: 7037-297
CURRENT APPLICATION NUMBER: US/09/043,981
CURRENT FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: US96/15712
EARLIER FILING DATE: 1996-09-30
EARLIER APPLICATION NUMBER: 08/536,891
EARLIER FILING DATE: 1995-09-29
EARLIER APPLICATION NUMBER: 60/024,169
EARLIER FILING DATE: 1996-08-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 271
TYPE: PRT
ORGANISM: Homo sapiens
US-09-043-981-1

Query Match 67.1%; Score 57; DB 10; Length 271;
Best Local Similarity 75.0%; Pred. No. 0.4;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YVTGLEPGIDY 14
Db 148 YVTGLOPGIDY 159

RESULT 13
US-09-775-964-1
Sequence 1, Application US/09775964
Publication No. US20030087437A1
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Koyama, No. US20030087437A1
Koyama, No. US20030087437A1
Kato, Ikunoshin
Hashino, Kimikazu
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS

ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
City: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-775-964-1

Query Match 67.1%; Score 57; DB 10; Length 271;
Best Local Similarity 75.0%; Pred. No. 0.4;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YVTGLGPGIDY 14
DB 148 YTTGLQPGTDY 159

RESULT 14
US-09-775-964-22
Sequence 22, Application US/09775964
Publication No. US20030087437A1
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Koyama, No. US20030087437A1uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
City: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-775-964-22

Query Match 67.1%; Score 57; DB 10; Length 457;
Best Local Similarity 75.0%; Pred. No. 0.71;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YVTGLGPGIDY 14
DB 334 YTTGLQPGTDY 345

RESULT 15
US-09-775-964-21
Sequence 21, Application US/09775964
Publication No. US20030087437A1
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Koyama, No. US20030087437A1uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
City: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/775,964
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-775-964-21

Query Match 67.1%; Score 57; DB 10; Length 472;

Best Local Similarity 75.0%; Pred. No. 0.73; 1; Indels 0; Gaps 0;

Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 YTVTGLEPGIDY 14

Db 426 YTIRGLQPGTDY 437

Search completed: September 21, 2004, 06:30:30
Job time: 100.154 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:47:40 ; Search time 8.60394 Seconds
(without alignments)
90.015 Million cell updates/sec

Title: US-10-676-049-2

Perfect score: 85
Sequence: 1 GYTTVTGLEPGIDYD 15

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

389414

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	1336	2	US-08-551-356-6
2	85	100.0	1336	5	PCT-US93-12687-6
3	85	100.0	2446	2	US-08-551-356-2
4	85	100.0	2446	5	PCT-US93-12687-2
5	57	67.1	225	3	US-08-933-100B-6
6	57	67.1	271	3	US-08-536-891A-1
7	57	67.1	271	3	US-08-923-100B-14
8	57	67.1	271	4	US-08-366-009-1
9	57	67.1	271	4	US-08-809-156B-1
10	57	67.1	271	4	US-09-043-981-1
11	57	67.1	296	2	US-08-836-854-18
12	57	67.1	367	2	US-08-836-854-16
13	57	67.1	457	2	US-08-836-854-15
14	57	67.1	457	4	US-08-366-009-22
15	57	67.1	457	4	US-08-809-156B-22
16	57	67.1	472	4	US-08-366-009-21
17	57	67.1	547	4	US-08-809-156B-21
18	57	67.1	547	4	US-09-366-009-13
19	57	67.1	549	4	US-08-809-156B-13
20	57	67.1	549	4	US-08-836-854-11
21	57	67.1	549	4	US-08-366-009-23
22	57	67.1	549	4	US-08-809-156B-23
23	57	67.1	573	4	US-09-366-009-30
24	57	67.1	573	4	US-08-809-156B-30
25	57	67.1	574	2	US-08-836-854-21
26	57	67.1	574	3	US-09-463-296-1
27	57	67.1	574	4	US-09-366-009-24

28	57	67.1	574	4	US-08-809-156B-24	Sequence 24, Appl
29	57	67.1	826	4	US-09-366-009-14	Sequence 14, Appl
30	57	67.1	826	4	US-08-809-156B-14	Sequence 14, Appl
31	57	67.1	2231	1	US-08-153-799-16	Sequence 16, Appl
32	57	67.1	2231	1	US-08-283-887-1	Sequence 1, Appl
33	57	67.1	2324	5	PCT-US95-09819-1	Sequence 1, Appl
34	57	67.1	2327	6	US-09-016-366A-12	Sequence 12, Appl
35	57	67.1	2386	2	US-08-933-100B-8	Sequence 8, Appl
36	49	57.6	32	3	US-08-933-100B-15	Sequence 15, Appl
37	49	57.6	89	1	US-08-241-883-32	Sequence 32, Appl
38	49	57.6	89	2	US-08-850-917-32	Sequence 32, Appl
39	49	57.6	94	2	US-08-717-169-8	Sequence 8, Appl
40	49	57.6	94	4	US-09-638-202A-110	Sequence 110, App
41	49	57.6	94	4	US-09-228-901A-8	Sequence 8, Appl
42	49	57.6	94	4	US-09-096-749A-110	Sequence 110, App
43	49	57.6	96	4	US-09-638-202A-112	Sequence 112, App
44	49	57.6	96	4	US-09-096-749A-112	Sequence 112, App
45	49	57.6	96	4	US-09-096-749A-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-08-551-356-6
Sequence 6, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Iranl, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,356
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
FILING DATE:
APPLICATION NUMBER: US/07/998,271
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holiy, Julie A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-356-6
Query Match 100.0%; Score 85; DB 2; Length 1336;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
|||||

Db 344 GYVTGTGLEPIDYD 358

RESULT 2

PCT-US93-12687-6
Sequence 6, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Iranl, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-6

Query Match 100.0%; Score 85; DB 5; Length 1336;

Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTGTGLEPIDYD 15

Db 344 GYVTGTGLEPIDYD 358

RESULT 3

US-08-551-356-2
Sequence 2, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Iranl, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/551,356
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
FILING DATE:
APPLICATION NUMBER: US/07/998,271
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holly, Julie A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-356-2

Query Match 100.0%; Score 85; DB 2; Length 2446;

Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVTGTGLEPIDYD 15

Db 1321 GYVTGTGLEPIDYD 1335

RESULT 4

PCT-US93-12687-2
Sequence 2, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Iranl, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-2

Query Match 100.0%; Score 85; DB 5; Length 2446;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYVTGLEGPDIDY 15
|||
Db 1321 GYVTGLEGPDIDY 1335

RESULT 5

US-08-933-100B-6
; Sequence 6, Application US/08933100B
; Patent No. 6274704
; GENERAL INFORMATION:
; APPLICANT: FUKAI, FUMIO
; APPLICANT: KATAYAMA, TAKASHI
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDE AND CANCER
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933.100B
; FILING DATE: 18-SEP-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRY, GLENN
; REGISTRATION NUMBER: 28458
; REFERENCE/DOCKET NUMBER: 7896/242094
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT:
; OTHER INFORMATION: Sequence of a part (1746 - 1770) of Heparin binding site
; Patent No. 6274704
; US-08-933-100B-6
Query Match 67.1%; Score 57; DB 3; Length 25;
Best Local Similarity 75.0%; Pred. No. 0.0062;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 3 YTVTGLEPDIDY 14
|||
Db 2 YTVTGLEPDIDY 13
|||
RESULT 6
US-08-536-891A-1
; Sequence 1, Application US/08536891A
; Patent No. 6033907
; GENERAL INFORMATION:
; APPLICANT: David A. Williams
; TITLE OF INVENTION: Enhanced Virus Mediated DNA Transfer
; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas O. Henry
; STREET: Bank One Tower, Suite 3700, 111 Monument Circle
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage

; COMPUTER: COMPAQ

; OPERATING SYSTEM: MSDOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/536.891A
; FILING DATE: September 29, 1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03817
; FILING DATE: March 27, 1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/218,355
; FILING DATE: March 25, 1994

; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas O. Henry

; REGISTRATION NUMBER: 28,309

; REFERENCE/DOCKET NUMBER: 7037-52/1U-33-CIP-2

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 634-3456
; TELEFAX: (317) 637-7561

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein fragment

US-08-536-891A-1

Query Match 67.1%; Score 57; DB 3; Length 271;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 YTVTGLEPDIDY 14
|||
Db 148 YTVTGLEPDIDY 159

RESULT 7
US-08-933-100B-14
; Sequence 14, Application US/08933100B
; Patent No. 6274704

; GENERAL INFORMATION:
; APPLICANT: FUKAI, FUMIO

; APPLICANT: KATAYAMA, TAKASHI

; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDE AND CANCER

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933.100B
; FILING DATE: 18-SEP-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

NAME: PERRY, GLENN
REGISTRATION NUMBER: 28458
REFERENCE/DOCKET NUMBER: 7898/242094
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 271
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: sequence of a part (1600-1870) of Heparin binding site
US-08-933-100B-14

Query Match 67.1%; Score 57; DB 3; Length 271;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
||:||||:|
Db 148 YTVTGLEPGIDY 159

RESULT 8
US-09-366-009-1
Sequence 1, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Ueno, Takashi
Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-366-009-1

Query Match 67.1%; Score 57; DB 4; Length 271;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
||:||||:|
Db 148 YTVTGLEPGIDY 159

RESULT 9
US-08-809-156B-1
Sequence 1, Application US/08809156B
Patent No. 6472204
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Ueno, Takashi
Koyama, No. 6472204uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-809-156B-1
Query Match 67.1%; Score 57; DB 4; Length 271;

Best Local Similarity 75.0%; Pred. No. 0.13; Indels 1; Gaps 0;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLPQGDY 14
DB 148 YTVTGLPQGDY 159

RESULT 10

US-09-043-981-1
Sequence 1, Application US/09043981
Patent No. 6670177
GENERAL INFORMATION:
APPLICANT: Williams, David A.
TITLE OF INVENTION: METHODS FOR ENHANCED VIRUS MEDIATED DNA TRANSFER USING
FILE REFERENCE: 7037-297
CURRENT APPLICATION NUMBER: US/09/043,981
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: US96/15712
EARLIER FILING DATE: 1996-09-30
EARLIER APPLICATION NUMBER: 08/536,891
EARLIER FILING DATE: 1995-09-29
EARLIER APPLICATION NUMBER: 60/024,169
EARLIER FILING DATE: 1996-08-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 271
TYPE: PRT
ORGANISM: Homo sapiens
US-09-043-981-1

Query Match 67.1%; Score 57; DB 4; Length 271;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLPQGDY 14
DB 148 YTVTGLPQGDY 159

RESULT 11

US-08-836-854-4
Sequence 4, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994

FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-4

Query Match 67.1%; Score 57; DB 2; Length 296;
Best Local Similarity 75.0%; Pred. No. 0.14;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLPQGDY 14
DB 148 YTVTGLPQGDY 159

RESULT 12

US-08-836-854-18
Sequence 18, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-18

Query Match 67.1%; Score 57; DB 2; Length 367;
Best Local Similarity 75.0%; Pred. No. 0.18;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
||:||||:|
Db 334 YTVTGLQPGTDY 345

RESULT 13

US-08-836-854-16
Sequence 16, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-5528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-16

Query Match 67.1%; Score 57; DB 2; Length 457;
Best Local Similarity 75.0%; Pred. No. 0.23;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
||:||||:|
Db 334 YTVTGLQPGTDY 345

RESULT 14
US-09-366-009-22
Sequence 22, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:

Uemori, Takashi
Ueno, Takashi
Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-AUG-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-366-009-22

Query Match 67.1%; Score 57; DB 4; Length 457;
Best Local Similarity 75.0%; Pred. No. 0.23;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLEPGIDY 14
||:||||:|
Db 334 YTVTGLQPGTDY 345

RESULT 15

US-08-809-156B-22
Sequence 22, Application US/08809156B
Patent No. 6472204
GENERAL INFORMATION:

APPLICANT: Asada, Kiyozo
APPLICANT: Uemori, Takashi
APPLICANT: Ueno, Takashi
APPLICANT: Koyama, No. 6472204uto
APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:

STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-809-1563-22

Query Match 67.1%; Score 57; DB 4; Length 457;
Best Local Similarity 75.0%; Pred. No. 0.23;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YTVTGLPRTDY 14
Db 334 YTVTGLPRTDY 345

Search completed: September 21, 2004, 06:15:26
Job time : 8.60294 secs

This Page Blank (uspto)

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53; Search time 7.5 Seconds
(without alignments)
192.383 Million cell updates/sec

Title: US-10-676-049-3

Perfect score: 77
Sequence: 1 TGLEPGIDYDISVIT 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR 78:1*
1: PIR1:1*
2: PIR2:1*
3: PIR3:1*
4: PIR4:1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	90	2 146162	fibronectin ED-B -
2	77	100.0	147	2 S00848	fibronectin, trans
3	77	100.0	1020	2 A29355	fibronectin - chic
4	77	100.0	2477	2 S14428	fibronectin precu
5	66	85.7	2481	2 A43908	fibronectin - Afri
6	53	68.8	273	2 A28512	fibronectin - chic
7	52	67.5	2265	1 FNBO	fibronectin - boyl
8	50	64.9	2386	1 FNBT	fibronectin precu
9	48	62.3	843	2 A40570	undulin 1 - human
10	47	61.0	2944	2 A54849	collagen alpha 1(V
11	46	59.7	1356	2 A45445	jannuin precursor
12	45	58.4	1036	2 T30311	S-layer protein -
13	45	58.4	1238	2 S68700	HPTP beta-like tyr
14	45	58.4	1353	1 JH0675	restriction precu
15	45	58.4	3488	2 T34418	hypothetical prote
16	44	57.1	933	2 A31930	cytoactin - chick
17	44	57.1	1746	1 S19694	tenascin precursor
18	44	57.1	1810	1 A32230	tenascin precursor
19	44	57.1	2019	1 JQ1322	tenascin-C - human
20	44	57.1	2201	2 A32160	fibronectin ED-A -
21	43	55.8	89	2 146161	fibronectin - gulin
22	43	55.8	123	2 A40790	choistmate synthas
23	43	55.8	356	2 E97010	protein-tyrosine-p
24	43	55.8	1997	1 S12050	tenascin-X - bovin
25	43	55.8	4135	2 T42629	titin - rabbit (fr
26	43	55.8	6805	2 S20901	hypothetical prote
27	42	54.5	133	2 D90445	hypothetical prote
28	42	54.5	271	2 A86796	hypothetical prote
29	42	54.5	438	2 F95984	probable guanine d

30	42	54.5	575	2 A54861	tenascin - rat (fr
31	42	54.5	662	2 B69274	acetyl-CoA synthet
32	42	54.5	1615	2 A49502	protein-tyrosine-p
33	42	54.5	1767	2 A49502	protein-tyrosine-p
34	42	54.5	26926	1 T38344	titin, cardiac mus
35	41	53.2	242	2 B82898	hypothetical prote
36	41	53.2	379	2 T19773	hypothetical prote
37	41	53.2	623	2 A13468	outer membrane pro
38	41	53.2	1185	2 T46428	hypothetical prote
39	41	53.2	1897	1 TDHUK	leukocyte antigen-
40	40	51.9	320	2 D87535	glutathione S-tran
41	40	51.9	377	2 AD1057	hypothetical prote
42	40	51.9	452	2 S37607	cyclin-like protei
43	40	51.9	572	2 T16865	hypothetical prote
44	40	51.9	613	2 H90160	conserved hypotet
45	40	51.9	654	2 T08600	hypothetical prote

ALIGNMENTS

RESULT 1

146162
fibronectin ED-B - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
C:Accession: 146162
R:Zhang, D.W.; Burton-Murster, N.; Lust, G.
J. Biol. Chem. 270, 1817-1822, 1995
A>Title: Alternative splicing of ED-A and ED-B sequences of fibronectin pre-mRNA differ
A:Reference number: 146161; MUID:95130563; PMID:7829518
A:Accession: 146162
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-90 <ZHA>
A:Cross-references: EMBL:U16208; NID:9562168; PIDN:AAA67749.1; PID:9562169
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II rep

Query Match 100.0%; Score 77; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. NO. 7.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 60 TGLEPGIDYDISVIT 74

RESULT 2

S00848
fibronectin, transformation-associated splice form - human (fragment)
N:Alternate names: fibronectin ED-B
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1988 #sequence_revision 01-Dec-1988 #text_change 21-Jul-2000
C:Accession: S00848; 159102; A28347
R:Paociella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
A>Title: Sequence analysis and in vivo expression show that alternative splicing of ED-
A:Reference number: S00848; MUID:88233940; PMID:3375063
A:Accession: S00848
A:Molecule type: DNA
A:Residues: 1-147 <PAO>
A:Cross-references: EMBL:X07717; NID:931406; PIDN:CAB52437.1; PID:95725425
R:Gutman, A.; Kornblith, A.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7179-7182, 1987
A>Title: Identification of a third region of cell-specific alternative splicing in huma
A:Reference number: 159102; MUID:88041070; PMID:3478690
A:Accession: 159102
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 26-134 <GUT>
A:Cross-references: GB:M18179; NID:9182693; PIDN:AAA52461.1; PID:9182695
R:Zardi, L.; Cammella, B.; Stili, A.; Petersen, T.E.; Sebastio, G.; Bara
EMBO J. 6, 2337-2342, 1987

A>Title: Transformed human cells produce a new fibronectin isoform by preferential alter
A/Reference number: A28347; MUID:86029324; PMID:2822387
A/Accession: A28347
A/Molecule type: protein
A/Residues: 3-146 <ZAR>
C/Genetics:
A/Gene: GDB:EN1
A/Cross-references: GDB:119135; OMIM:135600
A/Map position: 2q34-2q34
A/Intons: 35/1; 126/1
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C/Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter
F/35-118/Region: transformation-associated insert
F/35-118/Domain: fibronectin type III repeat homology <3PR>

Query Match 100.0%; Score 77; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGLEPGIDYDISVIT 15
Db 95 TGLEPGIDYDISVIT 109

RESULT 3
A29355
fibronectin - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 12-Feb-1999
C/Accession: A29355
R/Norton, P.A.; Hynes, R.O.
Mol. Cell. Biol. 7, 4297-4307, 1987
A>Title: Alternative splicing of chicken fibronectin in embryos and in normal and transfe
A/Reference number: A29355; MUID:86142820; PMID:2830487
A/Accession: A29355
A/Molecule type: mRNA
A/Residues: 1-1020 <NOR>
C/Genetics:
A/Intons: 176/3
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C/Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter
F/1-86/Domain: fibronectin type III repeat homology <FN3I>
F/92-177/Domain: fibronectin type III repeat homology <FN3I>
F/180-262/Domain: cell attachment (R-G-D) motif
F/257-359/Region: cell attachment (R-G-D) motif
F/274-356/Domain: fibronectin type III repeat homology <FN3I>
F/364-446/Domain: fibronectin type III repeat homology <FN3I>
F/444-536/Domain: fibronectin type III repeat homology <FN3I>
F/546-628/Domain: fibronectin type III repeat homology <FN3I>
F/636-718/Domain: fibronectin type III repeat homology <FN3I>
F/837-917/Domain: fibronectin type III repeat homology <FN3I>
F/940-979/Domain: fibronectin type I repeat homology <1F10>
F/940-969,967-979,985-1012/Disulfide bonds: #status predicted

Query Match 100.0%; Score 77; DB 2; Length 1020;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGLEPGIDYDISVIT 15
Db 154 TGLEPGIDYDISVIT 168

RESULT 4
S14428
fibronectin precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Aug-1999
C/Accession: S14428; S14455; A22319; S46203; S00459; A27252; I59049
R/Hynes, R.O.
submitted to the EMBL Data Library, July 1989
A/Reference number: S14428
A/Accession: S14428

A/Molecule type: mRNA
A/Residues: 1-2477 <HYN>
A/Cross-references: EMBL:X15906; NID:956163; PIDN:CAA34020.1; PID:956164
R/Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A>Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
A/Reference number: S12455; MUID:88054951; PMID:2445560
A/Accession: S12455
A/Molecule type: mRNA
A/Status: nucleic acid sequence not shown
A/Residues: 609-1810, 'T', 1812-2283 <SCH>
A/Cross-references: EMBL:X15906
R/Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A>Title: A single rat fibronectin gene generates three different mRNAs by alternative sp
A/Reference number: A22319; MUID:84298097; PMID:6089177
A/Accession: A22319
A/Molecule type: DNA
A/Residues: 2052-2237 <TM>
R/Falkenberg, C.; Enghild, J.O.; Thøgersen, I.B.; Salvesen, G.; Akerstrøm, B.
Biochem. J. 301, 745-751, 1994
A>Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in
A/Reference number: S46203; MUID:94330948; PMID:7519849
A/Accession: S46203
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1183-1192, 'Gln', 1268, 'P', 1270-1271, 'D', 1273, 'CF', 1276, 'Py', 1385-1399 <FAL>
R/Patel, R.S.; Odermatt, E.; Schwarzbauer, J.E.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1987
A>Title: Organization of the fibronectin gene provides evidence for exon shuffling durin
A/Reference number: S00459; MUID:88054950; PMID:3119323
A/Accession: S00459
A/Molecule type: DNA
A/Residues: 1-139,2382-2477 <PAT>
A/Cross-references: EMBL:X05831
A/Note: the authors translated the codon CCT for residues 51 and 94 as Ala
R/Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
Cell 35, 421-431, 1983
A>Title: Three different fibronectin mRNAs arise by alternative splicing within the codi
A/Reference number: A27252; MUID:84082067; PMID:6317187
A/Accession: A27252
A/Molecule type: mRNA
A/Residues: 1586-1720, 'T', 1722, 1813-2477 <SC2>
R/Odermatt, E.; Tamkun, J.W.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A>Title: Repeating modular structure of the fibronectin gene: Relationship to protein st
A/Reference number: I59049; MUID:86016741; PMID:3663113
A/Accession: I59049
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1722-1810 <RES>
A/Cross-references: GB:M11750; NID:9204164; PIDN:AAA41170.1; PID:9554437
C/Genetics:
A/Intons: 51/1; 94/1; 2416/3; 2454/3
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C/Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; dupli
F/1-32/Domain: signal sequence #status predicted <SIG>
F/33-2477/Product: fibronectin #status predicted <MAT>
F/53-88/Domain: fibronectin type I repeat homology <1F1>
F/98-136/Domain: fibronectin type I repeat homology <1F2>
F/142-180/Domain: fibronectin type I repeat homology <1F3>
F/187-226/Domain: fibronectin type I repeat homology <1F4>
F/232-271/Domain: fibronectin type I repeat homology <1F5>
F/308-342/Domain: fibronectin type I repeat homology <1F6>
F/360-401/Domain: fibronectin type II repeat homology <2F1>
F/420-461/Domain: fibronectin type II repeat homology <2F2>
F/478-508/Domain: fibronectin type I repeat homology <1F7>
F/518-555/Domain: fibronectin type I repeat homology <1F8>
F/561-589/Domain: fibronectin type I repeat homology <1F9>
F/603-692/Domain: fibronectin type III repeat homology <FN3A>
F/718-800/Domain: fibronectin type III repeat homology <FN3B>
F/805-890/Domain: fibronectin type III repeat homology <FN3C>
F/905-987/Domain: fibronectin type III repeat homology <FN3D>

F,995-1076/Domain: fibronectin type III repeat homology <FN3>
F,1085-1164/Domain: fibronectin type III repeat homology <FN3F>
F,1172-1257/Domain: fibronectin type III repeat homology <FN3G>
F,1265-1349/Domain: fibronectin type III repeat homology <FN3H>
F,1356-1439/Domain: fibronectin type III repeat homology <FN3I>
F,1447-1529/Domain: fibronectin type III repeat homology <FN3J>
F,1537-1619/Domain: fibronectin type III repeat homology <FN3K>
F,1614-1616/Region: cell attachment (R-G-D) motif
F,1631-1713/Domain: fibronectin type III repeat homology <FN3L>
F,1721-1803/Domain: fibronectin type III repeat homology <FN3M>
F,1811-1899/Domain: fibronectin type III repeat homology <FN3N>
F,1903-1984/Domain: fibronectin type III repeat homology <FN3O>
F,1992-2074/Domain: fibronectin type III repeat homology <FN3P>
F,2181-2183/Region: cell attachment (R-G-D) motif
F,2193-2273/Domain: fibronectin type III repeat homology <FN3Q>
F,2296-2335/Domain: fibronectin type I repeat homology <FI10>
F,2341-2378/Domain: fibronectin type I repeat homology <FI11>
F,2385-2420/Domain: fibronectin type I repeat homology <FI12>
F,53-79,79-88,98-126,124-136,142-170,168-180,167-216,214-226,237-261,259-271,308-335,333
368,236-2378,2385-2411,2409-2420/Disulfide bonds: #status predicted
F,2458/Disulfide bonds: interchain (to 2462) #status predicted
F,2462/Disulfide bonds: interchain (to 2458) #status predicted

Query Match 100.0%; Score 77; DB 2; Length 2477;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLPFGIDYDISVT 15
|||||
Db 1325 TGLPFGIDYDISVT 1339

RESULT 5
A43908
Fibronectin - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
C/Accession: A43908
R/Description: D.W.; Norton, P.A.; Hynes, R.O.
A/Title: Identification and characterization of alternatively spliced fibronectin mRNAs
A/Reference number: A43908; MUID:92111942; PMID:1730390
A/Accession: A43908
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-2481 <DES>
A/Cross-references: GB:M77820
A/Note: Sequence extracted from NCBI backbone (NCBI:P.77473)
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat homology
C/Keywords: duplication; extracellular matrix; glycoprotein; heterodimer
F,55-90/Domain: fibronectin type I repeat homology <FI1>
F,100-138/Domain: fibronectin type I repeat homology <FI2>
F,144-182/Domain: fibronectin type I repeat homology <FI3>
F,189-228/Domain: fibronectin type I repeat homology <FI4>
F,234-273/Domain: fibronectin type I repeat homology <FI5>
F,309-343/Domain: fibronectin type I repeat homology <FI6>
F,361-402/Domain: fibronectin type II repeat homology <FI7>
F,421-462/Domain: fibronectin type II repeat homology <FI8>
F,471-509/Domain: fibronectin type II repeat homology <FI9>
F,519-556/Domain: fibronectin type I repeat homology <FI10>
F,562-600/Domain: fibronectin type I repeat homology <FI11>
F,610-653/Domain: fibronectin type III repeat homology <FN3A>
F,719-801/Domain: fibronectin type III repeat homology <FN3B>
F,810-891/Domain: fibronectin type III repeat homology <FN3C>
F,906-988/Domain: fibronectin type III repeat homology <FN3D>
F,1096-1077/Domain: fibronectin type III repeat homology <FN3E>
F,1086-1165/Domain: fibronectin type III repeat homology <FN3F>
F,1173-1258/Domain: fibronectin type III repeat homology <FN3G>
F,1266-1349/Domain: fibronectin type III repeat homology <FN3H>
F,1357-1440/Domain: fibronectin type III repeat homology <FN3I>
F,1448-1530/Domain: fibronectin type III repeat homology <FN3J>
F,1538-1620/Domain: fibronectin type III repeat homology <FN3K>
F,1615-1611/Region: cell attachment (R-G-D) motif

F,1632-1714/Domain: fibronectin type III repeat homology <FN3L>
F,1722-1804/Domain: fibronectin type III repeat homology <FN3M>
F,1812-1894/Domain: fibronectin type III repeat homology <FN3N>
F,1904-1985/Domain: fibronectin type III repeat homology <FN3O>
F,1993-2075/Domain: fibronectin type III repeat homology <FN3P>
F,2197-2277/Domain: fibronectin type III repeat homology <FN3Q>
F,2301-2340/Domain: fibronectin type I repeat homology <FI10>
F,2346-2383/Domain: fibronectin type I repeat homology <FI11>
F,2390-2425/Domain: fibronectin type I repeat homology <FI12>
F,55-91,79-80,100-128,126-139,144-172,170-182,189-218,216-228,234-263,261-273,309-336,333
2373,2371-2383,2390-2416,2414-2425/Disulfide bonds: #status predicted
F,2459/Disulfide bonds: interchain (to 2463) #status predicted
F,2463/Disulfide bonds: interchain (to 2459) #status predicted

Query Match 85.7%; Score 66; DB 2; Length 2481;
Best Local Similarity 80.0%; Pred. No. 0.022;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLPFGIDYDISVT 15
|||||
Db 1326 TGLPFGIDYDISVT 1340

RESULT 6
A28512
Fibronectin - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Aug-1999
C/Accession: A28512
R/Rubomura, S.; Obata, M.; Karasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, B.
Biochim. Biophys. Acta 910, 171-181, 1987
A/Title: Genetic analysis of the cell binding domain region of the chicken fibronectin
A/Reference number: A28512; MUID:88050950; PMID:282899
A/Accession: A28512
A/Molecule type: DNA
A/Residues: 1-213 <KUB>
A/Cross-references: GB:X06533; NID:963393; PIDN:CA29781.1; PID:G295716
A/Note: The authors translated the codon CCG for residue 190 as Gln, CAG for residue 24
C/Genetics:
A/Insertion: 90/1, 129/1, 184/1, 236/1
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat homology
C/Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heterodimer
F,1-82/Domain: fibronectin type III repeat homology (fragment) <FN3I>
F,90-172/Domain: fibronectin type III repeat homology <FN3J>
F,167-169/Region: cell attachment (R-G-D) motif
F,184-266/Domain: fibronectin type III repeat homology <FN3K>

Query Match 68.8%; Score 53; DB 2; Length 273;
Best Local Similarity 69.2%; Pred. No. 0.28;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGLPFGIDYDISV 13
|||||
Db 149 TGLPFGIDYDISV 161

RESULT 7
FNBO
Fibronectin - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Oct-2000
C/Accession: A26452; E21165; A23292
R/Skorstgaard, K.; Jensen, M.S.; Sahi, P.; Petersen, T.E.; Magnusson, S.
Eur. J. Biochem. 161, 441-453, 1986
A/Title: Complete primary structure of bovine plasma fibronectin.
A/Reference number: A26452; MUID:87054047; PMID:3780752
A/Accession: A26452
A/Molecule type: protein
A/Residues: 1-2265 <SKO>
R/Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A/Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A/Reference number: A21165; MUID:83221567; PMID:6304699

A:Accession: B21165
A:Molecule type: mRNA
A:Residues: 2170-2265 <KOR>
A:Cross-references: GB:R00800; NID:g163055; PIDN:AA030521.2; PID:g5713323
R:Pedersen, T.E.; Thøgersen, H.C.; Skorsengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottr
Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983
A:Title: Partial primary structure of bovine plasma fibronectin: three types of internal
A:Reference number: A23292; MUID:83117805; PMID:6218503
A:Accession: A23292
A:Molecule type: Protein
A:Residues: 1-16 'C', 18-20, 'S', 22-432, 447-463, 1367-1517, 1567-1673, 2062-2176, 'N', 2178-226
C:Comment: Cys-1201 and Cys-2015 have free sulfhydryl groups.
C:Comment: The plasma fibronectin molecule consists of two chains, which are connected b
C:Comment: Fibronectins bind cell surfaces and various compounds including collagen, fib
aling, and maintenance of cell shape.
C:Comment: Plasma fibronectin is synthesized by hepatocytes.
C:Keywords: acute phase; alternative splicing; collagen binding; duplication; extracellular
F:21-24/Domain: fibrin and heparin binding <FBR>
F:21-56/Domain: fibronectin type I repeat homology <1F1>
F:66-104/Domain: fibronectin type I repeat homology <1F2>
F:110-148/Domain: fibronectin type I repeat homology <1F3>
F:155-194/Domain: fibronectin type I repeat homology <1F4>
F:200-239/Domain: fibronectin type I repeat homology <1F5>
F:227-577/Domain: collagen binding <CBR>
F:227-311/Domain: fibronectin type I repeat homology <1F6>
F:329-370/Domain: fibronectin type II repeat homology <2F1>
F:389-430/Domain: fibronectin type II repeat homology <2F2>
F:439-477/Domain: fibronectin type I repeat homology <1F7>
F:487-524/Domain: fibronectin type I repeat homology <1F8>
F:530-568/Domain: fibronectin type I repeat homology <1F9>
F:578-661/Domain: fibronectin type III repeat homology <FN3A>
F:688-770/Domain: fibronectin type III repeat homology <FN3B>
F:779-860/Domain: fibronectin type III repeat homology <FN3C>
F:875-957/Domain: fibronectin type III repeat homology <FN3D>
F:965-1046/Domain: fibronectin type III repeat homology <FN3E>
F:1055-1134/Domain: fibronectin type III repeat homology <FN3F>
F:1142-1227/Domain: fibronectin type III repeat homology <FN3G>
F:1235-1316/Domain: fibronectin type III repeat homology <FN3H>
F:1326-1404/Domain: fibronectin type III repeat homology <GN3I>
F:1410-1517/Domain: cell attachment <CAD>
F:1416-1502/Domain: cell attachment (R-G-D) motif
F:1493-1495/Region: cell attachment (R-G-D) motif
F:1510-1592/Domain: fibronectin type III repeat homology <FN3K>
F:1600-1870/Domain: heparin binding <HB2>
F:1600-1682/Domain: fibronectin type III repeat homology <FN3L>
F:1682-1773/Domain: fibronectin type III repeat homology <FN3M>
F:1781-1863/Domain: fibronectin type III repeat homology <FN3N>
F:1970-1972/Region: cell attachment (R-G-D) motif
F:1982-2063/Domain: fibronectin type III repeat homology <FN3O>
F:1985-2216/Domain: fibrin binding <FBR2>
F:2085-2124/Domain: fibronectin type I repeat homology <1F10>
F:2130-2167/Domain: fibronectin type I repeat homology <1F11>
F:2174-2209/Domain: fibronectin type I repeat homology <1F12>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status experime
F:21-47, 45-56, 66-94, 92-104, 110-138, 136-148, 155-184, 184-194, 200-229, 227-239, 277-304, 302-3
7, 2155-2176, 2174-2200, 2198-2209/Disulfide bonds: #status predicted
F:1399, 497, 511, 846, 976, 1213, 1987/Binding site: carbohydrate (Asn) (covalent) #status expe
F:1205, 1693/Binding site: carbohydrate (Thr) (covalent) #status absent
F:1943, 1944/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:2246/Disulfide bonds: interchain (to 2250) #status predicted
F:2250/Disulfide bonds: interchain (to 2246) #status predicted
F:2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 67.5%; Score 52; DB 1; Length 2265;
Best Local Similarity 71.4%; Pred. No. 4.4;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGLEPGIDYDISVT 14
Db 1840 TGLEPGTEYTIQVT 1853

RESULT 8
FNH

fibronectin precursor [validated] - human
N:Alternate names: fibronectin splice form ED-A
C:Species: Homo sapiens (man)
C:Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 08-Dec-2000
A:Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22
R:Dean, D.C.; Bowles, C.L.; Bourgeois, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A:Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A:Reference number: A26460; MUID:87175578; PMID:3031656
A:Accession: A26460
A:Molecule type: DNA
A:Residues: 1-49 <DEA>
A:Cross-references: GB:M1801; NID:g182686; PIDN:AA053376.1; PID:g553293
R:Oldberg, A.; Ruoslahti, E.
J. Biol. Chem. 261, 2113-2116, 1986
A:Title: Evolution of the fibronectin gene.
A:Reference number: A26284; MUID:86111901; PMID:3003095
A:Accession: A26284
A:Molecule type: DNA
A:Residues: 1447-1540 <OLD>
A:Cross-references: GB:M2549; NID:g182688
A:Note: the authors translated the codon TTC for residue 1494 as Glu
R:Paoliella, G.; Henschliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
A:Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B
A:Reference number: S00848; MUID:88233940; PMID:3375063
A:Accession: S03917
A:Molecule type: DNA
A:Residues: 1594-1767, 'V', 1769-1783 <PAO>
A:Cross-references: EMBL:X07718; NID:g31402
A:Note: the authors translated the codon AAC for residue 1631 as Asp
R:Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986
A:Title: Donor and acceptor splice signals within an exon of the human fibronectin gene.
A:Reference number: A24854; MUID:87030929; PMID:3770201
A:Accession: A24854
A:Molecule type: DNA
A:Residues: 1992-2147 <VIB>
A:Cross-references: GB:X04530; NID:g31436
R:Gutman, A.; Yamada, K.M.; Kornblith, A.
FEBS Lett. 207, 145-148, 1986
A:Title: Human fibronectin is synthesized as a pre-propolypeptide.
A:Reference number: A24476; MUID:87030890; PMID:3370189
A:Accession: A24476
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-14, 'Q', 16-38 <GUT>
R:Kornblith, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985
A:Title: Primary structure of human fibronectin: differential splicing may generate at l
A:Reference number: A91008; MUID:85284965; PMID:2992939
A:Accession: A91008
A:Molecule type: nucleic acid sequence not shown
A:Status: not compared with conceptual translation
A:Accession: A93529
A:Cross-references: GB:X02761
A:Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
Nucleic Acids Res. 12, 5853-5868, 1984
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
A:Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A:Reference number: A93529; MUID:84272258; PMID:6462919
A:Accession: A93529
A:Molecule type: mRNA
A:Residues: 973-2080, 2112-2386 <KOR>
A:Cross-references: GB:X00739
R:Oldberg, A.; Linney, E.; Ruoslahti, E.
U. Biol. Chem. 258, 10193-10196, 1983
A:Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell A
A:Reference number: A21011; MUID:83290929; PMID:6668418
A:Accession: A21011
A:Molecule type: mRNA

A:Residues: 1434-1537 <OL2>
A:Cross-references: GB:K00055; NID:g182680; PIDN:AAAS2459.1; PID:g182683
R:Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A:Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat
A:Reference number: A90495; MUID:85280409; PMID:2992573
A:Accession: A90495
A:Molecule type: mRNA
A:Residues: 1594-2386 <BBR>
A:Cross-references: GB:MT0905; NID:g182686; PIDN:AAAS2462.1; PID:g182687
R:Umezawa, K.; Kornblith, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A:Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A:Reference number: A22245; MUID:85231203; PMID:2989004
A:Accession: A22245
A:Molecule type: mRNA
A:Residues: 1948-2067 <UWE>
A:Cross-references: GB:M27589; NID:g182705; PIDN:AAAS2465.1; PID:g182706
A:Accession: B22245
A:Molecule type: mRNA
A:Residues: 1975-1991/2017-2039 <UW2>
A:Cross-references: GB:M27590
R:Seikiguchi, K.; Kios, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A:Title: Human liver fibronectin complementary DNAs: identification of two different mes
A:Reference number: 152394; MUID:87026578; PMID:3021206
A:Accession: 152394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1978-1990/2016-2018/'N', 2020-2081, 2113-2137 <SEK>
A:Cross-references: GB:M4060; NID:g182701; PIDN:AAAS2464.1; PID:g182704
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A:Reference number: A21165; MUID:83221567; PMID:6304699
A:Accession: A21165
A:Molecule type: mRNA
A:Residues: 2291-2386 <KO3>
A:Cross-references: GB:K00799; NID:g182681; PIDN:AAAS2460.1; PID:g182684
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 258, 12670-12674, 1983
A:Title: Primary structure of human plasma fibronectin.
A:Reference number: A92398; MUID:84032463; PMID:6650202
A:Accession: A92398
A:Molecule type: Protein
A:Residues: 32-47/'C', 49-51/'S', 53-72/'A', 74-290 <GAR1>
R:Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A:Title: Further characterization of the binding of fibronectin to gelatin reveals the p
A:Reference number: S34791; MUID:93312001; PMID:8323285
A:Accession: S34791
A:Molecule type: Protein
A:Residues: 291-300/551-560 <GAR2>
R:Griffith, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A:Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A:Reference number: A60904; MUID:87019725; PMID:3552418
A:Accession: A60904
A:Molecule type: Protein
A:Residues: 293-301 <GRI>
R:Calaycay, J.; Pandey, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A:Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pl
A:Reference number: A23901; MUID:86008277; PMID:3900070
A:Accession: A23901
A:Molecule type: Protein
A:Residues: 616-677/'Q', 679-703/'PT' <CAL>
R:Peterschbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A:Title: The cell attachment domain of fibronectin. Determination of the primary structu
A:Reference number: A92386; MUID:82265604; PMID:7050098
A:Accession: A92386
A:Molecule type: protein

A:Residues: 1441-1548 <PIR>
A:Note: residues 1524-1527 are responsible for the cell-binding activity
R:Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A:Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa do
A:Reference number: A32517; MUID:87241275; PMID:3599230
A:Accession: A32517
A:Molecule type: protein
A:Residues: 1589-1630/'T', 1722-2058 <GAR3>
R:Pressel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pan
Biochem. J. 274, 731-738, 1991
A:Title: Human plasma fibronectin. Demonstration of structural differences between the
A:Reference number: S14357; MUID:91190085; PMID:2012601
A:Accession: S14357
A:Molecule type: protein
A:Residues: 1614-1630/'T', 1722-2081, 2113-2244 <TRE>
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A:Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-da
A:Reference number: A23891; MUID:85261459; PMID:4019516
A:Accession: A23891
A:Molecule type: protein
A:Residues: 2071-2080/2113-2356 <GAR4>
C:Comment: The extra domain and connecting strand 3 are subject to developmental and ti
C:Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins
action, and transformation.
C:Genetics:
A:Gene: GDB:FNI
A:Cross-references: GDB:119135; OMIM:135600
A:Map position: 2q34-2q34
A:Functions: 49/3, 1266/1, 1357/1, 1447/1, 1487/1, 1541/1, 1631/1, 1721/1, 1991/1, 2145/1
C:Superfamily: fibronectin; fibronectin type I repeat homology <1F1>
C:Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplica
F:1-26/Domain: signal sequence #status predicted <SIG>
F:17-31/Domain: propeptide #status predicted <PRO>
F:32-2386/Product: fibronectin #status experimental <MNT>
F:32-272/Domain: fibrin and heparin binding <FHB>
F:32-87/Domain: fibronectin type I repeat homology <1F1>
F:37-135/Domain: fibronectin type I repeat homology <1F2>
F:141-179/Domain: fibronectin type I repeat homology <1F3>
F:186-225/Domain: fibronectin type I repeat homology <1F4>
F:231-270/Domain: fibronectin type I repeat homology <1F5>
F:308-342/Domain: collagen binding <CBR>
F:308-342/Domain: fibronectin type I repeat homology <1F6>
F:360-401/Domain: fibronectin type II repeat homology <2F1>
F:420-461/Domain: fibronectin type II repeat homology <2F2>
F:470-508/Domain: fibronectin type I repeat homology <1F7>
F:518-555/Domain: fibronectin type I repeat homology <1F8>
F:561-599/Domain: fibronectin type I repeat homology <1F9>
F:609-692/Domain: fibronectin type III repeat homology <3F1>
F:616-706/Domain: heparin binding <HPB>
F:719-801/Domain: fibronectin type III repeat homology <3F2>
F:810-891/Domain: fibronectin type III repeat homology <3F3>
F:906-988/Domain: fibronectin type III repeat homology <3F4>
F:996-1077/Domain: fibronectin type III repeat homology <3F5>
F:1086-1164/Domain: fibronectin type III repeat homology <3F6>
F:1172-1258/Domain: fibronectin type III repeat homology <3F7>
F:1266-1349/Domain: fibronectin type III repeat homology <3F8>

Query Match 64.9%; Score 50; DB 1; Length 2386;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGLRPGIDYDISVT 14
DB 1961 TGLRPGTEYTYIVT 1974

RESULT 9
AA0970
uncln1.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Sep-2003

C/Accession: A40970
 R/Unit: M.; Herbst, H.; Hummel, M.; Duerkop, H.; Tripiet, D.; Stein, H.; Schnuppan, D.
 J. Biol. Chem. 266, 17326-17332, 1991
 A/Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular m
 A/Reference number: A40970; MUID:91373351; PMID:1716629
 A/Accession: A40970
 A/Molecule type: mRNA
 A/Residues: 1-843 <UTS>
 A/Cross-references: GB:W64108; NID:9340081; PIND:AAA36794.1; PID:G340082
 C/Keywords: glycoprotein
 F/165-246/Domain: fibronectin type III repeat homology <FN3A>
 F/165-338/Domain: fibronectin type III repeat homology <FN3B>
 F/165-427/Domain: fibronectin type III repeat homology <FN3C>
 F/165-500/Domain: fibronectin type III repeat homology <FN3D>
 F/165-632/Domain: fibronectin type III repeat homology <FN3E>
 F/165-723/Domain: fibronectin type III repeat homology <FN3F>
 F/165-818/Domain: fibronectin type III repeat homology <FN3G>
 Query Match 62.3%; Score 48; DB 2; Length 843;
 Best Local Similarity 53.8%; Pred. No. 6.8;
 Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 GLEFGIDYISVI 14
 Db 495 GLEPGTEYEVSL 507
 RESULT 10
 A54849
 collagen alpha 1(VII) chain precursor - human
 N/Alternate names: procollagen alpha 1(VII) chain
 C/Species: Homo sapiens (man)
 C/Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text change 15-Sep-2003
 C/Accession: A54849; PH0844; S:6316; I56328; A30296; I84686
 R/Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
 J. Biol. Chem. 269, 20236-20262, 1994
 A/Title: Cloning of human type VII collagen. Complete primary sequence of the alpha1(VII
 A/Reference number: A54849; MUID:94327588; PMID:8051117
 A/Accession: A54849
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-2944 <CHR>
 A/Cross-references: GS:L02870; NID:9987124; PIND:AAA7438.1; PID:9987125
 R/Tanaka, T.; Takahashi, K.; Furukawa, F.; Imanura, S.
 Biochem. Biophys. Res. Commun. 183, 958-963, 1992
 A/Title: Molecular cloning and characterization of type VII collagen cDNA.
 A/Reference number: PH0844; MUID:92231902; PMID:1567409
 A/Accession: PH0844
 A/Molecule type: mRNA
 A/Residues: 1-340-475; RAUSTASHSTCMFATMPCNRCGSHWTRACBPCNRPASHPARAG, 524-528, 'C',
 A/Cross-references: DDBJ:D11152; DDBJ:D13694; NID:9453698; PIND:BA02853.1; PID:9453699
 A/Experimental source: keratinocyte
 A/Note: The authors translated the codon ACC for residues 394 and 397 as Tyr
 R/Parente, M.G.; Chung, L.C.; Ryttaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
 Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
 A/Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
 A/Reference number: S16316; MUID:91334380; PMID:1871109
 A/Accession: S16316
 A/Molecule type: mRNA
 A/Residues: 815-892, 'E', 894-1439 <PAR>
 A/Cross-references: GS:W65158; GB:S49017; NID:9180914; PIND:AAA6439.1; PID:9180915
 R/Experimental source: keratinocyte
 R/Gammot, W.R.; Bernethy, M.L.; Padilla, K.M.; Pitsayanh, P.S.; Cook, M.E.; Wright, J.;
 J. Invest. Dermatol. 99, 691-696, 1992
 A/Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot
 A/Reference number: I56328; MUID:9107742; PMID:1469284
 A/Accession: I56328
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
 A/Cross-references: GS:S51236; NID:9262308; PIND:AAA2637.1; PID:9262309
 R/Setzler, J.U.; Bissen, A.Z.; Baue, E.A.; Morris, N.P.; Glanville, R.W.; Burgess, R.E.
 J. Biol. Chem. 264, 3822-3826, 1989

A/Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagenase
 A/Reference number: A30296; MUID:85139437; PMID:2557292
 A/Accession: A30296
 A/Molecule type: protein
 A/Residues: 'A', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E', 2032, 'C', 2034-2041, '
 A/Note: two reported peptides cannot be reliably located
 R/Greenspan, D.S.
 Hum. Mol. Genet. 2, 273-278, 1993
 A/Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
 A/Reference number: I48103; MUID:93271985; PMID:8499916
 A/Accession: I48103
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 2395-2871, 'S', 2873-2944 <RE2>
 A/Cross-references: GB:L06862; NID:9388713; PIND:AAA89196.1; PID:9388714
 R/Christiano, A.M.; Ryttaenen, M.; Uitto, J.
 Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
 A/Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser subs
 A/Reference number: A55255; MUID:94224777; PMID:8170945
 A/Contents: annotation
 A/Comment: prolines and lysines at the third position of the tripeptide repeating unit (e
 ed and subsequently O-glycosylated.
 C/Genetics:
 A/Gene: GDB:COL7A1; EBR1; EBD1; EB
 A/Cross-references: GDB:128750; OMIM:120120
 A/Map position: 3p21.3-3p21.3
 A/Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
 A/Note: there are 118 introns
 C/Complex: type VII collagen is probably a homotrimer
 C/Function:
 A/Description: structural component of extracellular polymer associated with anchoring f
 C/Keywords: collid coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproli
 F/1-16/Domain: signal sequence #status predicted <SIG>
 F/17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
 F/17-1251/Domain: amino-terminal nonhelical #status predicted <NC1>
 F/36-201/Domain: von Willebrand factor type A repeat homology <WMA1>
 F/231-316/Domain: fibronectin type III repeat homology <FN1>
 F/327-413/Domain: fibronectin type III repeat homology <FN2>
 F/414-502/Domain: fibronectin type III repeat homology <FN3>
 F/508-593/Domain: fibronectin type III repeat homology <FN4>
 F/598-683/Domain: fibronectin type III repeat homology <FN5>
 F/686-771/Domain: fibronectin type III repeat homology <FN6>
 F/776-862/Domain: fibronectin type III repeat homology <FN7>
 F/864-952/Domain: fibronectin type III repeat homology <FN8>
 F/954-1045/Domain: fibronectin type III repeat homology <FN9>
 F/1052-1119/Domain: von Willebrand factor type A repeat homology <WMA2>
 F/1170-1172/Domain: cell attachment (R-G-D) motif
 F/1189-1253/Region: cysteine/proline-rich
 F/1254-2783/Region: interrupted helical
 F/1334-1336/Region: cell attachment (R-G-D) motif
 F/2008-2010/Region: cell attachment (R-G-D) motif
 F/2555-2555/Region: cell attachment (R-G-D) motif
 F/2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
 F/2876-2929/Domain: animal knutiz-type proteinase inhibitor homology <SPI>
 F/337-786, 1109/Binding site: carboxylate (Asn) (covalent) #status predicted
 F/2167-2176, 2185, 2189, 2664, 2667, 2673/Modified site: 4-hydroxyproline (Pro) #status exper
 F/2682, 2631/Modified site: 5-hydroxylysine (Lys) #status experimental
 F/2625, 2631/Binding site: carboxylate (Lys) (covalent) #status experimental
 F/2634, 2802, 2804/Disulfide bonds: interchain #status predicted
 Query Match 61.0%; Score 47; DB 2; Length 2944;
 Best Local Similarity 61.5%; Pred. No. 41;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Oy 3 LEFGIDYISVI 15
 Db 385 LEFGIDYEVST 397
 RESULT 11
 A55445
 juncin precursor, long form - rat
 N/Alternate names: neutral recognition glycoprotein J1-160/180, long form

N:Contains: neural recognition glycoprotein J1-160/180, short form
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 20-Aug-1999
C/Accession: A45445, B45445, S32023
R:Rus, B.; Wintergerst, E.S.; Bartsch, U.; Schachner, M.
J. Cell Biol. 120, 1237-1249, 1993
A>Title: Molecular characterization and in situ mRNA localization of the neural recognition glycoprotein J1-160/180
A/Reference number: A45445; MUID:9317267; PMID:7679676
A/Accession: A45445
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1356 <RUS>
A/Cross-references: GB:218630, NID:957961, PIDN:CAA79229.1, PID:957962
A/Accession: B45445
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-772,863-1356 <RUS>
A/Cross-references: GB:218630
R:Rus, B.; Wintergerst, E.; Bartsch, U.; Schachner, M.
Submitted to the EMBL Data Library, November 1992
A/Description: Molecular characterization and in situ mRNA localization of the neural recognition glycoprotein J1-160/180
A/Reference number: S32023
A/Accession: S32023
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1356 <RUS>
A/Cross-references: EMBL:218630, NID:957961, PIDN:CAA79229.1, PID:957962
C/Keywords: restriction; EGF homology; fibronogen beta/gamma homology; fibronectin type I; fibronectin type III repeat homology; extracellular matrix; glycoprotein; oligo
F:1-1356/Product: janusin, long form #status experimental <MAT>
F:1-772,863-1356/Product: janusin, short form #status experimental <MAT>
F:204-230/Domain: EGF homology <EG1>
F:235-261/Domain: EGF homology <EG2>
F:266-292/Domain: EGF homology <EG3>
F:297-323/Domain: EGF homology <EG4>
F:325-405/Domain: fibronectin type III repeat homology <FN1>
F:413-494/Domain: fibronectin type III repeat homology <FN2>
F:502-584/Domain: fibronectin type III repeat homology <FN3>
F:592-676/Domain: fibronectin type III repeat homology <FN4>
F:684-764/Domain: fibronectin type III repeat homology <FN5>
F:772-854/Domain: fibronectin type III repeat homology <FN6>
F:1038-1118/Domain: fibronectin type III repeat homology <FN7>
F:1133-1341/Domain: fibronogen beta/gamma homology <FBG>

Query Match 59.7%; Score 46; DB 2; Length 1356;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGLSPGIDYDISV 13
| | | | | : | | | |
DB 382 TELEPGITVMSV 394

RESULT 12
T30311
S-layer protein - Clostridium thermocellum
C/Species: Clostridium thermocellum
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C/Accession: T30311
R:Limaitre, M.; Miras, I.; Gounon, P.; Beguin, P.
Microbiology 144, 211-217, 1998
A>Title: Identification of a region responsible for binding to the cell wall within the A/Reference number: Z20818, MUID:98129094, PMID:9467913
A/Accession: T30311
A>Status: preliminary; translated from GB/EMBL/DBS
A/Molecule type: DNA
A/Residues: 1-1036 <LEM>
A/Cross-references: EMBL:U79117, NID:93493463, PID:93493464, PIDN:AAC33404.1
C/Genetics:
A/Gene: slpA

Query Match 58.4%; Score 45; DB 2; Length 1036;
Best Local Similarity 66.7%; Pred. No. 28;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LEFGIDYDISV 14
| | | | | : | | | |
DB 975 LEAGIDYDAAL 986

RESULT 13
HPP beta-like tyrosine phosphatase precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C/Accession: S68700
R:Kuzumochi, S.; Matsuda, S.; Matsuda, Y.; Saitoh, T.; Ohnishi, M.; Yamamoto, T.
FEBS Lett. 378, 7-14, 1996
A>Title: Molecular cloning and characterization of HPP, a murine receptor-type tyrosine A/Reference number: S68700, MUID:96140699, PMID:854806
A/Accession: S68700
A>Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1238 <KTR>
A/Cross-references: GB:D45212, NID:91208432, PIDN:BA08146.1, PID:91208433
C/Genetics:
A/Map position: 2E1-2
C/Superfamily: protein-tyrosine-phosphatase, receptor type I, fibronectin type III repe C/Keywords: phosphoprotein
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1238/Product: HPP beta-like tyrosine phosphatase #status predicted <MAT>
F:267-347/Domain: fibronectin type III repeat homology <FP>
F:966-1188/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1144/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1146/Binding site: substrate phosphate (Arg) #status predicted

Query Match 58.4%; Score 45; DB 2; Length 1238;
Best Local Similarity 53.3%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGLSPGIDYDISV 15
| | | | | : | | | |
DB 92 TGLSPGIDYDISV 106

RESULT 14
JH0675
restriccin precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: JH0675, PS0385, S21254
R:Noerenberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
Neuron 8, 849-863, 1992
A>Title: The chicken neural extracellular matrix molecule restriccin: similarity with E A/Reference number: JH0675, MUID:92265298, PMID:1375037
A/Accession: JH0675
A/Molecule type: mRNA
A/Residues: 1-1353 <NOE>
A/Cross-references: GB:X64649, NID:963613, PIDN:CAA45920.1, PID:963614
A/Experimental source: brain
A/Accession: PS0385
A/Molecule type: protein
A/Residues: 579-586,827-840 <NOE1>
C/Comment: This protein is a neural extracellular matrix protein implicated in neural c C/Superfamily: restriction; EGF homology; fibronogen beta/gamma homology; fibronectin ty C/Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycopro F:1-33/Domain: signal sequence #status predicted <MAT>
F:34-1353/Product: restriccin #status predicted <MAT>
F:203-229/Domain: EGF homology <EG1>
F:234-260/Domain: EGF homology <EG2>
F:265-291/Domain: EGF homology <EG3>
F:296-322/Domain: EGF homology <EG4>
F:324-405/Domain: fibronectin type III repeat homology <FN1>
F:413-494/Domain: fibronectin type III repeat homology <FN2>
F:502-584/Domain: fibronectin type III repeat homology <FN3>
F:592-676/Domain: fibronectin type III repeat homology <FN4>

F;684-764/Domain: fibronectin type III repeat homology <FN5>
 F;772-853/Domain: fibronectin type III repeat homology <FN6>
 F;861-941/Domain: fibronectin type III repeat homology <FN7>
 F;949-1027/Domain: fibronectin type III repeat homology <FN8>
 F;1035-1115/Domain: fibronectin type III repeat homology <FN9>
 F;1130-1338/Domain: fibronogen beta/gamma homology <FBG>
 F;1272-1286/Region: calcium binding #status predicted
 F;53,197,277,391,469,580,734,790,960,1031,1041,1256,1342/Binding site: carbohydrate (Asn

Query Match 58.4%; Score 45; DB 1; Length 1353;
 Best Local Similarity 50.0%; Pred. No. 37;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISV 14
 |||:|:|:|:
 Db 471 TGLKPGEEYTVTV 484

RESULT 15

T34418
 hypothetical protein F12F3.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T34418
 R;Fulton, B.; Wohldmann, P.
 submitted to the EMBL Data Library, July 1998
 A;Description: The sequence of C. elegans cosmid F12F3.
 A;Reference number: Z21521
 A;Accession: T34418
 A;Status: preliminary; translated from GB/EMBL/DDBO
 A;Molecule type: DNA
 A;Residues: 1-3488 <FUL>
 A;Cross-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3
 C;Genetics:
 A;Gene: CESP:F12F3.3
 A;Map position: 5
 A;Intons: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1

Query Match 58.4%; Score 45; DB 2; Length 3488;
 Best Local Similarity 66.7%; Pred. No. 1,1e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GLEPGIDYDISV 13
 |||:|:|:|:
 Db 3240 GLEPGIDYDKV 3251

Search completed: September 21, 2004, 05:48:43
 Job time : 8.75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

```
Run on: September 21, 2004, 05:46:37 ; Search time 4.30147 Seconds
        (without alignments)
        181.578 Million cell updates/sec
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Title:	US-10-676-049-3
Perfect score:	77
Sequence:	1 TGLEPGIDYDISVIT 15

Scoring table: BLOSUM62

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match		DB		ID	Description
No.	Score	Length	DB				
1	77	100.0	1256	1	PINC_CHICK	P11732	gallus galli
2	77	100.0	2477	1	PINC_MOUSE	P11276	mus musculus
3	77	100.0	2477	1	PINC_RAT	P04937	rattus norvegicus
4	73	94.8	1328	1	PINC_PLEWA	O91289	pleurodeles
5	66	85.7	2481	1	PINC_XENLA	O91740	xenopus laevis
6	52	67.5	522	1	PINC_CANPA	O28275	canis familiaris
7	52	67.5	522	1	PINC_HOSEE	O28377	equus caballus
8	52	67.5	2265	1	PINC_BOVIN	P07563	bos taurus
9	51	66.2	1329	1	KE10_HUMAN	O92218	homo sapiens
10	50	63.6	2386	1	PINC_HUMAN	P02751	homo sapiens
11	49	63.9	1560	1	TENN_MOUSE	O80271	mus musculus
12	47	61.0	1294	1	TENN_HUMAN	O90933	homo sapiens
13	47	61.0	2944	1	CA17_HUMAN	O02358	homo sapiens
14	45	58.4	1238	1	PRPJ_MOUSE	O04455	mus musculus
15	44	57.1	1746	1	TENA_PIG	O29116	sus scrofa
16	44	57.1	1808	1	TENA_CHICK	P10039	gallus gallus
17	44	57.1	2201	1	TENA_HUMAN	P24821	homo sapiens
18	43	55.8	1997	1	PRBE_HUMAN	P23467	homo sapiens
19	42	54.5	476	1	CYSN_VIBRA	O67899	vibrio parvulus
20	42	54.5	476	1	CYSN_VIBRU	O68793	vibrio vulnificus
21	42	54.5	476	1	CYSN_VIBRY	O68793	vibrio vulnificus
22	41	53.2	242	1	ORN_SHEON	O67178	shearwater
23	41	53.2	181	1	Y376_UREPA	O93055	ureaplasma urealyticum
24	41	53.2	1337	1	PRPJ_HUMAN	P102913	homo sapiens
25	41	53.2	1897	1	PRPF_HUMAN	P10566	homo sapiens
26	40	51.9	452	1	CIG1_YEAST	P25150	saccharomyces cerevisiae
27	40	51.9	1912	1	PRPD_HUMAN	P23468	homo sapiens
28	40	51.9	3063	1	CA1C_HUMAN	O99715	homo sapiens
29	39	50.6	219	1	BIOD_FUSMO	O87999	fusobacterium nucleatum
30	39	50.6	423	1	SACB_ZYMOO	O60114	zymomonas mobilis
31	39	50.6	446	1	LYS9_YEAST	P38939	saccharomyces cerevisiae
32	39	50.6	660	1	PG06_BP14	P29060	bacteriophage phi14
33	39	50.6	775	1	V506_MYCLE	O93750	mycobacterium tuberculosis

	34	38	49.4	1.1	1	PURF_THEMEA
	34	38	49.4	3.11	1	SYFA_CHLTM
	35	38	49.4	3.42	1	SYFA_CHLTR
	37	38	49.4	4.50	1	LYS3_YACGR
	38	38	49.4	4.93	1	MUR1_OCEIH
	38	38	49.4	4.94	1	MUR2_EACSU
	39	38	49.4	5.57	1	OCN2_HUMAN
	40	38	49.4	5.57	1	OCN2_MOUSE
	41	38	49.4	5.57	1	OCN2_RAT
	42	38	49.4	5.57	1	OCN2_MOUSE
	43	38	49.4	6.58	1	KPC1_LYPTI
	44	38	49.4	7.46	1	PKP_STRCO
	45	38	49.4	11.34	1	TIE1_MOUSE

ALIGNMENTS

```

RESULT 1
FINC_CHICK STANDARD; FRT; 1256 AA.
ID_FINC_CHICK_090921:
AC P11723; 090921:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin (FN) (Fragments).
GN FN1.
OS Gallus gallus (Chicken).
OC Embryos; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Galus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE OF 1-50 FROM N.A.
RX MEDLINE=63117850; PubMed=6572007;
RA Hirano H., Yamada Y., Sullivan M., de Crombrughe B., Pastan I.,
RA Yamada K.M.;
RT "Isolation of genomic DNA clones spanning the entire fibronectin
RT gene."
RT Proc. Natl. Acad. Sci. U.S.A. 80:46-50(1983).
RN [2]
RN SEQUENCE OF 51-1256 FROM N.A.
RX STRAIN=White leghorn;
RA Norton P.A.;
RN [3]
RN Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
RN [4]
RN SEQUENCE OF 227-415 FROM N.A.
RX MEDLINE=96183658; PubMed=8603103;
RA Gerlis A.L., Brandt D.W., Lewis S.D., Bennett V.D.;
RT "The exon encoding the fibronectin type III-9 repeat is
RT constitutively included in the mRNA from chick limb mesenchyme and
RT cartilage."
RN Biochim. Biophys. Acta 1311:5-12(1996).
RN [5]
RN SEQUENCE OF 327-599 FROM N.A.
RX MEDLINE=88050950; PubMed=2823899;
RA Kubomura S., Obara M., Karasaki Y., Taniguchi H., Gotoh S.,
RA Tada T., Higashi K., Ohara K., Hirano H.;
RT "Genetic analysis of the cell binding domain region of the chicken
RT fibronectin gene."
RN Biochim. Biophys. Acta 910:171-181(1987).
RN [6]
RN SEQUENCE OF 413-1256 FROM N.A.
RX MEDLINE=88142820; PubMed=2830487;
RA Norton P.A., Hynes R.O.;
RT "Alternative splicing of chicken fibronectin in embryos and in normal
RT and transformed cells."
RN Mol. Cell. Biol. 7:4297-4307(1987).
RN [7]
RN FUNCTION: Fibronectins bind cell surfaces and various compounds
RN including collagen, fibrin, heparin, DNA, and actin. Fibronectins
RN are involved in cell adhesion, cell motility, opsonization, wound
RN healing, and maintenance of cell shape.
RN [8]
RN SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
RN VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;

```

CC TO A LESSER EXTEND HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced. Each of the "extra
 CC domain" and the connecting strand 3 are present in some forms of
 CC fibronectin and absent in others;
 CC Name=1;
 CC IsoId=P11722-1; Sequence=Displayed;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 CC forms), made by fibroblasts, epithelial and other cell types, is
 CC deposited as fibrils in the extracellular matrix.
 CC -1- PMW: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains at least 2 fibronectin type I domains.
 CC -1- SIMILARITY: Contains at least 8 fibronectin type III domains.
 CC -----
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 CC -----
 CC DR EMBL; V00432; CAA23714.1; -;
 CC DR EMBL; U21327; AAA73566.1; -;
 CC DR EMBL; X06533; CAA29781.1; -;
 CC DR EMBL; M26186; AAA48772.1; ALT_SEQ.
 CC DR EMBL; U20386; AAB01062.1; -;
 CC DR PIR; A28512; A28512.
 CC DR PIR; A29355; A29355.
 CC DR PIR; S71465; S71465.
 CC DR HSSP; P02751; FNH.
 CC DR InterPro; IPR000083; Fibrnctn.
 CC DR InterPro; IPR008957; FN_III-like.
 CC DR InterPro; IPR003961; FN_III.
 CC DR InterPro; IPR000562; FN_Type_II.
 CC DR InterPro; IPR003962; FNIII_subd.
 CC DR PRINTS; PR00014; FNTPeptide.
 CC DR SMART; SM00058; FN1; 3.
 CC DR SMART; SM00060; FN3; 9.
 CC DR PROSITE; PS00023; FIBRONECTIN_2; PARTIAL.
 CC DR PROSITE; PS01253; FIBRONECTIN_1; 2.
 CC KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
 CC Repeat; Sulfation; Alternative splicing.
 CC FT NON_TER 1
 CC FT NON_CONS 50 51
 CC FT DOMAIN 236 509
 CC FT DOMAIN 690 961
 CC FT DOMAIN 1153 1226
 CC FT DOMAIN 327 415
 CC FT DOMAIN 416 509
 CC FT DOMAIN 510 599
 CC FT DOMAIN 600 689
 CC FT DOMAIN 690 781
 CC FT DOMAIN 781 871
 CC FT DOMAIN 872 961
 CC FT DOMAIN 962 1082
 CC FT DOMAIN 1083 1152
 CC FT DOMAIN 1174 1218
 CC FT DOMAIN 1219 1256
 CC FT SITE 493 495
 CC FT SITE 1176 1205
 CC FT DISULFID 1203 1215
 CC FT DISULFID 1221 1248
 CC FT CARBOHYD 1078 1078
 CC FT CARBOHYD 1078 1078
 CC FT CARBOHYD 1034 1034
 CC FT CARBOHYD 1035 1035
 CC FT CONFLICT 516 516
 CC FT CONFLICT 569 572
 CC FT NON_TER 1256 1256

SC SEQUENCE 1256 AA; 137435 MW; 3454ACAE047D1D9B CRC64;
 Query Match 100.0%; Score 77; DB 1; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGLSPGIDYDSVIT 15
 DB 204 TGLSPGIDYDSVIT 218
 RESULT 2
 AC P11726; G61567; G61568; G61569; G64233; Q80U14;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 GN Fibronectin precursor (FN).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX STRAIN=FVB/N-3; TISSUE=Breast tumor;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Muljaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huyls S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RA human and mouse cDNA sequences.";
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP SEQUENCE OF 1-28 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=941313; PubMed=8299972;
 RA Polly P., Nicholson R.C.;
 RT "Sequence of the mouse fibronectin-encoding gene promoter region.";
 RL Gene 137:353-354(1993).
 RN [13]
 RP SEQUENCE OF 562-834 FROM N.A.
 RC STRAIN=NR1;
 RX MEDLINE=9540556; PubMed=7673336;
 RA Tait J.F., Weller A., Timpi R., Ekblom M., Ekblom P.;
 RT "Regulation of mesenchymal extracellular matrix protein synthesis by
 RT transforming growth factor-beta and glucocorticoids in tumor
 RT stroma.";
 RL J. Cell Sci. 108:2153-2162(1995).
 RN [14]
 RP SEQUENCE OF 899-2376 FROM N.A.
 RC Gorski G., Aros M., Norton P.;
 RX Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RX MEDLINE=88124987; PubMed=3124113;
 RA Blatti S.P., Foster D.N., Rangathan G., Moses H.L., Getz M.J.;
 RT "Induction of fibronectin gene transcription and mRNA is a primary

RT response to growth-factor stimulation of AKR-2B cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).
 RN [6]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RC TISSUE=Kidney;
 RA Khandjian E.W., Salomon C., Leonard N., Tremblay S., Turler H.;
 RT "Fibronectin gene expression in proliferating, quiescent, and SV40-
 infected mouse kidney cells.";
 RL Exp. Cell Res. 202:464-470(1992).
 RN [7]
 RP STRUCTURE BY NMR OF 1447-1630.
 RA MEDLINE=9820578; PubMed=9533887;
 RX Copie V., Tomita Y., Akiyama S.K., Aota S., Yamada K.M., Venable R.M.,
 RA Pastor R.W., Krieger S., Torchia D.A.;
 RT "Solution structure and dynamics of linked cell attachment modules of
 mouse fibronectin containing the RGD and synergy regions: comparison
 with the human fibronectin crystal structure.";
 RL J. Mol. Biol. 277:663-682(1998).
 RN [8]
 RP DOWN-REGULATION BY GLUCOCORTICOIDS.
 RA MEDLINE=2160963; PubMed=1173725;
 RX Gu Y.-C., Tait J.F., Guilberg D., Timpl R., Ekblom M.;
 RT "Glucocorticoids down-regulate the extracellular matrix proteins
 fibronectin, fibrin-1 and fibrin-2 in bone marrow stroma.";
 RL Eur. J. Haematol. 67:176-184(2001).
 CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
 including collagen, fibrin, heparin, DNA, and actin. Fibronectins
 are involved in cell adhesion, cell motility, opsonization, wound
 healing, and maintenance of cell shape.
 CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
 variants, connected by 2 disulfide bonds near the carboxyl ends;
 to a lesser extend homodimers. Interacts with FHLN1 (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=1;
 Comment=A number of isoforms are produced. Each of the "extra
 domain" and the connecting strand 3 are present in some forms of
 fibronectin and absent in others;
 Name=1;
 CC -1- IsoId=B11276-1; Sequence=Displayed;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 forms), made by fibroblasts, epithelial and other cell types, is
 deposited as fibrils in the extracellular matrix.
 CC -1- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
 synthesis.
 CC -1- PTM: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; BC051082; AAHS1082.1; -
 DR EMBL; Z22729; CA80422.1; -
 DR EMBL; X82402; CA57796.1; -
 DR EMBL; X93167; CA63654.1; -
 DR EMBL; M18194; AA337636.1; -
 DR EMBL; S45680; AA23491.1; -
 DR FIR; A49173; A49173.
 DR PIR; I48349; I48349.
 DR PDB; IMFN; 29-APR-98.
 DR PDB; ZMFN; 29-APR-98.
 DR MGI; MGI:95566; Fnl.
 DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR000083; Fibronctn1.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR000562; FNII_Type_II.
 DR InterPro; IPR003962; FNIII_Subd.
 DR InterPro; IPR008924; MCR_alpha_beta_C.
 DR PRINTS; PR00014; FNTYPEIII.
 DR SMART; SM00058; FN1; 4.
 DR SMART; SM00060; FN3; 12.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
 KW Sulfation; Cell adhesion; Repeat; Alternative splicing; Signal;
 KW 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 33 2477
 FT DOMAIN 53 273
 FT DOMAIN 308 608
 FT DNA_BIND 906 1171
 FT DOMAIN 1357 1630
 FT DOMAIN 1811 2081
 FT DOMAIN 2296 2427
 FT DOMAIN 51 96
 FT DOMAIN 96 140
 FT DOMAIN 140 185
 FT DOMAIN 185 230
 FT DOMAIN 230 272
 FT DOMAIN 306 343
 FT DOMAIN 345 404
 FT DOMAIN 405 469
 FT DOMAIN 468 516
 FT DOMAIN 516 559
 FT DOMAIN 559 602
 FT DOMAIN 609 706
 FT DOMAIN 707 808
 FT DOMAIN 809 903
 FT DOMAIN 904 994
 FT DOMAIN 995 1084
 FT DOMAIN 1085 1172
 FT DOMAIN 1173 1264
 FT DOMAIN 1265 1355
 FT DOMAIN 1356 1446
 FT DOMAIN 1447 1536
 FT DOMAIN 1537 1630
 FT DOMAIN 1631 1720
 FT DOMAIN 1721 1810
 FT DOMAIN 1811 1902
 FT DOMAIN 1903 1991
 FT DOMAIN 1992 2081
 FT DOMAIN 2082 2201
 FT DOMAIN 2202 2283
 FT DOMAIN 2284 2358
 FT DOMAIN 2359 2381
 FT DOMAIN 2383 2426
 FT SITE 1614 1616
 FT SITE 2181 2183
 FT DISULFID 53 79
 FT DISULFID 77 88
 FT DISULFID 98 126
 FT DISULFID 124 136
 FT DISULFID 142 170
 FT DISULFID 168 180
 FT DISULFID 187 216
 FT DISULFID 214 226
 FT DISULFID 232 261
 Query Match 100.0%; Score 77; DB 1; Length 2477;
 Best Local Similarity 100.0%; Pred. No. 0.00019; Indels 0;
 Matches 15; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 TGLEPGIDYDISVIT 15


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FT  .DISULFID  1268  1284  BY SIMILARITY.
FT  .DISULFID  1320  1320  INTERCHAIN (WITH C-1324) (BY SIMILARITY).
FT  .DISULFID  1324  1324  INTERCHAIN (WITH C-1320) (BY SIMILARITY).
FT  SITE  461  463  CELL ATTACHMENT SITE.
FT  CARBOHYD  89  89  N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE  1328 AA;  145037 MW;  E31BF7968A1DIE74 CRC64;

QY  1 TGLEPGIDYDISVIT  15
    :|||||
    :|||||
Db  171 SGLPEGIDYDISVIT  185

RESULT 5
FINC_XENLA  STANDARD;  PRT;  2481 AA.
AC  Q91740;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Fibronectin precursor.
GN  FN1.
OC  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxId=8355;
OX  [1]
RN  R1
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92111942; PubMed=1730390;
RA  Deslions D.W., Norton P.A., Hynes R.O.;
RT  Identification and characterization of alternatively spliced
RT  fibronectin mRNAs expressed in early Xenopus embryos.";
RL  Dev. Biol. 149:357-369(1992).

CC  -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC  including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC  are involved in cell adhesion, cell motility, opsonization, wound
CC  healing, and maintenance of cell shape. (By similarity).
CC  -1- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
CC  CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
CC  SIMILARITY).
CC  -1- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=1;
CC  Comment=A number of isoforms are produced. Each of the "extra
CC  domain" and the connecting strand 3 are present in some forms of
CC  fibronectin and absent in others;
CC  Name=1;
CC  -1- IsoId=Q91740-1; Sequence=Displayed.
CC  -1- TISSUE SPECIFICITY: IN EARLY XENOPUS EMBRYO, CELLULAR FORMS OF
CC  FIBRONECTIN PREOMINATE WHICH INCLUDE BOTH EXTRA DOMAINS. IN
CC  FIBRONECTIN OF EMBRYONIC AND ADULT LIVER THE CONNECTING STRAND 3
CC  CAN BE EITHER COMPLETELY EXCLUDED OR INCLUDED.
CC  -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC  -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC  -1- SIMILARITY: Contains 17 fibronectin type III domains.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (see http://www.isb-sib.ch/announce/)
CC  or send an email to license@isb-sib.ch).
CC  -----
OR  EMBL; M77820; AAA49707.1; .
OR  HSSP; P02751; 2FN2.
OR  InterPro; IPR006209; EGF_like.
OR  InterPro; IPR000083; Fibrinctn1.
OR  InterPro; IPR008957; FN III-like.

```

[illegible]

FT DISULFID 562 590 BY SIMILARITY.
 FT DISULFID 568 600 BY SIMILARITY.
 FT DISULFID 2301 2330 BY SIMILARITY.
 FT DISULFID 2328 2340 BY SIMILARITY.
 FT DISULFID 2346 2373 BY SIMILARITY.
 FT DISULFID 2371 2383 BY SIMILARITY.
 FT DISULFID 2390 2414 BY SIMILARITY.
 FT DISULFID 2412 2428 BY SIMILARITY.
 FT DISULFID 2459 2459 INTERCHAIN (WITH C-2463) (BY SIMILARITY).
 FT DISULFID 2463 2463 INTERCHAIN (WITH C-2459) (BY SIMILARITY).
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 543 543 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 877 877 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1244 1244 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1291 1291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2202 2202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 2481 AA; 272678 MW; 7247DF4FC6C72C93 CRC64;

Query Match 85.7%; Score 66; DB 1; Length 2481;
 Best Local Similarity 80.0%; Pred. No. 0.013;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 TGLEPGIDYDISVT 15
 1326 SGLEPGIDYDISVT 1340

RESULT 6
 ID FINE CANFA STANDARD; PRT; 522 AA.
 AC Q28275; Q28276; 35; Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin (FN) (Fragment).
 GN FN1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Cartilage;
 RX MEDLINE=96324983; PubMed=8702559;
 RA MacLeod J.N., Burton-Wurster N., Gu D.N., Lust G.,
 RT "Fibronectin mRNA splice variant in articular cartilage lacks bases
 encoding the V, III-15, and I-10 protein segments.";
 RL J. Biol. Chem. 271:18954-18960(1996).
 CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
 including collagen, fibrin, heparin, DNA, and actin. Fibronectins
 are involved in cell adhesion, cell motility, opsonization, wound
 healing, and maintenance of cell shape.
 CC -1- FUNCTION: Isoform 2 is probably involved in matrix organization of
 cartilage.
 CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
 variants, connected by 2 disulfide bonds near the carboxyl ends;
 to a lesser extent homodimers.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Each of the "extra domain" and the connecting strand 3.
 CC are present in some forms of fibronectin and absent in others;
 CC Name=1;
 CC Name=2; Synonyms=(V+C)-;
 CC IsoId=Q28275-1; Sequence=Displayed;
 CC Name=2; Synonyms=(V+C)-;
 CC IsoId=Q28275-2; Sequence=VSP_003251, VSP_003252;
 CC Note=lacks repeat 15 of fibronectin type-III, repeat 10 of
 CC fibronectin type-I, and the connecting strand 3;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 CC form), made by fibroblasts, epithelial and other cell types, is
 CC deposited as fibrils in the extracellular matrix. Isoform 2 is the

CC major transcript in articular cartilage, but it is absent from
 CC liver.
 CC -1- PTM: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains at least 4 fibronectin type III domains.
 CC -1- SIMILARITY: Contains at least 3 fibronectin type I domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U52106; AAC48612.1; -;
 CC EMBL: U52105; AAC48611.1; -;
 CC HSPB: P02751; 1FNH.
 CC DR InterPro: IPR000083; Fibnrcnctn.
 CC DR InterPro: IPR008957; FN-III-like.
 CC DR InterPro: IPR003961; FN-III.
 CC DR InterPro: IPR003962; FNIII_subd.
 CC DR Pfam: PF00039; fn1; 3.
 CC DR Pfam: PF00041; fn3; 3.
 CC DR PRINTS: PR00014; FNTYPEIII.
 CC DR SMART: SM00058; FN1; 2.
 CC DR SMART: SM00060; FN3; 3.
 CC DR PROSITE: PS01253; FIBRONECTIN_1; 2;
 CC KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
 CC Repeat; Sulfation; Alternative splicing.
 CC FT NON TER 1 204
 CC FT DOMAIN <1 204 HEPARIN-BINDING 2 (BY SIMILARITY).
 CC FT DOMAIN 325 >522 FIBRIN-BINDING 2 (BY SIMILARITY).
 CC FT DOMAIN <1 25 FIBRONECTIN TYPE-III 13.
 CC FT DOMAIN 26 114 FIBRONECTIN TYPE-III 14.
 CC FT DOMAIN 115 204 FIBRONECTIN TYPE-III 15.
 CC FT DOMAIN 205 315 CONNECTING STRAND 3 (CS-3) (V REGION).
 CC FT DOMAIN 316 395 FIBRONECTIN TYPE-III 16.
 CC FT DOMAIN 417 461 FIBRONECTIN TYPE-I 10.
 CC FT DOMAIN 462 504 FIBRONECTIN TYPE-I 11.
 CC FT DOMAIN 506 >522 FIBRONECTIN TYPE-I 12.
 CC FT SITE 304 306 CELL ATTACHMENT SITE (POTENTIAL).
 CC FT DISULFID 419 448 BY SIMILARITY.
 CC FT DISULFID 446 458 BY SIMILARITY.
 CC FT DISULFID 464 491 BY SIMILARITY.
 CC FT DISULFID 489 501 BY SIMILARITY.
 CC FT DISULFID 508 >522 BY SIMILARITY.
 CC FT MOD RES 509 509 SULFATION (POTENTIAL).
 CC FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 CC FT CARBOHYD 277 277 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 CC FT CARBOHYD 278 278 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 CC FT VARSPLIC 205 205 D -> E (in isoform 2).
 CC FT VARSPLIC 206 462 /FTId=VSP_003251.
 CC FT VARSPLIC 462 Missing (in isoform 2).
 CC FT NON TER 522 522 /FTId=VSP_003252.
 CC SQ SEQUENCE 522 AA; 57700 MW; DB1D9A54C2BD4E26 CRC64;

Query Match 67.5%; Score 52; DB 1; Length 522;
 Best Local Similarity 71.4%; Pred. No. 0.51;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 TGLEPGIDYDISVT 14
 174 TGLEPGIDYDISVT 187

RESULT 7
 ID FINE HORSE STANDARD; PRT; 522 AA.
 AC Q28377; Q28378; 35; Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Fibronectin (FN) (Fragment).
GN FN1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_taxid=9796;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=layer:
RX MEDLINE=96324983; PubMed=8702559;
RA Medline J.N., Burton-Wurster N., Gu D N., Lust G;
RT "Fibronectin mRNA splice variant in articular cartilage lacks bases
RT encoding the V, III-15, and I-10 protein segments.";
RL J. Biol. Chem. 271:18954-18960(1996).
CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC are involved in cell adhesion, cell motility, opsonization, wound
CC healing, and maintenance of cell shape.
CC -1- FUNCTION: Isoform 2 is probably involved in matrix organization of
CC cartilage.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing: Named isoforms=2;
CC Comment=Additional isoforms seem to exist. Each of the "extra
CC domain and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC IsoId=Q28377-1; Sequence=displayed;
CC Name=2; Synonyms=(V+C)-;
CC IsoId=Q28377-2; Sequence=VSP_003253, VSP_003254;
CC Note=Lacks repeat 15 of fibronectin type-III, repeat 10 of
CC fibronectin type-I, and the connecting strand 3;
CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
CC forms), made by fibroblasts, epithelial and other cell types, is
CC deposited as fibrils in the extracellular matrix. Isoform 2 is the
CC major transcript in articular cartilage; very low levels in lymph
CC node, bone, aorta, and skin; absent from liver, spleen, placenta,
CC cardiac muscle, skeletal muscle, stomach, small intestine, and
CC kidney.
CC -1- PTM: Sulfated (by similarity).
CC -1- SIMILARITY: Contains at least 4 fibronectin type III domains.
CC -1- SIMILARITY: Contains at least 3 fibronectin type I domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U52107; AAC48613.1; -;
CC EMBL; U52108; AAC48614.1; -;
CC HSP; P02751; IPIH.
CC InterPro; IPR000063; Fibnrcnctn.
CC InterPro; IPR008857; FN_III-like.
CC InterPro; IPR003561; FN_III.
CC InterPro; IPR003962; FNIII_subd.
CC Pfam; PF00039; fnl; 3.
CC Pfam; PF00041; fn3; 3.
CC PRINTS; PR00014; FNTYPEIII..
CC SMART; SM00058; FN1; 2.
CC SMART; SM00060; FN3; 3.
CC PROSITE; PS01253; FIBRONECTIN_1; 2.
CC Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
CC Repeat; Sulfation; Alternative splicing.
CC NON_TER 1
CC DOMAIN 1 204
CC 325 522 HEPARIN-BINDING 2 (BY SIMILARITY).
CC FIBRIN-BINDING 2 (BY SIMILARITY).
CC

```

FT DOMAIN 1 25 FIBRONECTIN TYPE-III 13.
FT DOMAIN 26 114 FIBRONECTIN TYPE-III 14.
FT DOMAIN 115 204 FIBRONECTIN TYPE-III 15.
FT DOMAIN 205 315 CONNECTING STRAND 3 (CS-3) (V REGION).
FT DOMAIN 316 395 FIBRONECTIN TYPE-III 16.
FT DOMAIN 417 461 FIBRONECTIN TYPE-I 10.
FT DOMAIN 462 504 FIBRONECTIN TYPE-I 11.
FT DOMAIN 506 >522 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 304 306 BY SIMILARITY.
FT DISULEID 419 448 BY SIMILARITY.
FT DISULEID 446 458 BY SIMILARITY.
FT DISULEID 464 491 BY SIMILARITY.
FT DISULFID 489 501 BY SIMILARITY.
FT MOD_RBS 515 515 SUPRATON (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 277 277 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT CARBOHYD 278 278 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT CARBOHYD 205 205 D -> E (in isoform 2).
FT VARSPLIC /Frid=VSP_003253.
FT VARSPLIC 206 462 Missing (in isoform 2).
FT VARSPLIC /Frid=VSP_003254.
FT NON_TBR 522 522
FT SEQ SEQUENCE 522 AA; 57577 MM; 893BAC895864D41 CRC64;

Query Match 67.5%; Score 52; DB 1; Length 522;
Best Local Similarity 71.4%; Pred. No. 0.51;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGLPFGIDYISY 14
Db 174 TGLPFGTETTYQVI 187

RESULT 8
FINC_BOVIN
ID_FINC_BOVIN STANDARD; PRT; 2265 AA.
AC P07589;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin (FN).
GN FN1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
OX [1]
RX MEDLINE=67054047; PubMed=3780752;
RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin..";
RL Eur. J. Biochem. 161:441-453(1986).
LN [2]
LN PARTIAL SEQUENCE.
RP MEDLINE=63117805; PubMed=6218503;
RA Petersen T.E., Thorgeresen H.C., Skorstengaard K., Vibe-Pedersen K.,
RA Sahl P., Sottrup-Jensen L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
of internal homology ";
RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
LN [3]
LN SEQUENCE OF 2170-2265 FROM N.A.
RP MEDLINE=83221567; PubMed=6304699;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
fibronectins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
LN -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
including collagen, fibrin, heparin, DNA, and actin. Fibronectins
are involved in cell adhesion, cell motility, opsonization, wound
healing, and maintenance of cell shape.
LN -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein KIAA1510 precursor.
GN KIAA1510.
OS Homo sapiens (Human).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.W., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharasliho M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Patker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Pallimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans S., Vandin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:665-671(2001).
RN [2]
RP SEQUENCE OF 156-1329 FROM N.A. (ISOFORM 3).
RX TISSUE=Brain;
RA MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 7:143-150(2000).
RN [3]
RP SEQUENCE OF 1020-1329 FROM N.A. (ISOFORM 3).
RX TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heish F.,
RA Datchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong J.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Cassavan T.L., Schaefer T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pange C.,
RA Rata S.S., Loguailano N.A., Peters G.J., Abramson R.D., Millar S.J.,
RA Bosak S.A., McEwan P.D., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzey D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1060-1199 FROM N.A. (ISOFORM 1).
RA Hillier L., Allen M., Bowles L., Dubuque T., Getzel G., Jost S.,
RA Krizman D., Kucada T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore B., Schellberg K., Steptoe W., Tan F., Theising B., White Y.,
RA Wylie T., Waterston R., Wilson R.;
RT "Ashu-NCI human EST project."
RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probable collagen protein.
CC -1- SUBCELLULAR LOCATION: Extracellular (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=09P218-1; Sequence=Displayed;
CC Note=Inferred from EST source;
CC Name=2;
CC IsoId=09P218-2; Sequence=VSP_002436;
CC Note=Inferred from EST source;
CC Name=3;
CC IsoId=09P218-3; Sequence=VSP_002437;
CC -1- TISSUE SPECIFICITY: High expression in heart, lung, liver,
CC skeletal muscle, kidney, pancreas, spleen, testis, ovary,
CC subthalamic nucleus and fetal liver. Weak expression in other
CC tissues tested.
CC -1- SIMILARITY: Contains 1 collagenous domain.
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -1- SIMILARITY: Contains 1 VWFA domain.
CC -1- CAUTION: Ref.1 sequences differ from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL; AL121827; CAC6117.1; ALT_SEQ.
DR EMBL; AL121827; CAC6118.1; ALT_SEQ.
DR EMBL; ABC040943; BAA96034.1; -.
DR EMBL; BC013658; BAA13658.1; -.
DR EMBL; BC019637; AAH19637.1; ALT_INIT.
DR EMBL; A1272270; -. NOT ANNOTATED_CDS.
DR HSSP; P17301; IAOX.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003129; TSPN.
DR InterPro; IPR002035; VWFA.
DR Pfam; PF01391; collagen_3.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF02210; TSPN; 1.
DR Pfam; PF00092; vwa; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SMO0060; FN3; 6.
DR SMART; SMO0327; VWFA; 1.
DR SMART; SMO0210; TSPN; 1.
DR PROSITE; PS0234; VWFA; 1.
DR PROSITE; PS0234; VWFA; 1.
DR SIGNAL; 1; 22
DR CHAIN; 1; 1329
DR DOMAIN; 186; 361
DR DOMAIN; 384; 467
DR DOMAIN; 474; 552
DR DOMAIN; 564; 646
DR DOMAIN; 734; 827
DR DOMAIN; 747; 834
DR DOMAIN; 842; 1044
DR DOMAIN; 1079; 1230
DR CARPCHD; 614; 614
DR VASAPLIC; 1089; 1138

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FT VARSPLIC 1107 1138 Missing (in isoform 3).
 FT CONFLICT 619 619 /FTID=VSP_002437.
 SQ SEQUENCE 1329 AA; 140288 MW; 1429CDEE1DE86D CRC64;
 Query Match 66.2%; Score 51; DB 1; Length 1329;
 Best Local Similarity 75.0%; Pred. No. 2;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GLEPGIDYDISV 13
 DB 532 GLEPGRDYEVSV 543

RESULT 10
 FINE_HUMAN STANDARD; PRT; 2386 AA.
 AC P02751; Q95609; Q95610; Q14312; Q14325; Q14366; Q86727; Q81V18;
 AC Q96KP7; Q96KP8; Q96KP9; Q9H1B8; Q9HAP3; Q9UMK2;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).
 GN FN1 OR FN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=21600194; PubMed=11737888;
 RA Schor S.L., Schor A.M.;
 RT "Phenotypic and genetic alterations in mammary stroma: implications
 for tumour progression.";
 RL Breast Cancer Res. 3:373-379(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 3; 7 AND 10).
 RC TISSUE=Cervix;
 RA Ansoorge W., Krieger S., Regiert T., Riltmuller C., Schwager B.,
 RA Mewes H.-W., Weill B., Amd C., Osanger A., Fobo G., Han M.,
 RA Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE=87030890; PubMed=770189;
 RA Gutman A., Yamada K.M., Kornblith A.R.;
 RT "Human fibronectin is synthesized as a pre-propolypeptide.";
 RL FBS Lett. 207:145-148(1986).
 RN [4]
 RP SEQUENCE OF 1-49 FROM N.A.
 RX MEDLINE=87175578; PubMed=3031656;
 RA Dean D.C., Bowles C.L., Bourgeois S.;
 RT "Cloning and analysis of the promoter region of the human fibronectin
 gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).
 RN [5]
 RP SEQUENCE OF 28-2386 FROM N.A. (ISOFORM 3).
 RX MEDLINE=85284965; PubMed=2992939;
 RA Kornblith A.R., Umezawa K., Vide-Pedersen K., Baralle F.E.;
 RT "Primary structure of human fibronectin: differential splicing may
 generate at least 10 polypeptides from a single gene.";
 RL EMBO J. 4:1755-1759(1985).
 RN [6]
 RP SEQUENCE OF 103-481 AND 2228-2386 FROM N.A. (ISOFORMS 1; 3; 8 AND 9).
 RC TISSUE=Peripheral blood T-cell, and Umbilical vein endothelial cells;
 RA Godfrey H.P., Ebrahim A.A.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 973-2386 FROM N.A. (ISOFORM 3).
 RX MEDLINE=84272258; PubMed=6462919;
 RA Kornblith A.R., Vide-Pedersen K., Baralle F.E.;
 RT "Human fibronectin: cell specific alternative mRNA splicing generates
 polypeptide chains differing in the number of internal repeats.";

RL Nucleic Acids Res. 12:5853-5868(1984).
 RN [8]
 RP SEQUENCE OF 1232-1782 FROM N.A. (ISOFORM 7).
 RX MEDLINE=88233940; PubMed=3375063;
 RA Pacella G., Henchcliffe C., Sebastio G., Baralle F.E.;
 RT "Sequence analysis and in vivo expression show that alternative
 RT splicing of ED-B and ED-A regions of the human fibronectin gene are
 RT independent events.";
 RL Nucleic Acids Res. 16:3545-3557(1988).
 RN [9]
 RP SEQUENCE OF 1257-1365 FROM N.A. (ISOFORM 11).
 RX MEDLINE=88041070; PubMed=3478690;
 RA Gutman A., Kornblith A.R.;
 RT "Identification of a third region of cell-specific alternative
 RT splicing in human fibronectin mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7179-7182(1987).
 RN [10]
 RP SEQUENCE OF 1441-1548.
 RX MEDLINE=82265604; PubMed=7050098;
 RA Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
 RT "The cell attachment domain of fibronectin. Determination of the
 RT primary structure.";
 RL J. Biol. Chem. 257:9593-9597(1982).
 RN [11]
 RP SEQUENCE OF 1448-1540 FROM N.A.
 RX MEDLINE=83290929; PubMed=6688418;
 RA Oldberg A., Linney E., Ruoslahti E.;
 RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for
 RT the cell attachment domain in human fibronectin.";
 RL J. Biol. Chem. 258:10193-10196(1983).
 RN [12]
 RP SEQUENCE OF 1448-1540 FROM N.A.
 RX MEDLINE=86111901; PubMed=3003095;
 RA Oldberg A., Ruoslahti E.;
 RT "Evolution of the fibronectin gene. Exon structure of cell attachment
 RT domain.";
 RL J. Biol. Chem. 261:2113-2116(1986).
 RN [13]
 RP SEQUENCE OF 1594-2386 FROM N.A. (ISOFORM 1).
 RX MEDLINE=85280409; PubMed=2992573;
 RA Bernard M.P., Kolbe M., Weill D., Chu M.-L.;
 RT "Human cellular fibronectin: comparison of the carboxyl-terminal
 RT portion with rat identifies primary structural domains separated by
 RT hypervariable regions.";
 RL Biochemistry 24:2698-2704(1985).
 RN [14]
 RP SEQUENCE OF 1712-1739 FROM N.A.
 RX MEDLINE=87026578; PubMed=3021206;
 RA Sekiguchi K., Kios A.M., Kurachi K., Yoshitake S., Hakomori S.;
 RT "Human liver fibronectin complementary DNAs: identification of two
 RT different messenger RNAs possibly encoding the alpha and beta
 RT subunits of plasma fibronectin.";
 RL Biochemistry 25:4936-4941(1986).
 RN [15]
 RP SEQUENCE OF 1788-2386 FROM N.A. (ISOFORMS 4; 5 AND 6).
 RC TISSUE=Cartilage;
 RX MEDLINE=22126816; PubMed=12127832;
 RA Parker A.E., Boulell J., Carr A., Maciewicz R.A.;
 RT "Novel cartilage-specific splice variants of fibronectin.";
 RL Osteoarthritis Cartilage 10:528-534(2002).
 RN [16]
 RP SEQUENCE OF 32-290.
 RX MEDLINE=84032463; PubMed=6630202;
 RA Garcia-Pardo A., Pearlstein E., Frangione B.;
 RT "Primary structure of human plasma fibronectin. The 29,000-dalton
 RT NH2-terminal domain.";
 RL J. Biol. Chem. 258:12670-12674(1983).
 RN [17]
 RP SEQUENCE OF 309-608 AND COLLAGEN-BINDING.
 RX MEDLINE=87080265; PubMed=3024962;
 RA Owens R.J., Baralle F.E.;
 RT "Mapping the collagen-binding site of human fibronectin by expression
 RT in Escherichia coli.";

RL EMBL J. 5:2825-2830(1986).
RN
RP SUBPATION.
RX MEDLINE=86042625; Pubmed=2414772;
RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
RT "Tyrosine sulfation of proteins from the human hepatoma cell line HepG2."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
RN
RP O-GLYCOSYLATION OF THR-2064.
RX MEDLINE=91190085; Pubmed=2012601;
RA Tresselt T., McCarthy J.B., Calaycay J., Lee T.D., Legesse K.,
RA Shively J.R., Pande H.;
RT "Human plasma fibronectin. Demonstration of structural differences between the A- and B-chains in the III CS region."
RL Biochem. J. 274:731-738(1991).
RN
RP PLN1-BINDING SITE.
RX MEDLINE=93015879; Pubmed=1400330;
RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,
RA Argaves W.S.;
RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding region of fibronectin."
RL J. Biol. Chem. 267:20120-20125(1992).
RN
RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
RX MEDLINE=95081153; Pubmed=7989369;
RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
RT "Further characterization of the NH2-terminal fibrin-binding site on fibronectin."
RL J. Biol. Chem. 269:31938-31945(1994).
RN
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=9216710; Pubmed=1311202;
RA Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,
RA Campbell I.D.;
RT "1H NMR assignment and secondary structure of the cell adhesion type III module of fibronectin."
RL Biochemistry 31:2068-2073(1992).
RN
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=93046665; Pubmed=1423622;
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;
RT "The three-dimensional structure of the tenth type III module of fibronectin: an insight into RGD-mediated interactions."
RL Cell 71:671-678(1992).
RN
RP STRUCTURE BY NMR OF 182-275.
RX MEDLINE=94141923; Pubmed=8308892;
RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,
RA Campbell I.D.;
RT "Solution structure of a pair of fibronectin type I modules with fibrin binding activity."
RL J. Mol. Biol. 235:1302-1311(1994).
RN
RP STRUCTURE BY NMR OF 32-92.
RX MEDLINE=9606779; Pubmed=7583666;
RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;
RT "High-resolution structural studies of the factor XIIIa crosslinking site and the first type I module of fibronectin."
RL Nat. Struct. Biol. 2:946-950(1995).
RN
RP STRUCTURE BY NMR OF 406-464.
RX MEDLINE=98179558; Pubmed=9514732;
RA Steich H., Pickford A.R., Potts J.R., Campbell I.D.;
RT "Solution structure of the glycosylated second type 2 module of fibronectin."
RL J. Mol. Biol. 276:177-187(1998).
RN
RP STRUCTURE BY NMR OF EXTRA ED-B DOMAIN FROM ISOFORM 7.
Query Match 64.9%; Score 50; DB 1; Length 2386;
Best Local Similarity 71.4%; Pred. No. 5.5;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Cy 1 TGLEPGIDYDISY 14
Db 1961 TGLEPGREYTYTY 1974
RESULT 11
TENN_MOUSE
ID TENN_MOUSE STANDARD; PRT; 1560 AA.
AC Q80Z71;
DT 10-OCT-2003 (Rel. 42, Created)
DR 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tenascin N precursor.
GN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A., FUNCTION, ALTERNATIVE SPLICING, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC STRIN=C57BL/6;
RX MEDLINE=22697596; Pubmed=12812753;
RA Neidhardt J., Fehr S., Kutsche M., Loehler J., Schachner M.;
RT "Tenascin-N: characterization of a novel member of the tenascin family that mediates neurite repulsion from hippocampal explants."
RL Mol. Cell. Neurosci. 23:193-209(2003).
CC
CC -I- FUNCTION: Isoform 2 inhibits neurite outgrowth and cell migration in hippocampal explants while isoform 1 does not have this effect.
CC
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC
CC -I- IsoId=Q80Z71-1; Sequence=Displayed;
CC
CC -I- TISSUE SPECIFICITY: Highest expression in kidney followed by spleen and brain. In brain, highest expression is found in hippocampus, cerebellum and olfactory bulb.
CC
CC -I- DEVELOPMENTAL STAGE: Hardly detectable at embryonic day 14, then increases until post-natal day 17 and remains detectable in the adult.
CC
CC -I- SIMILARITY: Contains 3 EGF-like domains.
CC
CC -I- SIMILARITY: Contains 12 fibronectin type III domains.
CC
CC -I- SIMILARITY: Contains 1 fibronogen C-terminal domain.
CC
CC
CC THE SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL; AF455756; AAO63807.1; -
CC
CC MGD; MGI:2665790; Tnn.
DR GO; GO:0016049; P:cell growth, IDA.
DR GO; GO:0016477; P:cell migration, IDA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002181; Fibinogen_C.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_3.
DR Pfam; PF00147; fibritogen_C; 1.
DR Pfam; PF00041; fn3; 12.
DR SMART; SM00181; EGF_3.
DR SMART; SM00186; FBG; 1.
DR SMART; SM00060; FN3; 12.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.

KW Repeat; EGF-like domain; Signal. Alternative splicing.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 1560 TENASCIN N.
 FT DOMAIN 167 198 EGF-LIKE 1.
 FT DOMAIN 199 229 EGF-LIKE 2.
 FT DOMAIN 230 260 EGF-LIKE 3.
 FT DOMAIN 262 340 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 351 435 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 443 520 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 531 608 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 619 696 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 707 784 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 795 872 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 883 960 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 971 1048 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1059 1136 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 1147 1224 FIBRONECTIN TYPE-III 11.
 FT DOMAIN 1235 1312 FIBRONECTIN TYPE-III 12.
 FT DOMAIN 1328 1539 FIBRINOGEN C-TERMINAL.
 FT DISULFID 171 181 POTENTIAL.
 FT DISULFID 175 186 POTENTIAL.
 FT DISULFID 188 197 POTENTIAL.
 FT DISULFID 202 212 POTENTIAL.
 FT DISULFID 206 217 POTENTIAL.
 FT DISULFID 219 228 POTENTIAL.
 FT DISULFID 233 243 POTENTIAL.
 FT DISULFID 237 248 POTENTIAL.
 FT DISULFID 250 259 POTENTIAL.
 SQ SEQUENCE 1560 AA; 173115 MW; D6C4F46CC086D3A7F CRC64;
 Query Match 63.6%; Score 49; DB 1; Length 1560;
 Best Local Similarity 57.1%; Pred. No. 5.1;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TGLEPGIDYDISVI 14
 Db 411 TGLPGTEYKRTIV 424
 RESULT 12
 TENN HUMAN STANDARD; PRT; 1294 AA.
 ID CA17 HUMAN
 AC Q90Q93;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tenascin N precursor.
 GN TNN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RX NCBI_Taxid=9606;
 RN [1]
 RA Rhoeder S., Bird C.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Involved in neurite outgrowth and cell migration in
 CC hippocampal explants (By similarity).
 CC -!- SIMILARITY: Contains 3 EGF-like domains.
 CC -!- SIMILARITY: Contains 9 fibronectin type III domains.
 CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC EMBL; AL049689; CAB41260.1; -
 DR EMBL; Z99715; CAB16871.1; -
 DR HSPB; P02671; 1P2D.

DR Genew: HGNC:22942; TN.
 DR GO; GO:0016047; P:cell growth; ISS.
 DR GO; GO:0016477; P:cell migration; ISS.
 DR InterPro; IPR006209; EGF-Like.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR InterPro; IPR008957; FN III-Like.
 DR InterPro; IPR003961; FN III.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00147; fibrinogen_C; 1.
 DR Pfam; PF00041; FN3; 9.
 DR SMART; SMO0186; FBG; 1.
 DR SMART; SMO0060; FN3; 6.
 DR PROSITE; PS00022; EGF 1; 3.
 DR PROSITE; PS01186; EGF 2; 2.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
 KW Repeat; EGF-like domain; Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 1294 TENASCIN N.
 FT DOMAIN 162 193 EGF-LIKE 1.
 FT DOMAIN 194 224 EGF-LIKE 2.
 FT DOMAIN 225 255 EGF-LIKE 3.
 FT DOMAIN 257 335 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 346 430 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 438 515 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 526 604 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 615 692 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 703 781 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 792 869 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 880 957 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 968 1045 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1061 1272 FIBRINOGEN C-TERMINAL.
 FT DISULFID 166 176 POTENTIAL.
 FT DISULFID 170 181 POTENTIAL.
 FT DISULFID 183 192 POTENTIAL.
 FT DISULFID 197 207 POTENTIAL.
 FT DISULFID 201 212 POTENTIAL.
 FT DISULFID 214 223 POTENTIAL.
 FT DISULFID 228 238 POTENTIAL.
 FT DISULFID 232 243 POTENTIAL.
 FT DISULFID 245 254 POTENTIAL.
 SQ SEQUENCE 1294 AA; 143445 MW; 5FE3CDA30A3CF8E6 CRC64;
 Query Match 61.0%; Score 47; DB 1; Length 1294;
 Best Local Similarity 57.1%; Pred. No. 9;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TGLEPGIDYDISVI 14
 Db 406 TGLHPGTEYKRTIV 419
 RESULT 13
 CA17 HUMAN STANDARD; PRT; 2944 AA.
 ID CA17 HUMAN
 AC Q02388; Q14054; Q16507;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1(VII) chain precursor (Long-chain collagen) (LC
 DE collagen).
 GN COL7A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RX NCBI_Taxid=9606;
 RN [1]
 RA MEDLINE=94327588; PubMed=8051117;
 RX Christano A.M., Greenspan D.S., Lee S., Uitto J.,
 RT "Cloning of human type VII collagen. Complete primary sequence of the
 RT alpha 1(VII) chain and identification of intergenic polymorphisms."
 RL J. Biol. Chem. 269:20256-20262(1994).
 RN [2]

RP SEQUENCE OF 128-1493 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93338437; PubMed=1307247;
RA Christiano A.M., Rosenbaum L.M., Chung-Honet L.C., Parente M.G.,
RA Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Burgeson R.E.,
RA Uitto J.;
RT "The large non-collagenous domain (NC-1) of type VII collagen is
RT amino-terminal and chimeric. Homology to cartilage matrix protein,
RT the type III domains of fibronectin and the A domains of von
RT Willebrand factor.";
RL Hum. Mol. Genet. 1:475-481(1992).
RN [13]
RP SEQUENCE OF 815-1439 FROM N.A.
RX MEDLINE=91334380; PubMed=1871109;
RA Parente M.G., Chung L.C., Rymaenen J., Woodley D.T., Wynn K.W.,
RA Bauer E.A., Mattei M.-G., Chu M.-L., Uitto J.;
RT "Human type VII collagen: cDNA cloning and chromosomal mapping of the
RT gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:6931-6935(1991).
RN [14]
RP SEQUENCE OF 369-1255 FROM N.A.
RX MEDLINE=93107742; PubMed=1469284;
RA Gammon W.R., Abernethy M.L., Padilla K.M., Prisyavah P.S.,
RA Cook M.E., Wright J., Briggsman R.A., Hunt S.W. III;
RT "Noncollagenous (NC1) domain of collagen VII resembles multidomain
RT adhesion proteins involved in tissue-specific organization of
RT extracellular matrix.";
RL J. Invest. Dermatol. 99:691-696(1992).
RN [15]
RP SEQUENCE OF 340-675 FROM N.A.
RX TISSUE=Keratinocytes;
RC MEDLINE=92231902; PubMed=1567409;
RA Tanaka T., Takahashi K., Furukawa F., Imanura S.;
RT "Molecular cloning and characterization of type VII collagen cDNA.";
RL Biochem. Biophys. Res. Commun. 183:958-963(1992).
RN [16]
RP SEQUENCE OF 2395-2944 FROM N.A.
RX MEDLINE=93271985; PubMed=8499916;
RA Greenspan D.S.;
RT "The carboxyl-terminal half of type VII collagen, including the non-
RT collagenous NC-2 domain and intron/exon organization of the
RT corresponding region of the COL7A1 gene.";
RL Hum. Mol. Genet. 2:273-278(1993).
RN [17]
RP SEQUENCE OF 1-87 FROM N.A.
RX TISSUE=Placenta;
RC MEDLINE=94375010; PubMed=8088784;
RA Christiano A.M., Hoffman G.G., Chung-Honet L.C., Lee S., Cheng W.,
RA Uitto J., Greenspan D.S.;
RT "Structural organization of the human type VII collagen gene (COL7A1),
RT composed of more exons than any previously characterized gene.";
RL Genomics 21:169-179(1994).
RN [18]
RP VARIANT EBDSC ARG-2034.
RX MEDLINE=89227237; PubMed=2653224;
RA Fine J.D., Johnson L., Wright T.;
RT "Epidermolysis bullosa simplex superficialis. A new variant of
RT epidermolysis bullosa characterized by subcorneal skin cleavage
RT mimicking peeling skin syndrome.";
RL Arch. Dermatol. 125:633-638(1989).
RN [19]
RP REVIEW ON DEB VARIANTS.
RX MEDLINE=98041696; PubMed=9375848;
RA Jeevalakhallo A., Pulkkinen L., Uitto J.;
RT "Molecular basis of dystrophic epidermolysis bullosa: mutations in
RT the type VII collagen gene (COL7A1).";
RL Hum. Mutat. 10:338-347(1997).
RN [10]
RP VARIANT DEB LYS-2798.
RX MEDLINE=93291877; PubMed=8513326;
RA Christiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y.,
RA Iin A.N., Dietz H.C., Hovnanian A., Uitto J.;
RT "A missense mutation in type VII collagen in two affected siblings
RT with recessive dystrophic epidermolysis bullosa."

RL Nat. Genet. 4:62-66(1993).
RN [11]
RP VARIANT DEB SER-2040.
RX MEDLINE=94224777; PubMed=8170945;
RA Christiano A.M., Rymaenen M., Uitto J.;
RT "Dominant dystrophic epidermolysis bullosa: identification of a
RT gly--->ser substitution in the triple-helical domain of type VII
RT collagen.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3549-3553(1994).
RN [12]
RP VARIANT DEB CYS-2623.
RX MEDLINE=96081220; PubMed=8541842;
RA Christiano A.M., Lee J.Y.-Y., Chen W.J., Laforgia S., Uitto J.;
RT "Periapical epidermolysis bullosa: genetic linkage to COL7A1 and
RT identification of a glycine-to-cysteine substitution in the triple-
RT helical domain of type VII collagen.";
RL Hum. Mol. Genet. 4:1579-1583(1995).
RN [13]
RP VARIANT DEB ARG-2043.
RX MEDLINE=95164985; PubMed=7861014;
RA Christiano A.M., Morriconi A., Paradisi M., Angelo C., Mazzanti C.,
RA Cavallieri R., Uitto J.;
RT "A glycine-to-arginine substitution in the triple-helical domain of
RT type VII collagen in a family with dominant dystrophic epidermolysis
RT bullosa.";
RL J. Invest. Dermatol. 104:438-440(1995).
RN [14]
RP VARIANTS DEB.
RX MEDLINE=96220218; PubMed=8644729;
RA Christiano A.M., McGrath J.A., Tan K.C., Uitto J.;
RT "Glycine substitutions in the triple-helical region of type VII
RT collagen result in a spectrum of dystrophic epidermolysis bullosa
RT phenotypes and patterns of inheritance.";
RL Am. J. Hum. Genet. 58:671-681(1996).
RN [15]
RP VARIANT DEB ARG-2575.
RX MEDLINE=96154068; PubMed=8592061;
RA Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., Uitto J.;
RT "Molecular basis of recessive dystrophic epidermolysis bullosa:
RT genotype/phenotype correlation in a case of moderate clinical
RT severity.";
RL J. Invest. Dermatol. 106:119-124(1996).
RN [16]
RP VARIANT DEB ARG-1782.
RX MEDLINE=96183562; PubMed=8618018;
RA Christiano A.M., McGrath J.A., Uitto J.;
RT "Influence of the second COL7A1 mutation in determining the
RT phenotypic severity of recessive dystrophic epidermolysis bullosa.";
RL J. Invest. Dermatol. 106:766-770(1996).
RN [17]
RP VARIANT DEB ASP-2073.
RX MEDLINE=96310789; PubMed=8757758;
RA Dunnill M.G.S., McGrath J.A., Richards A.J., Christiano A.M.,
RA Uitto J., Pope F.M., Bady R.A.J.;
RT "Clinicopathological correlations of compound heterozygous COL7A1
RT mutations in recessive dystrophic epidermolysis bullosa.";
RL J. Invest. Dermatol. 107:171-177(1996).
RN [18]
RP VARIANTS DEB TRP-1982; GLY-2008; ALA-2025; GLU-2049; TRP-2063 AND
RP ARG-2575.
RX MEDLINE=97465605; PubMed=9326325;
RA Hovnanian A., Rochat A., Bodemer C., Petit E., Rivers C.A., Prost C.,
RA Freitag S., Christiano A.M., Uitto J., Lathrop M., Barrandon Y.,
RA de Prost Y.;
RT "Characterization of 18 new mutations in COL7A1 in recessive
RT dystrophic epidermolysis bullosa provides evidence for distinct
RT molecular mechanisms underlying defective anchoring fibril
RT formation.";
RL Am. J. Hum. Genet. 61:599-610(1997).
RN [19]
RP VARIANT DEB ARG-1652.
RX MEDLINE=98106792; PubMed=9444387;

FT CARBOHYD 662 662 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 668 668 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 691 691 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 725 725 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 838 838 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1238 AA; 136782 MM; 939479EDC8016835 CRC64;

Query Match 58.4%; Score 45; DB 1; Length 1238;
Best Local Similarity 53.3%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
Db 92 TGLSPGTYSTFSLIS 106

RESULT 15

TENA_PIG STANDARD; PRT; 1746 AA.

AC Q29116; P98142;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Tenascin precursor (TN) (Hexabrachion) (Cytosactin) (Neurectin)

DE (GEMM) (J1) (Motendinous antigen) (Glioma-associated-extracellular

DE matrix antigen) (GP 150-225) (Tenascin-C) (TN-C) (P230).

GN TNC OR HXB.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxId=9823;

RP SEQUENCE FROM N.A. (ISOFORMS MAJOR; MINOR-1 AND MINOR-2).

RC TISSUE=Submaxillary gland;

RC MEDLINE=92104189; PubMed=1722152;

RA Nishi T., Weinstein J., Gillespie W.M., Paulson J.C.;

RT "Complete primary structure of porcine tenascin: detection of

RT tenascin transcript in adult submaxillary glands.";

RL Eur. J. Biochem. 202:643-648(1991).

RN [2]

RP SEQUENCE OF 813-825; 887-917; 998-1011; 1597-1608 AND 1719-1730.

RC TISSUE=Petal brain;

RC MEDLINE=98158323; PubMed=9498558;

RA Wakasuki S., Ho S.H., Arioka M., Yamasaki M., Kitamoto K.;

RT "Isolation and characterization of a 230 kDa protein (p230)

RT specifically expressed in fetal brains: its involvement in neurite

RT outgrowth from rat cerebral cortex neurons grown on monolayer of

RT astrocytes.";

RL J. Biochem. 122:1146-1152(1997).

CC -1- FUNCTION: SAM (substrate-adhesion molecule) that appears to

CC inhibit cell migration. May play a role in supporting the growth

CC of epithelial tumors. Is a ligand for integrins alpha-8/beta-1,

CC alpha-9/beta-1, alpha-V/beta-3 and alpha-V/beta-6.

CC -1- FUNCTION: Plays a role during early brain development particularly

CC in growth cone guidance. Involved in neurite outgrowth from

CC cortical neurons grown on the monolayer of astrocytes.

CC -1- SUBUNIT: Hexameric. A homotrimer may be formed in the triple

CC coiled-coil region and may be stabilized by disulfide linked

CC both ends. Two of such half-hexabrachions may be disulfide linked

CC within the central globule.

CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Comment=isoforms are produced in a tissue and time-specific

CC manner during development;

CC Name=Minor-2;

CC IsoId=Q29116-1; Sequence=Displayed;

CC Name=Major;

CC IsoId=Q29116-2; Sequence=VSP_001416;

CC Name=Minor-1;

CC IsoId=Q29116-3; Sequence=VSP_001417;

CC -1- TISSUE SPECIFICITY: Submaxillary glands and brain.
CC -1- DEVELOPMENTAL STAGE: Predominantly expressed in the embryonic and
CC early postnatal stages. Little or no detection in adult brain.
CC -1- INDUCTION: By TGF-beta.
CC -1- SIMILARITY: Contains 15 EGF-like domains.
CC -1- SIMILARITY: Contains 11 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 fibronogen C-terminal domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X61599; CAA43796.1; -.

DR PIR; S19684; S19694.

DR HSSP; P24821; ITEN.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR002181; Fibronogen C.

DR InterPro; IPR008957; FN III-like.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR002049; Laminin_EGF.

DR Pfam; PF00006; EGF_12.

DR Pfam; PF00147; Fibronogen C_1.

DR Pfam; PF00041; fn3_10.

DR PRINTS; PR00011; EGF1AMININ.

DR SMART; SM00181; EGF_8.

DR SMART; SM00186; FBG_1.

DR SMART; SM00060; FN3_8.

DR PROSITE; PS00022; EGF_1; 15.

DR PROSITE; PS01186; EGF_2; 14.

DR PROSITE; PS50026; EGF_3; 5.

KW Glycoprotein; Cell adhesion; Repeat; EGF-like domain; Coiled coil;

KW Extracellular matrix; Alternative splicing; Signal.

FT SIGNAL 1 22

FT CHAIN 23 1746

FT DOMAIN 23 185

FT DOMAIN 118 145

FT DOMAIN 174 186

FT DOMAIN 187 217

FT DOMAIN 218 249

FT DOMAIN 250 280

FT DOMAIN 281 311

FT DOMAIN 312 342

FT DOMAIN 343 373

FT DOMAIN 374 404

FT DOMAIN 405 435

FT DOMAIN 436 466

FT DOMAIN 467 497

FT DOMAIN 498 528

FT DOMAIN 529 559

FT DOMAIN 560 589

FT DOMAIN 590 620

FT DOMAIN 621 710

FT DOMAIN 711 801

FT DOMAIN 802 891

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FT DOMAIN 1072 1162

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FT DOMAIN 1254 1342

FT DOMAIN 1343 1430

FT DOMAIN 1431 1518

FT DOMAIN 1527 1733

FT DISULFID 64

FT DISULFID 190

FT DISULFID 194

FT DISULFID 207

FT DISULFID 221

FT DISULFID 225

FT DISULFID 236

POTENTIAL.

TENASCIN.

INVOLVED IN HEXAMER FORMATION.

COILED COIL (POTENTIAL).

EGF-LIKE 1 (INCOMPLETE).

EGF-LIKE 2.

EGF-LIKE 3.

EGF-LIKE 4.

EGF-LIKE 5.

EGF-LIKE 6.

EGF-LIKE 7.

EGF-LIKE 8.

EGF-LIKE 9.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 12.

EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 15.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 4.

FIBRONECTIN TYPE-III 5.

FIBRONECTIN TYPE-III 6.

FIBRONECTIN TYPE-III 7.

FIBRONECTIN TYPE-III 8.

FIBRONECTIN TYPE-III 9.

FIBRONECTIN TYPE-III 10.

FIBRINOGEN C-TERMINAL.

INTERCHAIN (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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FT DISULFID 238 247 BY SIMILARITY.
FT DISULFID 252 263 BY SIMILARITY.
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FT DISULFID 563 573 BY SIMILARITY.
FT DISULFID 567 578 BY SIMILARITY.
FT DISULFID 580 589 BY SIMILARITY.
FT DISULFID 594 604 BY SIMILARITY.
FT DISULFID 598 609 BY SIMILARITY.
FT DISULFID 611 620 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 788 788 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1034 1034 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1079 1079 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1121 1121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1354 1354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 1072 1162 Missing (in isoform Major).
FT VARSPPLIC 1072 1253 /Frid=VSP 001416.
FT VARSPPLIC 1072 1253 Missing (in isoform Minor-1).
FT CONFLICT 1007 1007 T -> M (IN REF. 2).
FT SEQUENCE 1746 AA; 191399 MW; 56549B1CFE5E5C88 CRC64;
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Query Match 57.1%; Score 44; DB 1; Length 1746;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 TGLEPGIDYDISV 13
DB 771 TGLAFGEYEYISL 783
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Search completed: September 21, 2004, 05:47:31
Job time : 5.30147 secs

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Alignment Scores:

Pred. No.:	5,096-42	Length:	447
Score:	592.00	Matches:	120
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Best Local Similarity:	98.36%	Mismatches:	1
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DB:	9	Gaps:	0

US-10-001-885-125 (1-121) x AA452397 (1-447)

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QY 1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspProArgValArgThr 20
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QY 21 ThrThgInProProArgGlySerIleProArgInserPheAsnArgGlyHisGly 40
DB 105 ACTACCCAGCCCAAGAGGTAGCATCTCTCGACGAGCTTCTTCAACAGGGGCCATGCT 164
QY 41 AlaProProGlyGlyProGlyProArgGlnGlnAlaGlyAlaArgLeuGlyAla 60
DB 165 GTCCTCCCGAGGGGCTCCGTGGCCCGCCGACAGAGGAGGAGTGC-AGGCTGGGCTGTC 223
QY 60 AgInserProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpH 80
DB 224 TCAGTCCCTTCATGATGACCTCAACCGGACGCTGTAACATGGGCTTTCGGCAGTGCA 283
QY 80 sLeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuPheLeuMetMe 100
DB 284 TCTTGACCAACATGCTGAGAGCCGTCACCTCATCTCTCTCTCTCTCTCTCTCTCATGAT 343
QY 100 cLeuGlyValArgGlyLeuLeuValGlyLeuValIleValIleValSerHisLeuSerG 120
DB 344 GCTTGCTGTTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 403
QY 120 TATG 121
DB 404 GCGG 407

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RESULT 12
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LOCUS BP230010B10B9 Soares normalized bovine placenta Bos taurus cDNA
DEFINITION
ACCESSION AM462809
VERSION AM462809.1 GI:7032977
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 454)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
Larson,J.H.
Bovine ESTs
Unpublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801 USA
Tel.: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross-match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATGACCTCATATAGG
BACKWARD: ATTACCTCATATAGG

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High quality sequence stop: 454.
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/lab_host="DH10B"
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/note="Organ: placenta; Vector: pTRT3fac; Site_1: EcorI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lemmon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "

ORIGIN

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US-10-001-885-125 (1-121) x AA462809 (1-454)

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QY 21 ThrThgInProProArgGlySerIleProArgInserPheAsnArgGlyHisGly 40
DB 149 ACTACCCAG---CAACGCGAGTGTACTCTCTCGACAGAGCTTCTCAATAGGGGCCACCGT 205
QY 41 AlaProProGlyGlyProGlyProArgGlnGlnAlaGlyAlaArgLeuGlyAla 60
DB 206 GCTCTCCCTGGGGGCTCCGCGCCCGCCGACGAGGAGGAGGCTGCTCTCTCT 265
QY 61 gInserProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 80
DB 266 CAGTCCCTTCATGATGACCTCAACCGGACGCTGTAATAGGGCTTCCACAGTGGCAT 325
QY 81 LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuPheLeuMetMe 100
DB 326 CTGGGCAACCAAGCGGTGAGCGGAGCTTCATCTGCTGCTCTCTCTCTCTCTCTCT 385
QY 101 LeuGlyValArgGlyLeuLeuValGlyLeuValIleValIleValSerHisLeuSerGln 120
DB 386 CTGGGAGTGGCGGGGCTCTGCTGTTGGGCGCTCGTCTACCTGCTGCCACCTGAGTCA 445
QY 121 Arg 121
DB 446 CGG 448

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RESULT 13
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DEFINITION 146771 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
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VERSION BE237464.1 GI:9022182
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 468)
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahnenkrug,S.C.,

REFERENCE
AUTHORS

Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
 Chitko-McKown, C.G., Perlea, G., Holt, I., Karanycheva, S., Liang, F.,
 Quackenbush, J., and Keefe, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)

JOURNAL MEDLINE
 PUBMED
 21180013
 11282978
 CONTACT: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -mismatch 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
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 /lab_host="DH10B"
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 embryos."

ORIGIN

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 Pred. No.: 1.83e-40 Length: 468
 Score: 574.50 Matches: 114
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 Query Match: 90.90% Indels: 1
 Gaps: 10

US-10-001-885-125 (1-121) x BE237464 (1-468)

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 QY 101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGln 120
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 BE664644.1 GI:10024339
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 SOURCE
 ORGANISM
 Bos taurus (cow)
 Bos taurus
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 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE
 AUTHORS
 Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Cnaas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
 Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
 Chitko-McKown, C.G., Perlea, G., Holt, I., Karanycheva, S., Liang, F.,
 Quackenbush, J., and Keefe, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)

JOURNAL MEDLINE
 PUBMED
 21180013
 11282978
 CONTACT: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
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 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCACGACG
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 Seq primer: ATTATGCTGACCTATAG.
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 /lab_host="DH10B"
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 /note="Vector: PCMV SPOR6; Site 1: NotI; Site 2: SalI;
 library made from pooled tissue from day 20 and day 40
 embryos."

ORIGIN

Alignment Scores:
 Pred. No.: 2.14e-40 Length: 523
 Score: 574.50 Matches: 114
 Percent Similarity: 94.21% Conservative: 0
 Best Local Similarity: 94.21% Mismatches: 6
 Query Match: 90.90% Indels: 1
 Gaps: 10

US-10-001-885-125 (1-121) x BE664644 (1-523)

QY 1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspProArgValArgThr 20
 Db 79 ATGATTGGAGCTTGGCCAAATGGGAGATTGTGACGATGATGACCCCGCGTACGAAAT 138
 QY 21 ThrThrGlnProProArgGlySerIleProArgGlnSerPheAsnArgGlyHis 40
 Db 139 ACTACCCAG--CCACGCAAGTAGTACTCTCGACAGAGCTTTCTCAATAGGGGCCACGGT 195
 QY 41 AlaProProGlyGlyProGlyProArgGlnGlnIleValGlnIleValGlnIleVal 60
 Db 196 GCTCTCCCTGGGGGGGTCCCGGCCCGCCAGCAGCAGGCGCGCAGGCTGGGTGCTGCT 255
 QY 61 GlnSerProPheAsnAspLeuAsnArgGlnIleValAsnMetGlyPheProGlnTrpHis 80

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Db      256 CAGTCCCTTCATGACCTCAACCGGAGCTGTGATATGGCTCCACAGTGGCAT 315
QY      81 LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMet 100
Db      316 CTGGGCAACCAACGCGGTGGAGCCGCTGACCTCCATCTGCTGCTGCTGCTGCTGATG 375
QY      101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGln 120
Db      376 CTGGGCGGCGGCGGCTCTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 435
QY      121 Arg 121
Db      436 CGG 438

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RESULT 15

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LOCUS      BP046179                      537 bp    mRNA    linear    EST 10-OCT-2000
DEFINITION BP250022B10D2 Soares normalized bovine placenta Bos taurus cDNA
clone BP250022B10D2 5', mRNA sequence.
ACCESSION  BP046179
VERSION     BP046179.1  GI:10763234
KEYWORDS   EST.
SOURCE      Bos taurus (cow)
ORGANISM   Bos taurus

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REFERENCE  1 (bases 1 to 537)
AUTHORS   Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
          Larson,J.H.
TITLE      Bovine ESTs
JOURNAL    Unpublished (2000)
COMMENT    Contact: Lewin, H. A.
          W. M. Keck Center for Comparative and Functional Genomics
          University of Illinois at Urbana-Champaign
          340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
          61801, USA
          Tel: 217 333 5998
          Fax: 217 244 5617
          Email: h-lewin@uiuc.edu

```

```

          Funding for cattle EST sequencing was provided by the USDA National
          Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
          to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
          from Washington University Genome Center. Vector Trimmi g:
          Cross match from Washington University Genome Center PHRAP suite.
          This sequence is vector free and at least 200 bp in length.
          PCR Primers
          FORWARD: TAATGACACTCATATAGAG
          BACKWARD: ATTACCGCTCATTAAG
          Insert Length: 537 Std Error: 0.00
          Plate: BP250022B10 row: D column: 2
          Seq primer: AGCGATACCAATTCACACGGA
          High quality sequence stop: 537.
          Location/Qualifiers

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1. 537
/organism="Bos taurus"
/mol_type="cDNA"
/db_xref="taxon:9913"
/clone="BP250022B10D2"
/sex="female"
/lab_host="DH10B"

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/clone_1ib="Soares normalized bovine placenta"
/note="Organ: placenta; Vector: pTT3pac; Site 1: EcoRI;
Site 2: NotI; The cDNA library was constructed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."

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ORIGIN

Alignment Scores:

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Prid. No.:      2 22e-40      Length:      537
Score:          574.50      Matches:      114

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Percent Similarity: 94.21%
Best Local Similarity: 94.21%
Query Match: 90.90%
DB: 10
US-10-001-885-125 (1-121) x BP046179 (1-537)
Conservative: 0
Mismatch: 6
Indels: 1
Gaps: 1

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QY      1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspAspProArgValArgThr 20
Db      95 ATGTTTCGATCTTGGCCAAATGGGAGATTTGACGAGATGAGACCCCGGTGAGGAT 154
QY      21 ThrThgInProProArgGlySerIleProArgGlnSerPheAsnArgGlyHisGly 40
Db      155 ACTACCCAG--CCAGCAGTGTACTCTCTGACAGACCTTTCTCAATAGGGGCCACGGT 211
QY      41 AlaProProGlyGlyProGlyProArgGlnGlnGlnAlaGlyAlaArgLeuGlyAla 60
Db      212 GCCTCCCTGGGGGGTCCCGGCCCGCCAGCAGCAGGAGCGCCAGGCTGGTCTCT 271
QY      61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 80
Db      272 CAGTCCCTTCAATGACCTCAACCGGACGCTGTGATATGGCTTCCACAGTGGCAT 331
QY      81 LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMet 100
Db      332 CTGGGCAACCAACGCGGTGGAGCCGCTGACCTCCATCTGCTGCTGCTCTCTCATGATG 391
QY      101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValSerHisLeuSerGln 120
Db      392 CTGGGCGTGGCGGCTCTCTGCTGAGGCTCTGCTCTCTCTCTCTCTCTCTCTCTCT 451
QY      121 Arg 121
Db      452 CGG 454

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Search completed: August 22, 2004, 09:53:23
Job time : 2470 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2004, 08:21:50 ; Search time 79 Seconds

(without alignments)
849.988 Million cell updates/sec

Title: US-10-001-885-125

Perfect score: 632

Sequence: 1 MVRILANGELVQDDPRVTR.....GVKGLLVGLVIVLSLQR 121

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 682703 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO.spool/p/US10001885/runat.17082004.151719.25929/app.query.fasta_1.263

-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=p2n.mf -MINMATCH=0.1 -LOOPEXT=0

-LOOPEXT=0 -UNITS=dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.ctd

-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFMT=pco -NOM=ext -HEAPSIZE=900 -MINLEN=0 -MAXLEN=2000000000

-USER=US10001885.@CGN.1.1-105@runat.17082004.151719.25929 -NCPU=6 -ICPU=3

-NO MMAP -LARGEORDER -NRG SCORES=0 -WAIT -DSBLOCCK=100 -LONGIOG

-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA.*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seg.*

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5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seg.*

6: /cgn2_6/ptodata/2/ina/backfile1.seg.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	632	100.0	1049	4	US-09-149-476-58 Sequence 58, Appl
2	551	87.2	483	4	US-09-621-976-864 Sequence 864, Ap
3	503	79.6	519	4	US-09-621-976-3064 Sequence 3064, Ap
4	101	16.0	1383	4	US-09-489-039A-1795 Sequence 1795, Ap
5	93.5	14.8	1032	4	US-09-252-991A-6591 Sequence 6591, Ap
6	93.5	14.8	1329	4	US-09-252-991A-6714 Sequence 6714, Ap
7	93.5	14.8	1656	4	US-09-252-991A-6620 Sequence 6620, Ap
8	93.5	14.8	2469	4	US-09-252-991A-6679 Sequence 6679, Ap
9	85.5	13.5	2010	4	US-09-252-991A-9306 Sequence 9306, Ap
10	85.5	13.5	3729	4	US-09-252-991A-9272 Sequence 9272, Ap
11	84.5	13.4	1550	3	US-09-378-528-1 Sequence 1, Appl1
12	81.5	12.9	1441	1	US-08-136-277-18 Sequence 18, Appl1

13	81.5	12.9	1441	2	US-08-479-403-18	Sequence 18, Appl1
14	81.5	12.9	1441	3	US-08-835-734-18	Sequence 18, Appl1
15	81.5	12.9	2750	1	US-08-136-277-1	Sequence 1, Appl1
16	81.5	12.9	2750	2	US-08-479-403-1	Sequence 1, Appl1
17	81.5	12.9	2750	3	US-08-835-734-1	Sequence 1, Appl1
18	81.5	12.8	1297	2	US-08-727-688-9	Sequence 9, Appl1
19	81.5	12.8	1524	3	US-09-020-956-109	Sequence 109, Appl
20	81.5	12.8	1524	4	US-09-030-607-109	Sequence 109, Appl
21	81.5	12.8	1524	3	US-09-439-513-109	Sequence 109, Appl
22	81.5	12.8	1524	4	US-09-352-616A-109	Sequence 109, Appl
23	81.5	12.8	1524	4	US-09-232-149A-109	Sequence 109, Appl
24	81.5	12.8	1524	4	US-09-159-812-109	Sequence 109, Appl
25	81.5	12.8	1524	4	US-09-636-215-109	Sequence 109, Appl
26	81.5	12.8	1524	4	US-09-685-166A-109	Sequence 109, Appl
27	81.5	12.8	1524	4	US-09-115-453-109	Sequence 109, Appl
28	81.5	12.8	1524	4	US-09-688-489-109	Sequence 109, Appl
29	81.5	12.7	13857	4	US-09-620-312D-75	Sequence 75, Appl
30	79.5	12.6	348	4	US-09-252-991A-13677	Sequence 13677, A
31	79.5	12.6	990	4	US-09-252-991A-1381	Sequence 1381, Ap
32	79.5	12.6	1548	4	US-09-252-991A-2688	Sequence 2688, Ap
33	79.5	12.6	1992	4	US-09-252-991A-13575	Sequence 13575, A
34	79.5	12.6	2175	4	US-09-252-991A-13771	Sequence 13771, A
35	79.5	12.6	2292	4	US-09-252-991A-13657	Sequence 13657, A
36	79.5	12.6	2523	4	US-09-252-991A-2990	Sequence 2990, Ap
37	79.5	12.6	7065	4	US-09-874-923-115	Sequence 115, Ap
38	78.5	12.4	981	4	US-09-252-991A-5003	Sequence 5003, Ap
39	78.5	12.4	1242	4	US-09-372-448A-3	Sequence 3, Appl1
40	78.5	12.4	1818	1	US-08-889-402-6	Sequence 6, Appl1
41	78.5	12.4	1818	1	US-08-889-402-6	Sequence 6, Appl1
42	78.5	12.4	3259	5	PCT-US95-03747-1	Sequence 1, Appl1
43	78.5	12.4	9354	4	US-09-579-181-10	Sequence 10, Appl
44	77.5	12.3	984	4	US-09-252-991A-2798	Sequence 2798, Ap
45	77.5	12.3	1236	4	US-09-252-991A-3079	Sequence 3079, Ap

ALIGNMENTS

RESULT 1	US-09-149-476-58
Sequence 58, Application US/09149476	
Patent No. 6420526	
GENERAL INFORMATION:	
APPLICANT: Rosen et al.	
TITLE OF INVENTION: 186 Human Secreted proteins	
FILE REFERENCE: P2002P1	
CURRENT APPLICATION NUMBER: US/09/149,476	
EARLIER FILING DATE: 1998-09-08	
EARLIER APPLICATION NUMBER: PCT/US98/04493	
EARLIER FILING DATE: 1998-03-06	
EARLIER APPLICATION NUMBER: 60/040,162	
EARLIER FILING DATE: 1997-03-07	
EARLIER APPLICATION NUMBER: 60/040,333	
EARLIER FILING DATE: 1997-03-07	
EARLIER APPLICATION NUMBER: 60/038,621	
EARLIER FILING DATE: 1997-03-07	
EARLIER APPLICATION NUMBER: 60/040,626	
EARLIER FILING DATE: 1997-03-07	
EARLIER APPLICATION NUMBER: 60/040,334	
EARLIER FILING DATE: 1997-03-07	
EARLIER APPLICATION NUMBER: 60/040,336	
EARLIER FILING DATE: 1997-03-07	
EARLIER APPLICATION NUMBER: 60/040,163	
EARLIER FILING DATE: 1997-03-07	
EARLIER APPLICATION NUMBER: 60/047,600	
EARLIER FILING DATE: 1997-05-23	
EARLIER APPLICATION NUMBER: 60/047,615	
EARLIER FILING DATE: 1997-05-23	
EARLIER APPLICATION NUMBER: 60/047,597	
EARLIER FILING DATE: 1997-05-23	
EARLIER APPLICATION NUMBER: 60/047,502	
EARLIER FILING DATE: 1997-05-23	
EARLIER APPLICATION NUMBER: 60/047,633	
EARLIER FILING DATE: 1997-05-23	

[illegible]

EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Alignment Scores:

Pred. No.: 1,26e-55 Length: 1049
Score: 632.00 Matches: 121
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-001-885-125 (1-121) x US-09-149-476-58 (1-1049)

QY 1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspProArgValArgThr 20
DB 116 ATGGTGGGATCTTGGCCAAATGGGAAATCGTGAGAGACGACCCCGAGTGAAGACC 175
QY 21 ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40
DB 176 ACTACCCAGCCACCAAGAGTACATTCCTGACAGGCTTCTTCATATAGGGCCATGGT 235
QY 41 AlaProProGlyGlyProGlyProArgGlnGlnAlaGlyAlaArgLeuGlyAlaAla 60
DB 236 GCTCCCCCAGGGGCTCTGCGCCCGCCAGCAGAGGCAAGTCCAGGCTGGTGTGCT 235
QY 61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 80
DB 296 CAGTCCCCCTTCATATGACCTCAACCGGAGCTGTGAACATGGGCTTCCGAGTGGCAT 355
QY 81 LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuPheLeuLeuMetMet 100
DB 356 CTCGGCAACATGCTGTGAGCCGCTGACCTCCATCTCTCTCTCTCTCTCTCATGATG 415
QY 101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTrpLeuValSerHisLeuSerGln 120
DB 416 CTGTGTGTGTGGCTCTCTCTCTCTCTCTGTGCTGTCTACCTGCTGCCACCTGAGTCAG 475
QY 121 Arg 121
DB 476 CGG 478

RESULT 2

US-09-621-976-864
Sequence 864, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm

SEQ ID NO 864
LENGTH: 483
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 171..482
US-09-621-976-864

Alignment Scores:

Pred. No.: 8.48e-48 Length: 483
Score: 551.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.18% Indels: 0
DB: 4 Gaps: 0

US-10-001-885-125 (1-121) x US-09-621-976-864 (1-483)

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QY 21 ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40
DB 231 ACTACCCAGCCACCAAGAGTACATTCCTGACAGGCTTCTTCATATAGGGCCATGGT 290
QY 41 AlaProProGlyGlyProGlyProArgGlnGlnAlaGlyAlaArgLeuGlyAlaAla 60
DB 291 GCTCCCCCAGGGGCTCTGCGCCCGCCAGCAGGAGTCCAGGCTGGTGTGCTGCT 350
QY 61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 80
DB 351 CAGTCCCCCTTCATATGACCTCAACCGGAGCTGTGAACATGGGCTTCCGAGTGGCAT 410
QY 81 LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuPheLeuLeuMetMet 100
DB 411 CTGGGCAACATGCTGTGAGCCGCTGACCTCCATCTCTCTCTCTCTCTCATGATG 470
QY 101 LeuGlyValArg 104
DB 471 CTGTGTGTGCT 482

RESULT 3

US-09-621-976-3064
Sequence 3064, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3064
LENGTH: 519
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 93..431
US-09-621-976-3064

Alignment Scores:

Pred. No.: 7.28e-43 Length: 519
Score: 503.00 Matches: 99
Percent Similarity: 99.00% Conservative: 0
Best Local Similarity: 99.00% Mismatches: 1
Query Match: 79.59% Indels: 1
DB: 4 Gaps: 0

TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
TITLE OF INVENTION: CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Young & Thompson
STREET: 745 South 23rd Street
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,277
FILING DATE: 15-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: B2272
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1441 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-136-277-18
Alignment Scores:
Pred. No.: 25.2 Length: 1441
Score: 81.50 Matches: 44
Percent Similarity: 32.45% Conservative: 5
Best Local Similarity: 29.14% Mismatches: 42
Query Match: 12.90% Indels: 60
Gaps: 6
US-10-001-885-125 (1-121) x US-08-136-277-18 (1-1441)
QY 13 AspAspAPProArgValArgThrThrGlnProPro----- 25
DB 289 GACACAGGCCCGAGGTGAGACCAATCTTCAGCCACTGCTCACTGCTGCCCC 348
QY 26 -----ArgGlySerIleProArg----- 31
DB 349 AGGACACAGGCCCGAGTCCCTAGCGGAGAGCCAGCCAGTGACATGCGGCTCTCCAG 408
QY 32 -----GlnSerPhePheAsnArgGlyHisGlyAlaProProGlyGly----- 45
DB 409 GCCCGCGCCCTGGCGGGGAAACAGCTGACGCGCCGCTGCTCGTCCGCGGC 468
QY 46 -----ProGlyProArgGlnGln 52
DB 469 CTATGAGGCCCAAGTCTACCCCTGTGTGCGCCAGTGGCTGCCCCGCGCAGGGCTCT 528
QY 53 AlaGlyAlaArgGlyAlaAlaGlnSerProPheAsnAspLeuAsnArgGlnLeuVal 72
DB 529 TCAGCGCGCCCGCGGAGCCACGACAGA-----GGCTCCGG 567
QY 73 AsnMetGlyPheProGlnIlePheIleuGlyAsnHisAlaValGluPro-ValThrSerIle 92
DB 568 GGTGCGCGCGCCAAAGCTGGCAT-----GAACCGGGTATTCTCTGCA 609
QY 92 IleuLeuPheLeuLeuLeuMetLeuGlyValArg-----GlyLe 106
DB 610 GCGGCTCTGTGTGCTCTGCGGCTGCTGCTCCCGGCTCTGTGCGGAGACGGGCT 669

QY 106 IleuLeuValGlyLeuValTyrLeuValSer 116
DB 670 GCTGCGCCCTGACTCGCGCGCTGTGTGAGC 700
RESULT 13
US-08-479-403-18
Sequence 18, Application US/08479403
Patent No. 5869039
GENERAL INFORMATION:
APPLICANT: MANDEL, Jean-Louis
APPLICANT: AUBOURG, Patrick
APPLICANT: MOSSER, Jean
APPLICANT: SARDE, Claude
TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Young & Thompson
STREET: 745 South 23rd Street
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,403
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: B2272DIV
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1441 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-479-403-18
Alignment Scores:
Pred. No.: 25.2 Length: 1441
Score: 81.50 Matches: 44
Percent Similarity: 32.45% Conservative: 5
Best Local Similarity: 29.14% Mismatches: 42
Query Match: 12.90% Indels: 60
Gaps: 6
US-10-001-885-125 (1-121) x US-08-479-403-18 (1-1441)
QY 13 AspAspAPProArgValArgThrThrGlnProPro----- 25
DB 289 GACACAGGCCCGAGGTGAGACCAATCTTCAGCCACTGCTCACTGCTGCCCC 348
QY 26 -----ArgGlySerIleProArg----- 31
DB 349 AGGACACAGGCCCGAGTCCCTAGCGGAGAGCCAGCCAGTGACATGCGGCTCTCCAG 408
QY 32 -----GlnSerPhePheAsnArgGlyHisGlyAlaProProGlyGly----- 45
DB 409 GCCCGCGCCCTGGCGGGGAAACAGCTGACGCGCCGCTGCTCGTCCGCGGC 468
QY 46 -----ProGlyProArgGlnGln 52

Db 469 CTATGAGGCCCAAAAGTCACTACCCCTGTGTGGCCAGTCGCTGGACCCCGGCAAGGGTCT 528
Qy 53 ALaGlyValArgLeuGlyValAlaIleInserProPheAnaApyLeuAnaGlyLeuVal 72
Db 529 TCAGGGGCCCCGCGGGAGCCACGAGGA-----GGCTTCGG 567
Qy 73 AsMetGlyPheProGlnTrpHisLeuGlyAsnHisAlaValGluPro-ValThrSerIle 92
Db 568 GGTCTGGGGGGGCCCAAGCTGGCAT-----GAACGGGGATTTCCTGCA 609
Qy 92 eLeuLeuLeuPheLeuLeuMetLeuGlyValArg-----GlyLe 106
Db 610 GCGGCTCTGTGTGCTCTCTCGGCTGTGTTCCCGGGGCTGCTGTGCGCGAGACGGGGCT 669
Qy 106 uLeuLeuValGlyLeuValTyrLeuValSer 116
Db 670 GCTGGCCCTTGCACTCGGCGCCCTGTGTAGC 700

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1      RESULT 14 734-18
2      US-08-835-734-18
3      Sequence 18, Application US/08835734
4      Patent No. 6013769
5      GENERAL INFORMATION:
6      APPLICANT: MANDEL, Jean-Louis
7      APPLICANT: AUBOURG, Patrick
8      APPLICANT: MOSSER, Jean
9      APPLICANT: SARDE, Claude
10     TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
11     TITLE OF INVENTION: CORRESPONDING PROTEIN
12     NUMBER OF SEQUENCES: 23
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: Young & Thompson
15     STREET: 745 South 23rd Street
16     CITY: Arlington
17     STATE: VA
18     COUNTRY: USA
19     ZIP: 22202
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: Patent In Release #1.0, Version #1.25
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/08/835,734
27     FILING DATE:
28     CLASSIFICATION: 536
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: US 08/479,403
31     FILING DATE: 07-JUN-1995
32     ATTORNEY/AGENT INFORMATION:
33     NAME: PATCH, Andrew J.
34     REGISTRATION NUMBER: 32,925
35     REFERENCE/DOCKET NUMBER: B2272DIV
36     TELECOMMUNICATION INFORMATION:
37     TELEPHONE: 703-521-2297
38     TELEFAX: 703-685-0573
39     TELEX: 248425 EMBON
40     INFORMATION FOR SEQ ID NO: 18:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 1441 base pairs
43     TYPE: nucleic acid
44     STRANDEDNESS: single
45     TOPOLOGY: linear
46     MOLECULE TYPE: DNA (genomic)
47     US-08-835-734-18

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Pred. No.:	25.2
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Percent Similarity:	32.45%
Best Local Similarity:	29.14%
Query Match:	12.90%
Length:	1441
Matches:	44
Conservative:	5
Mismatches:	42
Indels:	60

DB:	3	Gaps:	6
US-10-001-885-125 (1-121) x US-08-835-734-18 (1-1441)			
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DB	289	GACAAACAGCGCCAGGGTCAGAACCAACATCCTTCACGACCTGCACTGCTGCCCC	348
QY	26	-----ArgGlySerLeuProArg-----	31
DB	349	AGGACACACAGCCCAAGTCCTTAGCGGGCAGACGCCACAGTACATGCGCGGTCTTCAG	408
QY	32	-----GlnSerPhePheAsnArgGlyHisGlyAlaProProGlyGly-----	45
DB	409	GCCCGCGCCCTGAGCGGGGAAACACGCTAGACGACGCGCGCTGCTCGGCGCTCGCGGC	468
QY	46	-----ProGlyProArgGlnGlnGln	52
DB	469	CTATGAGAGCCCAACAAAGTCTACCCCTTGGTGGGCCAGTGCGTGGCCGCGCAGGAGTCT	528
QY	53	AlAGlyValArgLeuGlyValAlaGlnSerProPheAsnAspLeuAsnArgGlnLeuVal	72
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DB	529	TCAGGGGCGCCCGCGGGGAGCCACGACGAGA-----GGCTTCGG	567
QY	73	AsnMetGlyPheProGlnTrpHisLeuGlyAsnHisAlaValGluPro-ValThrSerI	92
DB	568	GCTGGCGGGCGGCCAAGCTGGCAT-----GAACGGGATATCTCGCA	609
QY	92	eLeuLeuLeuPheLeuLeuMetLeuGlyValArg-----GlyLe	106
		:::	
DB	610	GCGGCTCTCGTGGCTCTCTCGGCTCTCTCTTCGCCCGGGTCTGTGCGGGAGACGAGGAGCT	669
QY	106	uLeuLeuValGlyLeuValTrpLeuValSer	116
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DB	670	GCTGGCCCTGCACTCGGCGCGCTTGATAGC	700

RESULT 15
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 ; Sequence 1, Application US/08136277
 ; Patent No. 5644045
 ; GENERAL INFORMATION:
 ; APPLICANT: MANDEL, Jean-Louis
 ; APPLICANT: AUBOURG, Patrick
 ; APPLICANT: MOSSER, Jean
 ; APPLICANT: SARDE, Claude
 ; TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
 ; TITLE OF INVENTION: CORRESPONDING PROTEIN
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Young & Thompson
 ; STREET: 745 South 23rd Street
 ; CITY: Arlington
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/136,277
 ; FILING DATE: 15-OCT-1993
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PATCH, Andrew J.
 ; REGISTRATION NUMBER: 32,925
 ; REFERENCE/DOCKET NUMBER: B2272
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-521-2297
 ; TELEFAX: 703-685-0573
 ; TELEX: 248425 EMBON
 ; INFORMATION FOR SEQ ID NO: 1:

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2750 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 387..2624
US-08-136-277-1

Alignment Scores:
Pred. No.: 57.3 Length: 2750
Score: 81.50 Matches: 44
Percent Similarity: 32.45% Conservative: 5
Best Local Similarity: 29.14% Mismatches: 42
Query Match: 12.90% Indels: 60
DB: 1 Gaps: 6

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QY 26 -----ArgGlySerIleProArg----- 31
DB 344 AGGACACAGCCCACTCCCTACGCGGACGACCCAGCGATGCCGATCTCCAG 403
QY 32 -----GlnSerPhePheAsnArgGlyHisGlyAlaProProGlyGly----- 45
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QY 46 -----ProGlyProArgGlnGln 52
DB 464 CTATGAGCCCAACAAAGTCTACCCCTTGTCGCGCAGTGCCTGCGCGGAGGTCT 523
QY 53 AlaGlyAlaArgLeuGlyAlaAlaGlnSerProPheAsnAspLeuAsnArgGlnLeuVal 72
DB 524 TCAGGCGCGCCCGCGGAGCCACGACGAGA-----GGCTCCGG 562
QY 73 AsnMetGlyPheProGlnTrpHisLeuGlyAsnHisAlaValGluPro-ValThrSerIle 92
DB 563 GATGCGCGCGGCGCAAGCTGCGAT-----GAACCGGATATTCCTGCA 604
QY 92 eleuLeuLeuPheLeuLeuMetMetLeuGlyValArg-----GlyLe 106
DB 605 GCGGCTCTGTGGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 664
QY 106 uLeuLeuValGlyLeuValTyrLeuValSer 116
DB 665 GCTGCGCTGCACTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695
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Search completed: August 22, 2004, 09:54:52
Job time : 83 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 22, 2004, 09:14:46 ; Search time 360 Seconds

(without alignments)
1651.023 Million cell updates/sec

Title: US-10-001-885-125

Perfect score: 632

Sequence: 1 MVRILANGELVQDDPRVTR.....GVRGLLVGLVIVSHLSQR 121

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Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 3228839 seqs, 245606551 residues

Total number of hits satisfying chosen parameters: 645678

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62
-TRANS=trans40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US1001885@cgn2_1.1.723/runat_17082004_151721_26002
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
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1	632	100.0	365	15	US-10-076-747-65	Sequence 65, Appl
2	632	100.0	1049	10	US-09-809-391-58	Sequence 58, Appl
3	632	100.0	1049	13	US-09-882-171-58	Sequence 58, Appl
4	632	100.0	1049	13	US-10-164-861-58	Sequence 58, Appl
5	632	100.0	1052	16	US-10-302-172-94	Sequence 94, Appl
6	632	100.0	1108	13	US-10-264-237-619	Sequence 619, Appl
7	632	100.0	1192	13	US-10-001-885-31	Sequence 31, Appl
8	110.5	17.5	2594	16	US-10-108-260A-439	Sequence 1439, Ap
9	107	16.9	2668	14	US-10-071-766-116	Sequence 116, Ap
10	100	15.8	1233	17	US-10-437-963-11056	Sequence 12056, A
11	99.5	15.7	669	15	US-10-156-761-3430	Sequence 3430, Ap
12	99.5	15.7	9025608	15	US-10-156-761-1	Sequence 1, Appl1
13	98.5	15.6	2361	17	US-10-437-963-80030	Sequence 80030, A
14	94.5	15.0	738	13	US-10-389-647-274	Sequence 274, App
15	90.5	14.3	9025608	15	US-10-156-761-1	Sequence 1, Appl1
16	89.5	14.2	576	13	US-10-027-632-125723	Sequence 125723,
17	89.5	14.2	576	16	US-10-027-632-125723	Sequence 158, App
18	89	14.1	4177	13	US-10-221-278-158	Sequence 158, App
19	89	14.1	4177	16	US-10-291-172-158	Sequence 10, Appl
20	89	14.1	4351	15	US-10-251-186-10	Sequence 4038, Ap
21	88.5	14.0	2172	9	US-09-815-242-4038	Sequence 7386, Ap
22	88.5	14.0	2172	13	US-10-282-132A-7386	Sequence 7, Appl1
23	88.5	14.0	2172	15	US-10-246-330-7	Sequence 1744, Ap
24	88	13.9	53885	13	US-10-087-192-1744	Sequence 112, App
25	86.5	13.7	397	17	US-10-322-281-112	Sequence 63692, A
26	86.5	13.7	397	17	US-10-437-963-63692	Sequence 30941, A
27	86.5	13.7	484	10	US-09-918-995-30941	Sequence 258, App
28	86.5	13.7	2332	16	US-10-108-260A-258	Sequence 601, App
29	86.5	13.6	2417	17	US-09-823-245A-601	Sequence 42670, A
30	86	13.6	1647	13	US-10-437-963-42670	Sequence 41632, A
31	85.5	13.5	416	13	US-10-424-559-31632	Sequence 41632, Ap
32	85	13.4	817	16	US-10-260-238-4633	Sequence 21, Appl
33	85	13.4	2507	17	US-10-664-705-21	Sequence 84668, A
34	85	13.4	2511	17	US-10-437-963-84668	Sequence 40534, A
35	85	13.4	4500	17	US-10-437-963-40534	Sequence 9856, Ap
36	85	13.4	8031	10	US-09-764-891-9856	Sequence 283755,
37	85	13.4	8066	10	US-09-764-891-9856	Sequence 283755,
38	84.5	13.4	423	13	US-10-027-632-283755	Sequence 26612, A
39	84.5	13.4	423	16	US-10-027-632-283755	Sequence 35, Appl
40	84.5	13.4	1024	13	US-10-425-114-4848	Sequence 3686, App
41	84.5	13.4	1091	13	US-10-425-114-26612	
42	84.5	13.4	1170	13	US-10-243-552-4	
43	84.5	13.4	1484	17	US-10-471-115-35	
44	84.5	13.4	1550	9	US-09-880-107-3686	
45	84.5	13.4	1550	9	US-09-954-531-166	

ALIGNMENTS

RESULT 1
US-10-076-747-65
; Sequence 65, Application US/10076747
; Publication No. US20030180726A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Hervé
APPLICANT: Kaira, Kalpana
APPLICANT: Cafferty, Robert
APPLICANT: Sun, Yorgming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and P
FILE REFERENCE: DEX-0315
CURRENT APPLICATION NUMBER: US/10/076,747
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,290
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/268,834
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1

SEQ ID NO 65
LENGTH: 365
TYPE: DNA
ORGANISM: Homo sapien
US-10-076-747-65

Alignment Scores:
Pred. No.: 2,19e-67 Length: 365
Score: 632.00 Matches: 121
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

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QY 21 ThrTngInProProArgGlySerIleProArgGlnSerPheAsnArgGlyHisGly 40
DB 61 ACTACCCAGCCACCAAGAGTGAATCTCTGACAGAGCTTCTTCAATAGGGCCATGCT 120
QY 41 AlaProProGlyGlyProGlyProArgGlnGlnAlaGlyAlaArgLeuGlyAlaAla 60
DB 121 GCTCCCCCAGGGGGTCTGGCCCCCGCAGCAGCAGGAGTGCAGGCTGGTGGCT 180
QY 61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 80
DB 181 CAGTCCCCCTTCAATGACCTCAACCGCAGCTGGTGAACATGGGCTTTCGACGTGGCAT 240
QY 81 LeuGlyAsnHisAlaValGlnProValThrSerIleLeuLeuPheLeuMetMet 100
DB 241 CTCGGCAACCATCTGTGGAGCCGCTGACCTCCATCTCTCTCTCTCTCATGATG 300
QY 101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuValIleLeuValSerHisLeuSerGln 120
DB 301 CTGGGTGTTGGTGGCTCTCTCTGGTGGCTTGTCTACCTGCTGCCACCTGATGATG 360
QY 121 Arg 121
DB 361 CGG 363

RESULT 2

US-09-809-391-58
Sequence 58, Application US/09809391
Publication No. US20030049618A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 1049
TYPE: DNA
ORGANISM: Homo sapiens
US-09-809-391-58

Alignment Scores:

Pred. No.: 8.49e-67 Length: 1049
Score: 632.00 Matches: 121
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-001-885-125 (1-121) x US-09-809-391-58 (1-1049)

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QY 21 ThrTngInProProArgGlySerIleProArgGlnSerPheAsnArgGlyHisGly 40
DB 176 ACTACCCAGCCACCAAGAGTGAATCTCTGACAGAGCTTCTTCAATAGGGCCATGCT 235
QY 41 AlaProProGlyGlyProGlyProArgGlnGlnAlaGlyAlaArgLeuGlyAlaAla 60
DB 236 GCTCCCCCAGGGGGTCTGGCCCCCGCAGCAGCAGGAGTGCAGGCTGGTGGCT 295
QY 61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 80
DB 296 CAGTCCCCCTTCAATGACCTCAACCGCAGCTGTGAACATGGGCTTTCGACGTGGCAT 355
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DB 356 CTCGGCAACCATCTGTGGAGCCGCTGACCTCCATCTCTCTCTCTCTCATGATG 415
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DB 476 CGG 478

RESULT 3

US-09-882-171-58
Sequence 58, Application US/09882171
Publication No. US20030175858A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
Prior application number: 09/809,391
Prior filing date: 2001-03-16
Prior application number: 09/149,476
Prior filing date: 1998-09-08
Prior application number: PCT/US98/04493
Prior filing date: 1998-03-06
Prior application number: 60/040,162
Prior filing date: 1997-03-07
Prior application number: 60/040,333
Prior filing date: 1997-03-07
Prior application number: 60/038,621
Prior filing date: 1997-03-07
Prior application number: 60/040,626
Prior filing date: 1997-03-07
Prior application number: 60/040,334
Prior filing date: 1997-03-07
Prior application number: 60/040,336
Prior filing date: 1997-03-07
Prior application number: 60/040,163
Prior filing date: 1997-03-07
Prior application number: 60/047,600
Prior filing date: 1997-05-23
Prior application number: 60/047,615
Prior filing date: 1997-05-23
Prior application number: 60/047,597
Prior filing date: 1997-05-23
Prior application number: 60/047,502
Prior filing date: 1997-05-23
Prior application number: 60/047,633
Prior filing date: 1997-05-23
Prior application number: 60/047,583
Prior filing date: 1997-05-23
Prior application number: 60/047,617
Prior filing date: 1997-05-23
Prior application number: 60/047,618

1 PRIOR FILING DATE: 1997-05-23
2 PRIOR APPLICATION NUMBER: 60/047,503
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6 PRIOR APPLICATION NUMBER: 60/047,581
7 PRIOR FILING DATE: 1997-05-23
8 PRIOR APPLICATION NUMBER: 60/047,584
9 PRIOR FILING DATE: 1997-05-23
10 PRIOR APPLICATION NUMBER: 60/047,500
11 PRIOR FILING DATE: 1997-05-23
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14 PRIOR APPLICATION NUMBER: 60/047,492
15 PRIOR FILING DATE: 1997-05-23
16 PRIOR APPLICATION NUMBER: 60/047,598
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18 PRIOR APPLICATION NUMBER: 60/047,613
19 PRIOR FILING DATE: 1997-05-23
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21 PRIOR FILING DATE: 1997-05-23
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23 PRIOR FILING DATE: 1997-05-23
24 PRIOR APPLICATION NUMBER: 60/047,612
25 PRIOR FILING DATE: 1997-05-23
26 PRIOR APPLICATION NUMBER: 60/047,632
27 PRIOR FILING DATE: 1997-05-23
28 PRIOR APPLICATION NUMBER: 60/047,601
29 PRIOR FILING DATE: 1997-05-23
30 PRIOR APPLICATION NUMBER: 60/043,580
31 PRIOR FILING DATE: 1997-04-11
32 PRIOR APPLICATION NUMBER: 60/043,568
33 PRIOR FILING DATE: 1997-04-11
34 PRIOR APPLICATION NUMBER: 60/043,314
35 PRIOR FILING DATE: 1997-04-11
36 PRIOR APPLICATION NUMBER: 60/043,569
37 PRIOR FILING DATE: 1997-04-11
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39 PRIOR FILING DATE: 1997-04-11
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50 PRIOR APPLICATION NUMBER: 60/043,672
51 PRIOR FILING DATE: 1997-04-11
52 PRIOR APPLICATION NUMBER: 60/043,315
53 PRIOR FILING DATE: 1997-04-11
54 PRIOR APPLICATION NUMBER: 60/048,974
55 PRIOR FILING DATE: 1997-06-06
56 PRIOR APPLICATION NUMBER: 60/056,886
57 PRIOR FILING DATE: 1997-08-22
58 PRIOR APPLICATION NUMBER: 60/056,877
59 PRIOR FILING DATE: 1997-08-22
60 PRIOR APPLICATION NUMBER: 60/056,889
61 PRIOR FILING DATE: 1997-08-22
62 PRIOR APPLICATION NUMBER: 60/056,893
63 PRIOR FILING DATE: 1997-08-22
64 PRIOR APPLICATION NUMBER: 60/056,630
65 PRIOR FILING DATE: 1997-08-22
66 PRIOR APPLICATION NUMBER: 60/056,878
67 PRIOR FILING DATE: 1997-08-22
68 PRIOR APPLICATION NUMBER: 60/056,662
69 PRIOR FILING DATE: 1997-08-22
70 PRIOR APPLICATION NUMBER: 60/056,872
71 PRIOR FILING DATE: 1997-08-22
72 PRIOR APPLICATION NUMBER: 60/056,882
73 PRIOR FILING DATE: 1997-08-22

74 PRIOR APPLICATION NUMBER: 60/056,637
75 PRIOR FILING DATE: 1997-08-22
76 PRIOR APPLICATION NUMBER: 60/056,903
77 PRIOR FILING DATE: 1997-08-22
78 PRIOR APPLICATION NUMBER: 60/056,888
79 PRIOR FILING DATE: 1997-08-22
80 PRIOR APPLICATION NUMBER: 60/056,879
81 PRIOR FILING DATE: 1997-08-22
82 PRIOR APPLICATION NUMBER: 60/056,880
83 PRIOR FILING DATE: 1997-08-22
84 PRIOR APPLICATION NUMBER: 60/056,894
85 PRIOR FILING DATE: 1997-08-22
86 PRIOR APPLICATION NUMBER: 60/056,911
87 PRIOR FILING DATE: 1997-08-22
88 PRIOR APPLICATION NUMBER: 60/056,636
89 PRIOR FILING DATE: 1997-08-22
90 PRIOR APPLICATION NUMBER: 60/056,874
91 PRIOR FILING DATE: 1997-08-22
92 PRIOR APPLICATION NUMBER: 60/056,910
93 PRIOR FILING DATE: 1997-08-22
94 PRIOR APPLICATION NUMBER: 60/056,864
95 PRIOR FILING DATE: 1997-08-22
96 PRIOR APPLICATION NUMBER: 60/056,631
97 PRIOR FILING DATE: 1997-08-22
98 PRIOR APPLICATION NUMBER: 60/056,845
99 PRIOR FILING DATE: 1997-08-22
100 PRIOR APPLICATION NUMBER: 60/056,892
101 PRIOR FILING DATE: 1997-08-22
102 PRIOR APPLICATION NUMBER: 60/057,761
103 PRIOR FILING DATE: 1997-08-22
104 PRIOR APPLICATION NUMBER: 60/047,595
105 PRIOR FILING DATE: 1997-05-23
106 PRIOR APPLICATION NUMBER: 60/047,588
107 PRIOR FILING DATE: 1997-05-23
108 PRIOR APPLICATION NUMBER: 60/047,585
109 PRIOR FILING DATE: 1997-05-23
110 PRIOR APPLICATION NUMBER: 60/047,586
111 PRIOR FILING DATE: 1997-05-23
112 PRIOR APPLICATION NUMBER: 60/047,590
113 PRIOR FILING DATE: 1997-05-23
114 PRIOR APPLICATION NUMBER: 60/047,594
115 PRIOR FILING DATE: 1997-05-23
116 PRIOR APPLICATION NUMBER: 60/047,589
117 PRIOR FILING DATE: 1997-05-23
118 PRIOR APPLICATION NUMBER: 60/047,593
119 PRIOR FILING DATE: 1997-05-23
120 PRIOR APPLICATION NUMBER: 60/047,614
121 PRIOR FILING DATE: 1997-05-23
122 PRIOR APPLICATION NUMBER: 60/043,578
123 PRIOR FILING DATE: 1997-04-11
124 PRIOR APPLICATION NUMBER: 60/043,576
125 PRIOR FILING DATE: 1997-04-11
126 PRIOR APPLICATION NUMBER: 60/047,501
127 PRIOR FILING DATE: 1997-05-23
128 PRIOR APPLICATION NUMBER: 60/043,670
129 PRIOR FILING DATE: 1997-04-11
130 PRIOR APPLICATION NUMBER: 60/056,632
131 PRIOR FILING DATE: 1997-08-22
132 PRIOR APPLICATION NUMBER: 60/056,664
133 PRIOR FILING DATE: 1997-08-22
134 PRIOR APPLICATION NUMBER: 60/056,876
135 PRIOR FILING DATE: 1997-08-22
136 PRIOR APPLICATION NUMBER: 60/056,881
137 PRIOR FILING DATE: 1997-08-22
138 PRIOR APPLICATION NUMBER: 60/056,909
139 PRIOR FILING DATE: 1997-08-22
140 PRIOR APPLICATION NUMBER: 60/056,875
141 PRIOR FILING DATE: 1997-08-22
142 PRIOR APPLICATION NUMBER: 60/056,862
143 PRIOR FILING DATE: 1997-08-22
144 PRIOR APPLICATION NUMBER: 60/056,887

PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-05

Alignment Scores:

Pred. No.:	8,49e-67	Length:	1049
Score:	632.00	Matches:	121
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	10	Gaps:	0

US-10-001-885-125 (1-121) x US-09-882-171-58 (1-1049)

QY 1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspProArgValArgThr 20
DB 116 ATGATCGCGATCTTGCCCAATGGGGAAATCGTCAGAGACGACGCCCGAGTGAAGACC 175
QY 21 ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgIleValArg 40
DB 176 ACTACCCAGCCACCAAGAGTGAATCTCTCGACAGAGCTTCTTCATATAGGGGCATGAT 235
QY 41 AlaProProGlyGlyProGlyProArgGlnGlnIleValArgValArgValArgValArg 60
DB 236 GCTCCCCCAGGGGGCTCGGCCCGCCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAG 295
QY 61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 80
DB 296 CAGTCCCTTCATAGACTCAACCGGACGCTGTGAACATGAGGCTTCCGCGATGCGCAT 355
QY 81 LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuMetMet 100
DB 356 CTCGGCAACCAATGCTGTGAGCCGCTGACCTCCATCCGCTCTCTCTCTCTCTCTCT 415
QY 101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuValIleValValSerHisLeuSerGln 120
DB 416 CTGGTGTCTTGGGCT 475
QY 121 Arg 121
DB 476 CGG 478

RESULT 4

US-10-164-861-58
Sequence 58, Application US/10164861
Publication No. US20030225248A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 166 Human Secreted proteins
FILE REFERENCE: P2002p1
CURRENT APPLICATION NUMBER: US/10/164,861
PRIOR FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 1049
TYPE: DNA
ORGANISM: Homo sapiens
US-10-164-861-58

Pred. No.: 8,49e-67 Length: 1049
Score: 632.00 Matches: 121
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-001-885-125 (1-121) x US-10-164-861-58 (1-1049)

QY 1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspProArgValArgThr 20
DB 116 ATGATCGCGATCTTGCCCAATGGGGAAATCGTCAGAGACGACGCCCGAGTGAAGACC 175
QY 21 ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgIleValArg 40
DB 176 ACTACCCAGCCACCAAGAGTGAATCTCTCGACAGAGCTTCTTCATATAGGGGCATGAT 235
QY 41 AlaProProGlyGlyProGlyProArgGlnGlnIleValArgValArgValArgValArg 60
DB 236 GCTCCCCCAGGGGGCTCGGCCCGCCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAG 295
QY 61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValAsnMetGlyPheProGlnTrpHis 80
DB 296 CAGTCCCTTCATAGACTCAACCGGACGCTGTGAACATGAGGCTTCCGCGATGCGCAT 355
QY 81 LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuMetMet 100
DB 356 CTCGGCAACCAATGCTGTGAGCCGCTGACCTCCATCCGCTCTCTCTCTCTCTCTCT 415
QY 101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuValIleValValSerHisLeuSerGln 120
DB 416 CTGGTGTCTTGGGCT 475
QY 121 Arg 121
DB 476 CGG 478

RESULT 5

US-10-302-172-94
Sequence 94, Application US/10302172
Publication No. US20040053250A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Dymnac, Radoje T.
TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids and
FILE REFERENCE: 803 ICNCP
CURRENT APPLICATION NUMBER: US/10/302,172
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 950
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 94
LENGTH: 1052
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (365)..(508)
US-10-302-172-94

Alignment Scores:

Pred. No.:	8,52e-67	Length:	1052
Score:	632.00	Matches:	121
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
	0	Indels:	0
	0	Gaps:	0

DB: 13 Gaps: 0

US-10-001-885-125 (1-121) x US-10-302-172-94 (1-1052)

QY 1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspAspProArgValArgThr 20

DB 146 ATGGTGGGATCTTGGCCAAATGGGAAATCTGCAGACGACCCCGAGTGAAGACC 205

QY 21 ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40

DB 206 ACTACCCAGCCACCAAGAGGTAGCATTCCTCGACGAGACTTCTCAATAGGGGCGCATGT 265

QY 41 AlaProProGlyGlyProGlyProArgGlnGlnGlnIleValIleValIleValIleVal 60

DB 266 GCTCCCGCAGGGGGGTCTGGCCCGCCGACGAGGAGGTGCGAGGCTGGGTGGTCT 325

QY 61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValIleValIleValIleValIleVal 80

DB 326 CAGTCCCGCTTCAATGACCTCAACCGGAGCTGTGTGAACATGGGCTTCCGCAATGGCAT 385

QY 81 LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMet 100

DB 386 CTCGGCAACCAATGCTGTGAGCCGCGTGAACCTCCATCCCTGCTCTGCTGATGATG 445

QY 101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValIleSerHisLeuSerGln 120

DB 446 CTGGTGTTCGTGGCTCTCTCTGTTGGCTTGTCTTACCTGTGTCTCCACCTGAGTCA 505

QY 121 Arg 121

DB 506 CGG 508

RESULT 6

US-10-264-237-619

/ Sequence 619, Application US/10264237

/ Publication No. US20040009491A1

/ GENERAL INFORMATION:

/ APPLICANT: Birse et al.

/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

/ FILE REFERENCE: PA313P1

/ CURRENT APPLICATION NUMBER: US/10/264,237

/ PRIOR FILING DATE: 2002-10-04

/ PRIOR APPLICATION NUMBER: PCT/US01/16450

/ PRIOR FILING DATE: 2001-05-18

/ PRIOR APPLICATION NUMBER: US 60/205,515

/ PRIOR FILING DATE: 2000-05-19

/ NUMBER OF SEQ ID NOS: 2876

/ SOFTWARE: PatentIn Ver. 3.1

/ SEQ ID NO 619

/ LENGTH: 1108

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ PEATTRE:

/ NAME/KEY: misc feature

/ LOCATION: (1101)..(1101)

/ OTHER INFORMATION: n equals a,t,g, or c

US-10-264-237-619

Alignment Scores:

Pred. No.: 91e-67 Length: 1108

Score: 632.00 Matches: 121

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 16 Gaps: 0

US-10-001-885-125 (1-121) x US-10-264-237-619 (1-1108)

QY 1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspAspProArgValArgThr 20

DB 147 ATGGTGGGATCTTGGCCAAATGGGAAATCTGCAGACGACCCCGAGTGAAGACC 206

QY 21 ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40

DB 207 ACTACCCAGCCACCAAGAGGTAGCATTCCTCGACGAGACTTCTCAATAGGGGCGCATGT 266

QY 41 AlaProProGlyGlyProGlyProArgGlnGlnGlnIleValIleValIleValIleVal 60

DB 267 GCTCCCGCAGGGGGGTCTGGCCCGCCGACGAGGAGGTGCGAGGCTGGGTGGTCT 326

QY 61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValIleValIleValIleValIleVal 80

DB 327 CAGTCCCGCTTCAATGACCTCAACCGGAGCTGTGTGAACATGGGCTTCCGCAATGGCAT 386

QY 81 LeuGlyAsnHisAlaValGluProValThrSerIleLeuLeuLeuPheLeuLeuMetMet 100

DB 387 CTGGCAACCAATGCTGTGAGCCGCGTGAACCTCCATCCCTGCTCTGCTGATGATG 446

QY 101 LeuGlyValArgGlyLeuLeuLeuValGlyLeuValTyrLeuValIleSerHisLeuSerGln 120

DB 447 CTGGTGTTCGTGGCTCTCTCTGTTGGCTTGTCTTACCTGTGTCTCCACCTGAGTCA 506

QY 121 Arg 121

DB 507 CGG 509

RESULT 7

US-10-001-885-31

/ Sequence 31, Application US/10001885

/ Publication No. US20040058319A1

/ GENERAL INFORMATION:

/ APPLICANT: Saiceda, Susana

/ APPLICANT: Macina, Roberto

/ APPLICANT: Racipon, Hervé

/ APPLICANT: Cafferey, Robert

/ APPLICANT: Sun, Yongsang

/ APPLICANT: Liu, Chenghua

/ TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro

/ FILE REFERENCE: DEX-0279

/ CURRENT APPLICATION NUMBER: US/10/001,885

/ PRIOR FILING DATE: 2001-11-20

/ PRIOR APPLICATION NUMBER: 60/252,061

/ PRIOR FILING DATE: 2000-11-20

/ PRIOR APPLICATION NUMBER: 60/253,257

/ PRIOR FILING DATE: 2000-11-27

/ NUMBER OF SEQ ID NOS: 167

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 31

/ LENGTH: 1192

/ TYPE: DNA

/ ORGANISM: Homo sapien

US-10-001-885-31

Alignment Scores:

Pred. No.: 1e-66 Length: 1192

Score: 632.00 Matches: 121

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 13 Gaps: 0

US-10-001-885-125 (1-121) x US-10-001-885-31 (1-1192)

QY 1 MetValArgIleLeuAlaAsnGlyGluIleValGlnAspAspAspProArgValArgThr 20

DB 161 ATGGTGGGATCTTGGCCAAATGGGAAATCTGCAGACGACCCCGAGTGAAGACC 220

QY 21 ThrThrGlnProProArgGlySerIleProArgGlnSerPhePheAsnArgGlyHisGly 40

DB 221 ACTACCCAGCCACCAAGAGGTAGCATTCCTCGACGAGCTTCTCAATAGGGGCGCATGT 280

QY 41 AlaProProGlyGlyProGlyProArgGlnGlnGlnIleValIleValIleValIleVal 60

DB 281 GCTCCCGCAGGGGGGTCTGGCCCGCCGACGAGGAGGTGCGAGGCTGGGTGGTCT 340

QY 61 GlnSerProPheAsnAspLeuAsnArgGlnLeuValIleValIleValIleValIleVal 80

QY 16 ProArgValArgThrThrInProProArg-----GlySerile 29
Db 517 CGCGGGGTTG-----GCCGCCCGCGCGCGCGTTTGCCAGCGGCTTTGTG 467
QY 30 Pro-----ArgInSerPhePheAsnArgGly 38
Db 466 CGCGTGTGTGCCCGACCGCGCGCCCTGCGCGCTGATCGTTGGCCGATCCGAGC 407
QY 39 His-----GlyAlaProPro-GlyGlyProGlyProArgInGlnGln 52
Db 406 CATCGGTTCCCGTGGACCGCGCGGTGGACCGCTTGCTGCTCCGGTCCACGGTGGACCGG 347
QY 52 nAla-----GlyAlaArgLeuGlyAlaAlaGlnSerProPheAsnAs 66
Db 346 CGCCCTTGTCCCGCTGACCGCGGTGGGGCCCGCTTGCGCGCGCCCTCCCTTTGATGA 287
QY 66 PleuAsnArgInLeuValaAsnMetGlyPheProGlnTrpHis 80
Db 286 CGTCAGCAACCTCTTTCTCTGCTTACCTATCCCTTGGAAT 244
RESULT 11
US-10-156-761-3430
Sequence 3430, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156, 761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3430
LENGTH: 669
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(669)
US-10-156-761-3430
Alignment Scores:
Pred. No.: 0.0148 Length: 669
Score: 99.50 Matches: 32
Percent Similarity: 38.94% Conservative: 12
Best Local Similarity: 28.32% Mismatches: 27
Query Match: 15.74% Indels: 43
Gaps: 4
US-10-001-885-125 (1-121) x US-10-156-761-3430 (1-669)
QY 11 ValGlnAspAspAspProArgVal-----ArgThrThrThrGlnProProArgGlySer 28
Db 23 ATCCGTAAGGACAGCGGACGAGAACCCCGACAGGTTACGGCTACCCCGACAGGCGCAGC 82
QY 29 IlePro-----ArgGlnSerPhePheAsnArgGlyHisGlyAlaPro----- 42
Db 83 CGCCCTACCCCGACGCGCGCGGAGGAGCATTCG-CAGCAGGTTACGGCTACCCCGACAG 141
QY 43 -----ProGlyGlyProGlyProArgGlnGlnGln 52
Db 142 GGGCAGCCCGGCTACGGCTACCCCGGCGGACCGGGCGGACCGCGCGCTGCCCTCG 201
QY 53 AlaGlyAlaArgLeuGlyAlaAlaGlnSerProPheAsnAspLeuAsnArgInLeuVal 72

Db 202 ATGGCGCGCGCGCTCGCGCC----- 222
QY 73 AsnMetGlyPheProGlnTrpHisLeuGlyAsnHisAlaValGlnProValThrSerile 92
Db 223 -----CGGCGCATGACGCGCGCTGCGCTTCTTC 249
QY 93 LeuLeuLeuPheLeuLeuLeuMetLeuGlyValArgGly 105
Db 250 GTCATCTACTTCACTCTCGCGCGCATCGCGCGCGGT 288
RESULT 12
US-10-156-761-1
Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156, 761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
Alignment Scores:
Pred. No.: 2.94e+03 Length: 9025608
Score: 99.50 Matches: 32
Percent Similarity: 38.94% Conservative: 12
Best Local Similarity: 28.32% Mismatches: 27
Query Match: 15.74% Indels: 43
Gaps: 4
US-10-001-885-125 (1-121) x US-10-156-761-1 (1-9025608)
QY 11 ValGlnAspAspAspProArgVal-----ArgThrThrThrGlnProProArgGlySer 28
Db 4267023 ATCCGTAAGGACAGCGGACGAGAACCCCGACAGGTTACGGCTACCCCGACAGGCGCAGC 4267082
QY 29 IlePro-----ArgGlnSerPhePheAsnArgGlyHisGlyAlaPro----- 42
Db 4267083 CGCCCTACCCCGACGCGCGCGGAGGAGCATTCG-CAGCAGGTTACGGCTACCCCGACAG 4267141
QY 43 -----ProGlyGlyProGlyProArgGlnGlnGln 52
Db 4267142 GGGCAGCCCGGCTACGGCTACCCCGGCGGACCGGGCGGACCGCGCGCTGCCCTCG 4267201
QY 53 AlaGlyAlaArgLeuGlyAlaAlaGlnSerProPheAsnAspLeuAsnArgInLeuVal 72
Db 4267202 ATGGGCGCGCGCTCGCGCG----- 4267222
QY 73 AsnMetGlyPheProGlnTrpHisLeuGlyAsnHisAlaValGlnProValThrSerile 92
Db 4267223 -----CGGCGCATGACGCGCGCTGCGCTTCTTC 4267249
QY 93 LeuLeuLeuPheLeuLeuLeuMetLeuGlyValArgGly 105

Tue Aug 24 09:48:28 2004

us-10-001-885-125.p2n.rnpb

Page 8

Db 4267250 GTCATCTACTTCATCCTCGGCGCATCGGCGTGGCCGGT 4267288

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RESULT 13
US-10-437-963-80030
/ Sequence 80030, Application US/10437963
/ Publication NO. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 80030
/ LENGTH: 2361
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_79695C.1
/ US-10-437-963-80030

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Alignment Scores:	
Pred. No.:	0.0966
Score:	96.50
Percent Similarity:	42.59%
Best Local Similarity:	31.33%
Query Match:	15.53%
GB:	17
Gaps:	6

US-10-001-885-125 (1-121) X US-10-437-963-80030 (1-2361

QY	1	ProArgValArgThrThrThrInPro--ProAGSylSerIleProArgInsPhe	34
Db	30	CGGCGCGGCGGCGCGCGCGCGCTCGGCTCGGCTCGGCACCT-----	77
QY	35	PheAsnArgGLYHISGLYAlaProProGLYGLYProGLYProArgInsGlnGlnAlaGLY	54
Db	78	-----CGGCGCGCGCGCGCTCGCGCGGAGCACCGCGCGCGCGCGCGCGGCGGCG	132
QY	55	---AlaArgLeuGLYAlaAlaGlnSer-----	62
Db	132	CGTCTCGGCTCGGCGCTGCTCTCTGTTGSCACGCGCGGCGCTCGGCACCTCCCGCGCT	199
QY	63	---Pro-PheAsnAspLeuAsnArgGlnLeuValAsnMetGLYPheProGlnTPHISle	81
Db	192	CCACCTCTTTCGCGCATGCGGACCTGCTC-----GGCGTCCCAAC-----	234
QY	81	uGLYAsnHISAlaValGluProValTPHSerIleLeuLeuAspPheLeuAsnMetMetIle	101
Db	235	-----ACGCTCAAGTGTCTACCGCGCTACCGGCTCTCTCTGGC	272
QY	101	uGLYValArgGLYLeuLeuLeu	108
Db	273	GGCGGTGCGCGGCGCTCGTCTTC	284

RESULT 14
US-10-389-6647-274/c
Sequence 274, Application US/10389647
Publication No. US2004003549A1
GENERAL INFORMATION:
APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIAL

```

? FILE REFERENCE: UII-0383CP
? CURRENT APPLICATION NUMBER: US/10/389,647
? CURRENT FILING DATE: 2003-03-14
? PRIOR APPLICATION NUMBER: 09/653730
? PRIOR FILING DATE: 2000-09-01
? PRIOR APPLICATION NUMBER: 60/153022
? PRIOR FILING DATE: 1999-09-03
? NUMBER OF SEQ ID NOS: 710
? SOFTWARE: PseSTSEQ for Windows Version 4.0
? SEQ ID NO 274
? LENGTH: 738
? TYPE: DNA
? ORGANISM: Pseudomonas aeruginosa
? US-10-389-647-274

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Alignment Scores:	
Pred. No.:	0.0677
Score:	94.50
Percent Similarity:	44.83
Best Local Similarity:	43.10%
Query Match:	14.95%
DB:	13
Length:	733
Matches:	25
Conservative:	1
Mismatches:	25
Indels:	7
Gaps:	2

US-10-001-885-125 (1-121) X US-10-389-647-274 (1-738)

QY ARGGLVHISGLVLAPro-----ProGLVGLYProGLVProArgGln 50
Db CGAGGCGCTGGTGGCGCTTCGGGTGCTTCAGAGTTTCCAGCAGGAGCTGTACTCGGCC 266
QY GINGLINALGLVALArgPheuglVAlaIaInseRProPheAspLeuAsnArgGln 70
Db TGGCCGGCGGGTGGCCGATCCGAGCCAGAGATCAGCGCTTTCTCTCGGCGACGTCCAGCA 200
QY LeuValAsnMetGlyPheProGlnTrpHisLeuGlyAsnHisAlaValGluPro 88
Db ACCCGCGCGGATGCTTTCAGGTTGGCA---GGCGCGCATGAGGCGGCGCTT 149

RESULT 15
US-10-156-761-1/c
; Sequence 1, Application US/10156761

```

1  PREDICTION NO.: 06200301190101
2  GENERAL INFORMATION:
3  APPLICANT: OKURA, SATOSHI
4  APPLICANT: IKEDA, HARUO
5  APPLICANT: ISHIKAWA, JUN
6  APPLICANT: HORIKAWA, HIROSHI
7  APPLICANT: SHIBA, TADAYOSHI
8  APPLICANT: SAKAI, YOSHIYUKI
9  APPLICANT: HATTORI, MASAHIRA
10 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
11 FILE REFERENCE: 249-262
12 CURRENT APPLICATION NUMBER: US/10/156,761
13 CURRENT FILING DATE: 2002-05-29
14 PRIOR APPLICATION NUMBER: JP 2001-204089
15 PRIOR FILING DATE: 2001-05-30
16 PRIOR APPLICATION NUMBER: JP 2001-272697
17 PRIOR FILING DATE: 2001-08-02
18 NUMBER OF SEQ ID NOS: 15109
19 SEQ ID NO 1
20 LENGTH: 9025608
21 TYPE: DNA
22 ORGANISM: Streptomyces avermitilis
23 FEATURE:
24 NAME/KEY: misc feature
25 LOCATION: (4187715)
26 OTHER INFORMATION: a, t, c, g, other or unknown
27 IS-10-156-761-1

```

Alignment Scores:	
Pred. No.:	3.61e+04
Score:	90.50
Percent Similarity:	42.97%
Best Local Similarity:	30.47%
	Length:
	Matches:
	Conservative:
	Mismatches:

Job time : 6674 secs

Blank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53 ; Search time 23.6029 Seconds

(without alignments)
200.516 Million cell updates/sec

Title: US-10-676-049-3

Perfect score: 77

Sequence: 1 TGAEPGIDYDISVIT 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	90	6 Q28253	Q28253 canis fam11
2	77	100.0	134	6 Q28253	Q28253 bos taurus
3	64	83.1	2478	13 Q93406	Q93406 brachydanio
4	53	68.8	215	13 Q710K8	Q710K8 ambystoma m
5	52	67.5	320	6 Q95KV4	Q95KV4 bos taurus
6	52	67.5	347	6 Q95KV5	Q95KV5 bos taurus
7	51	66.2	637	4 Q81VX1	Q81VX1 homo sapien
8	50	64.9	120	4 Q95608	Q95608 homo sapien
9	50	64.9	189	11 Q8CQ36	Q8CQ36 mus sp. fib
10	50	64.9	354	4 Q8U0S6	Q8U0S6 mus sapien
11	50	64.9	379	4 Q95617	Q95617 homo sapien
12	50	64.9	810	11 Q8R3F3	Q8R3F3 mus muscula
13	48	62.3	843	4 Q05707	Q05707 homo sapien
14	48	62.3	1253	6 Q97566	Q97566 canis fam11
15	48	62.3	2936	6 Q7YRK8	Q7YRK8 canis fam11
16	46	59.7	757	10 Q941U9	Q941U9 oryza sativ

17	46	59.7	757	10 Q7XCQ3	Q7XCQ3 oryza sativ
18	46	59.7	1356	11 Q05546	Q05546 rattus norv
19	46	59.7	1358	4 Q92752	Q92752 homo sapien
20	46	59.7	1358	4 Q15568	Q15568 homo sapien
21	46	59.7	2944	11 Q63870	Q63870 mus musculu
22	45	58.4	293	6 Q9XSG0	Q9XSG0 oryctolagus
23	45	58.4	1036	2 Q86999	Q86999 clostridium
24	45	58.4	1238	11 Q8K3Q2	Q8K3Q2 mus musculu
25	45	58.4	1238	11 Q8C1M9	Q8C1M9 mus musculu
26	45	58.4	1353	13 Q05346	Q05346 gallus gall
27	45	58.4	1797	11 Q80X19	Q80X19 mus musculu
28	45	58.4	3484	5 P91257	P91257 caenorhabdi
29	45	58.4	18519	5 Q8ISF6	Q8ISF6 caenorhabdi
30	45	58.4	18534	5 Q8ISF7	Q8ISF7 caenorhabdi
31	44	57.1	232	17 Q8T0A7	Q8T0A7 methanosarc
32	44	57.1	233	4 Q8H6T5	Q8H6T5 homo sapien
33	44	57.1	264	16 Q8EFK5	Q8EFK5 streptococ
34	44	57.1	413	9 Q8SD78	Q8SD78 pseudomonas
35	44	57.1	590	10 Q8S134	Q8S134 oryza sativ
36	44	57.1	832	11 Q80YX0	Q80YX0 mus musculu
37	44	57.1	885	16 Q8PPJ3	Q8PPJ3 xanthomonas
38	44	57.1	1532	13 Q90994	Q90994 gallus gall
39	44	57.1	1714	13 Q90995	Q90995 gallus gall
40	44	57.1	1810	13 Q90824	Q90824 gallus gall
41	44	57.1	2019	11 Q64706	Q64706 mus musculu
42	44	57.1	2019	11 Q80YX2	Q80YX2 mus musculu
43	44	57.1	2110	11 Q80YX1	Q80YX1 mus musculu
44	43	55.8	190	6 Q28252	Q28252 canis fam11
45	43	55.8	190	11 Q921Z8	Q921Z8 mus musculu

ALIGNMENTS

RESULT 1

Q28253 PRELIMINARY: PRT; 90 AA.

AC Q28253; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB Fibronectin ED-B (Fragment).

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

NC NCBI_TaxID=9615;

XP MEDLINE=95130563; PubMed=7829518;

RA Zhang D.W., Burton-Murster N., Lust G.;

RT "Alternative splicing of ED-A and ED-B sequences of fibronectin pre-

RT mRNA differs in chondrocytes from different cartilaginous tissues and

RT can be modulated by biological factors.";

U J. Biol. Chem. 270:1817-1822(1995).

DR EMBL: U16208; AA67749.1; -.

DR PIR: I46162; I46162.

DR HSSP: P02751; IITP.

DR InterPro: IPR003961; FN_III.

DR InterPro: IPR008957; FN_III-like.

DR Pfam: PF00041; FN3; 1.

DR SMART: SM00060; FN3; 1.

FT NON_TER 1

FT NON_TER 90

SQ SEQUENCE 90 AA; 9585 MW; 766781BDF8511848 CRC64;

Query Match 100.0%; Score 77; DB 6; Length 90;

Best local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAEPGIDYDISVIT 15

Db 60 TGAEPGIDYDISVIT 74

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RESULT 2
ID 09M232 PRELIMINARY; PRT; 134 AA.
AC 09M232;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2003 (TREMBlrel. 15, Last sequence update)
DE Fibronectin ED-B+ region (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA De Cardia L.M., Rodgers R.J.;
RT "Characterization of the expression of the alternative splicing of ED-
RT A, ED-B and V regions of fibronectin mRNA in bovine ovarian follicles
RT and corpora lutea."
RL Reprod. Fertil. Dev. 0:0-0(2000).
DR EMBL; AF260304; AAF91380.1; -.
DR HSSB; P02751; 1FNF.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
FT NON_TER 1
FT NON_TER 134
SQ SEQUENCE 134 AA; 14408 MW; 820971B2619A48A5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 134;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
DB 89 TGLEPGIDYDISVIT 103

RESULT 3
ID 093406 PRELIMINARY; PRT; 2478 AA.
AC 093406;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibronectin.
GN FN1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7953;
RN (1)
RP SEQUENCE FROM N.A.
RA Zhao Q., Colliodi P.;
RT "Characterization and expression of zebrafish fibronectin."
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081128; AAC31947.1; -.
DR HSSB; P02751; 1FNF.
DR ZFIN; ZDB-GENE-000426-1; fn1.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibnctn1.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00013; FNTYPEII.

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DR Prodom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1_12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 14.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 11.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
SQ SEQUENCE 2478 AA; 271652 MW; A03475C5A385750 CRC64;

Query Match
Best Local Similarity 83.1%; Score 64; DB 13; Length 2478;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGLEPGIDYDISVIT 15
DB 1325 TGLEPGIDYDISVIT 1338

RESULT 4
ID 070K8 PRELIMINARY; PRT; 215 AA.
AC 070K8;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibronectin (Fragment).
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
OC Ambystoma.
NCBI_TaxID=8296;
RN (1)
RP SEQUENCE FROM N.A.
RA Saif R., Bertrand S., De Luze A., Vanacker J.M., Marchand O.,
RA Carregli A., Demeneix B., Laudet V.;
RT "Thyroid Hormone Response In A Neotenic Amphibian, The Axolotl
RT (Ambystoma mexicanum)."
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139973; AAN37600.1; -.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23438 MW; 5207871B67C64CA3 CRC64;

Query Match
Best Local Similarity 68.8%; Score 53; DB 13; Length 215;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
DB 199 TGLEPGIDYDISVIT 213

RESULT 5
ID 095KV4 PRELIMINARY; PRT; 320 AA.
AC 095KV4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fibronectin (Fragment).
GN FN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RA Parker A.E., Boutell J., Carr A., Maciewicz R.A.;
RT "Novel Cartilage-Specific Splice Variants of Fibronectin."
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ320529; CAC86917.1; -.

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DR GO:0005576; C:extracellular; IEA.
DR InterPro; IPR000083; Fibrinctn.
DR InterPro; IPR003962; FN_III.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00039; fn3; 3.
DR Pfam; PF00041; fn3; 2.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00058; FN1; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 2.
DR Repeat.
KW NON_TER
FT NON_TER
SQ SEQUENCE 320 AA; 35485 MW; 93E2F4AF2AC2F0E CRC64;

Query Match 67.5%; Score 52; DB 6; Length 320;
Best Local Similarity 71.4%; Pred. No. 1.4;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGLEPGIDYDISVI 14
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
Db 174 TGLEPGTEYTIQVI 187

RESULT 6
O95KV5 PRELIMINARY; PRT; 347 AA.
ID O95KV5
AC O95KV5
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fibronectin (Fragment).
GN FN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Parker A.E.; Boulell J.; Carr A.; Maciewicz R.A.;
RT "Novel Cartilage-Specific Splice Variants of Fibronectin."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ30528; CAC86918.1; -.
DR GO:0005576; C:extracellular; IEA.
DR InterPro; IPR000083; Fibrinctn.
DR InterPro; IPR003962; FN_III subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00039; fn1; 2.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR Repeat.
KW NON_TER
FT NON_TER
SQ SEQUENCE 347 AA; 38344 MW; 3DCA859100BEA461 CRC64;

Query Match 67.5%; Score 52; DB 6; Length 347;
Best Local Similarity 71.4%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGLEPGIDYDISVI 14
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
Db 174 TGLEPGTEYTIQVI 187

RESULT 7
O8IVX1

ID O8IVX1 PRELIMINARY; PRT; 637 AA.
AC O8IVX1
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041767; AAH41767.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00092; vwa; 1.
DR Pfam; PF00453; VWFADOMAIN.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWF_A; 1.
DR Hypothetical protein.
KW SEQUENCE 637 AA; 68118 MW; 463B1A5A2711B80E CRC64;

Query Match 66.2%; Score 51; DB 4; Length 637;
Best Local Similarity 75.0%; Pred. No. 4.5;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGLEPGIDYDISV 13
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
Db 526 TGLEPGTEYEVSV 537

RESULT 8
O95608 PRELIMINARY; PRT; 120 AA.
ID O95608
AC O95608
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fibronectin (Fragment).
GN FN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Godfrey H.P.; Ebrahim A.A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41724; AAD00013.1; -.
DR HSSP; P02751; 1FNH.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR0041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR Repeat.
KW NON_TER
FT NON_TER
SQ SEQUENCE 120 AA; 13341 MW; 05E5C3277046ED2F CRC64;

Query Match 64.9%; Score 50; DB 4; Length 120;
Best Local Similarity 71.4%; Pred. No. 1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGLEPGIDYDISVI 14
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
Db 43 TGLEPGTEYTIYVI 56

RESULT 9

08CG36
ID 08CG36 PRELIMINARY; PRT; 189 AA.
AC 08CG36;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fibronectin (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10095;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96262744; PubMed=8691328;
RA Bergijk B.C., Baalde H.J., Kootstra C.J., De Heer E., Killen P.D.,
RA Bruijn J.A.,
RT "Cloning of the mouse fibronectin V-region and variation of its
RT splicing pattern in experimental immune complex glomerulonephritis."
RL J. Pathol. 178:462-468(1996).
DR EMBL; S82292; AAN86743.1; -.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
FT NON_TER 1
FT NON_TER 189
SQ SEQUENCE 189 AA; 20763 MW; BDF6B16ECC274662 CRC64;

Query Match 64.9%; Score 50; DB 11; Length 189;
Best Local Similarity 71.4%; Pred. No. 1.7;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGLSPGIDYDISVI 14
Db 23 TGLEPGTEYTYVI 36

RESULT 10

090Q06 PRELIMINARY; PRT; 354 AA.
AC 090Q06;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fibronectin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Dutt P., Yoder M.C.;
RT "Alternative splicing of fibronectin in human bone marrow stromal
RT cells."
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60068; AAD10853.1; -.
DR HSSP; P02751; 1FNH.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00014; FNTYPEIIT.
DR SMART; SM00060; FN3; 2.
FT NON_TER 1
FT NON_TER 354
SQ SEQUENCE 354 AA; 38656 MW; 596107AF3078F9F9 CRC64;

Query Match 64.9%; Score 50; DB 4; Length 354;
Best Local Similarity 71.4%; Pred. No. 3.5;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 254 TGLEPGTEYTYVI 267

RESULT 11

095617 PRELIMINARY; PRT; 379 AA.
AC 095617;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fibronectin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Dutt P., Yoder M.C.;
RT "Alternative splicing of fibronectin in human bone marrow stromal
RT cells."
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60067; AAD11500.1; -.
DR HSSP; P02751; 1FNH.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00014; FNTYPEIIT.
DR SMART; SM00060; FN3; 2.
FT NON_TER 1
FT NON_TER 379
SQ SEQUENCE 379 AA; 41370 MW; 7E1CA4B9428AC7C2 CRC64;

Query Match 64.9%; Score 50; DB 4; Length 379;
Best Local Similarity 71.4%; Pred. No. 3.8;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGLSPGIDYDISVI 14
Db 254 TGLEPGTEYTYVI 267

RESULT 12

08R3F3 PRELIMINARY; PRT; 810 AA.
AC 08R3F3;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025521; AAG25521.1; -.
DR MGD; MGI:95566; Fn1.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibinctnl.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00039; fn1; 3.
DR Pfam; PF00041; fn3; 6.
DR SMART; SM00058; FN1; 3.

DR PROSITE; PS01253; FIBRONECTIN_1, 3.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 810 AA; 89228 MW; 9A7A4DD0ED3437F CRC64;
Query Match 64.9%; Score 50; DB 11; Length 810;
Best Local Similarity 71.4%; Pred. No. 8.8;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISV 14
DB 409 TGLEPGTEYTYVI 422
RESULT 13
ID 005707 PRELIMINARY; PRT; 843 AA.
AC 005707;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
RT Undulin 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90256812; PubMed=2187872;
RA Schuppen D., Cantaluppi M., Becker J., Veit A., Bunce T., Troyer D.,
RT Schuppen F., Schmid W., Ackermann R., Hahn E.;
RT "Undulin, an Extracellular Matrix Glycoprotein Associated with
Collagen Fibrils."
RL J. Biol. Chem. 265:8823-8832(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91373351; PubMed=1716629;
RA Uuet M., Herbst H., Hummel M., Durkop H., Tripiet D., Stein H.,
RT Schuppen D.;
RT "Undulin is a novel member of the fibronectin-tenascin family of
extracellular matrix glycoproteins."
RL J. Biol. Chem. 266:17326-17332(1991).
DR EMBL; M64108; AAA36794.1; -.
DR PIR; A40970; A40970.
DR Gene; HGNC:2191; COL14A1.
DR GO; GO:0005578; C:extracellular matrix; NAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
DR GO; GO:0030199; P:collagen fibril organization; NAS.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF00041; fn3; 7.
DR Pfam; PF00092; vwa; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PSS0234; VWF_A; 1.
FT NON TER 1
SQ SEQUENCE 843 AA; 92638 MW; 1507710067E1C781 CRC64;
Query Match 62.3%; Score 48; DB 4; Length 843;
Best Local Similarity 53.8%; Pred. No. 20;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 2 GLEPGIDYDISV 14
DB 495 GLEPGTEYVSL 507
RESULT 14
ID 097566 PRELIMINARY; PRT; 1253 AA.
AC 097566;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
RT VII collagen non-collagenous (NC1) domain, the target antigen of
autoimmune disease epidermolysis bullosa acquisita (EBA).";
RL Biochim. Biophys. Acta 1408:25-34(1998).
DR EMBL; AF042093; AAC72024.1; -.
DR HSSP; F02751; 1FNA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00060; FN3; 9.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PSS0234; VWF_A; 2.
KM Collagen.
FT NON TER 1253
SQ SEQUENCE 1253 AA; 133696 MW; 7FF2B500E48CA89 CRC64;
Query Match 62.3%; Score 48; DB 6; Length 1253;
Best Local Similarity 69.2%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISV 13
DB 1016 TGLEPGISTYFSL 1028
RESULT 15
ID 07YRK8 PRELIMINARY; PRT; 2936 AA.
AC 07YRK8;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
RT Type VII collagen.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22756273; PubMed=12874109;
RA Baldeschi C., Gache Y., Rattenholl A., Bouille P., Danos O.,
RT Ortonne J.P., Bruckner-Tuderman L., Meneguzzi G.;
RT "Genetic correction of canine dystrophic epidermolysis bullosa
mediated by retrieval vectors."
RL Hum. Mol. Genet. 12:1897-1905(2003).
DR EMBL; AY183408; AAO64414.1; -.
KM Collagen.
SQ SEQUENCE 2936 AA; 293983 MW; F80CAFA0E1F69B9 CRC64;
Query Match 62.3%; Score 48; DB 6; Length 2936;
Best Local Similarity 69.2%; Pred. No. 83;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISV 13
DB 1016 TGLEPGISTYFSL 1028

Tue Sep 21 07:04:11 2004

us-10-676-049-3.open.rspt

Page 6

Search completed: September 21, 2004, 05:57:07
Job time : 24.6029 secs

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53 ; Search time 30.2206 Seconds
(without alignments)
140.243 Million cell updates/sec

Title: US-10-676-049-3

Perfect score: 77

Sequence: 1 TGLPEIDIDIVIT 15

Scoring table: BLOSUM62
Gapco 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	15	AAO17877	AAO17877 EDB fibro
2	77	100.0	31	AAU79568	AAU79568 Epitope #
3	77	100.0	91	AA25405	AA25405 ED-B.1/1
4	77	100.0	91	AA23838	AA23838 The ED2 d
5	77	100.0	91	ABG98132	ABG98132 Anti-neov
6	77	100.0	91	AAO17878	AAO17878 EDB fibro
7	77	100.0	91	ABP74705	ABP74705 Human ED-
8	77	100.0	91	ADCO9564	ADCO9564 Epitope w
9	77	100.0	146	ADCO9565	ADCO9565 Epitope w
10	77	100.0	147	ABG98133	ABG98133 Human fib
11	77	100.0	147	ABP74706	ABP74706 Human ED-
12	77	100.0	1336	AA60019	AA60019 Tissue-b1
13	77	100.0	2220	ABO01289	ABO01289 Human pro
14	77	100.0	2446	AA60021	AA60021 Fibronoge
15	77	100.0	2446	AA650377	AA650377 Human fib
16	77	100.0	2477	AAW95955	AAW95955 Human fib
17	77	100.0	2477	AADE63323	AADE63323 Rat Prote
18	64	83.1	15	AA604093	AA604093 Antigenic
19	64	83.1	15	AA608821	AA608821 ED-B anti
20	56	72.7	15	AAO17876	AAO17876 EDB fibro
21	53	68.8	90	ABP78883	ABP78883 Tumour ne
22	53	68.8	92	ABP78893	ABP78893 Tumour ne
23	53	68.8	94	ABP78837	ABP78837 Fibronect
24	52	67.5	93	ABP78839	ABP78839 Fibronect
25	52	67.5	93	ABP78840	ABP78840 Fibronect

26	50	64.9	21	2	AAW56675	AAW56675 Peptide d
27	50	64.9	21	4	AA670558	AA670558 Human pla
28	50	64.9	22	4	AA670559	AA670559 Human pla
29	50	64.9	90	2	AA651358	AA651358 Met-casab1
30	50	64.9	90	7	ADD49009	ADD49009 Fibronect
31	50	64.9	270	5	AA678414	AA678414 Human fib
32	50	64.9	271	2	AA682247	AA682247 Heparin-I
33	50	64.9	271	2	AA621689	AA621689 Heparin-I
34	50	64.9	271	2	AAW33336	AAW33336 Human fib
35	50	64.9	271	2	AAW13570	AAW13570 Mouse fib
36	50	64.9	271	2	AAW13567	AAW13567 Human fib
37	50	64.9	271	2	AAV05458	AAV05458 Fibronect
38	50	64.9	271	6	ABP59433	ABP59433 Human fib
39	50	64.9	271	6	ADD49012	ADD49012 Fibronect
40	50	64.9	276	7	ABP59443	ABP59443 Human fib
41	50	64.9	276	7	ADD49022	ADD49022 Fibronect
42	50	64.9	296	2	AA698815	AA698815 Cell adhe
43	50	64.9	296	2	AAW13571	AAW13571 Escherich
44	50	64.9	296	2	AAV05455	AAV05455 Fibronect
45	50	64.9	296	6	ABP59434	ABP59434 Human fib

ALIGNMENTS

RESULT 1					
AAO17877	ID	AAO17877	standard; peptide; 15 AA.		
XX	XX	AAO17877;			
AC	XX	20-AUG-2002 (first entry)			
DT	XX	EDB fibronectin domain binding peptide #3.			
DE	XX	EDB fibronectin domain; EDBFD; angiogenesis; gene therapy; transplant;			
XX	XX	implant; receptor molecule interaction.			
KM	XX	Unidentified.			
OS	XX	WO200220563-A2.			
XX	XX	14-MAR-2002.			
PD	XX	30-AUG-2001; 2001WO-EP010016.			
XX	XX	07-SEP-2000; 2000DE-01045803.			
PR	XX	02-MAY-2001; 2001DE-01023133.			
XX	XX	(SCHD) SCHERING AG.			
PA	XX	(REDL/) REDLITZ A.			
PA	XX	(KOPF/) KOPFITZ W.			
PA	XX	(EGNE/) EGNER U.			
PA	XX	(BAHR/) BAHR I.			
PA	XX	(MENR/) MENRAD A.			
XX	XX	Mentrad A;			
PI	XX	WPI; 2002-479458/51.			
DR	XX	New proteins binding specifically to the ED-B fibronectin domain, are			
PT	XX	cell adhesion and proliferation mediators useful e.g. in screening tests.			
XX	XX	Claim 2; Page 41; 66pp; German.			
XX	XX	The present invention relates to a new protein which binds specifically			
CC	CC	to the EDB fibronectin domain (EDBFD), is specifically expressed or			
CC	CC	activated in endothelial cells, stromal cells of a tumour and tumour			
CC	CC	cells, and has an apparent molecular weight of 120-130 kDa for the light			
CC	CC	chain and 150-160 kDa for the heavy chain. The protein can be used to			
CC	CC	screen compounds which bind to EDBFD or its receptor, for coating			
CC	CC	surfaces to which endothelial cells bind, in cell cultures, in			
CC	CC	combination with transplants or in combination with implants			

CC (specifically lung implants, artificial heart pacemakers or valves,
CC vascular implants, endoprostheses, screws, bars, plates, wires, nails,
CC rods, artificial joints, breast implants, artificial cranial plates,
CC false teeth, tooth fillings or tooth bridges, as it improves the
CC integration of transplants or implants in the body. The protein is also
CC useful in clarifying ED8-specific adhesion mechanisms and receptor
CC molecule interactions involved in angiogenesis. The present sequence is a
CC protein of the invention
XX

SO Sequence 15 AA;

Query Match 100.0%; Score 77; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
Db 1 TGLEPGIDYDISVIT 15

RESULT 2
AAU79568
ID AAU79568 standard; peptide; 31 AA.
XX
XX AAU79568;
XX

DT 03-SEP-2002 (first entry)

DE Epitope #3 of the Fibronectin ED-B domain.

XX Antibody: single chain antibody variable region fragment; scFv; ME-4C;
KW human; Fibronectin; ED-B; antiangiogenic; CD33;
KM complementarity determining region 3; heavy chain; VH; DP-47;
XX light chain; VL; DPL-16; 7B89; angiogenesis; epitope.
XX

OS Homo sapiens.

XX WC020246455-A2.

XX 13-JUN-2002.

XX 06-DEC-2001; 2001WO-EP014330.

XX 06-DEC-2000; 2000IT-F1000247.

XX (PHIL-) PHILGEN SRL.

XX Giovannoni L;

XX WPI; 2002-455060/48.

XX Novel process for selecting anti-angiogenesis antibody fragments.

XX Disclosure; Fig 3; 18pp; English.

XX The invention discloses a process for selecting anti-angiogenesis
CC antibody fragments, in which, starting from a highly complex system
CC containing billions of different binding specificities, several cycles of
CC filter selection of colonies and of amplification of positive clones are
CC carried out. The method is an improvement on existing antibody selection
CC methods by allowing the selection from a large repertoire of antibody
CC fragments expressed in bacteria. It can also avoid the use of phage
CC display, identifying directly, the clones expressing the antibody,
CC fragments in soluble form. The invention discloses, in particular, a
CC monoclonal antibody fragment scFv, ME-4C, produced according to the
CC process, with the CDR3 sequences of the heavy chain VH (DP-47) and the
CC light chain VL (DPL-16) characterised. The monoclonal antibody was
CC isolated by the recognition of epitopes from a decapeptide library of the
CC recombinant protein, 7B89, containing the domains 7, 8 and 9, and more
CC particularly, ED-B (not defined), of human Fibronectin. The identified
CC monoclonal antibody fragment scFv ME-4C can act as a reagent in the
CC determination of angiogenesis in tissue samples in vivo and/or in vitro

CC domain. The epitope binds to the monoclonal scFv antibody, ME-4C, which
CC was isolated from the ETH-2000 library

SO Sequence 31 AA;

Query Match 100.0%; Score 77; DB 5; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
Db 1 TGLEPGIDYDISVIT 15

RESULT 3
AAR25405
ID AAR25405 standard; protein; 91 AA.
XX
XX AAR25405;
XX

DT 18-JAN-1993 (first entry)

DE ED-B.

KM Fibronectin; antibody; cancer.

XX Homo sapiens.

XX JP04169195-A.

XX 17-JUN-1992.

XX 31-OCT-1990; 90JP-00295820.

XX 31-OCT-1990; 90JP-00295820.

XX (HOJI/) HOJIN G.

XX (GAKU/) GAKUEN F.

XX (SAKA) OTSUKA PHARM CO LTD.

XX WPI; 1992-253398/31.

XX Monoclonal antibody to fragment ED-B of fibronectin - for determining

XX fibronectin in cancerous tissue.

XX Claim 1; Page 1; 17pp; Japanese.

XX The sequence given is ED-B which is isolated from fibronectin. This
CC peptide was used in the production of an anti-ED-B monoclonal antibody.
CC This antibody is reactive against fibronectin, particularly in cancerous
CC tissue. The antibody recognises ED-B specifically and has reaction
CC specificity to cancerous fibronectin. This antibody is useful as a tracer
CC in determination of immunogen and cancerous fibronectin
XX

SO Sequence 91 AA;

Query Match 100.0%; Score 77; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
Db 61 TGLEPGIDYDISVIT 75

RESULT 4
AAR23838
ID AAR23838 standard; protein; 91 AA.
XX
XX AAR23838;
XX

DT 05-NOV-1992 (first entry)

DE The ED2 domain of fibronectin.
 XX
 XX FN; toxemia; pregnancy; type III.
 XX
 OS Homo sapiens.
 XX
 XX US5108898-A.
 XX
 XX 28-APR-1992.
 XX
 XX 18-JAN-1989; 89US-00298622.
 XX
 XX 18-JAN-1989; 89US-00298622.
 XX
 XX (PETE/) PETERS J H.
 XX
 XX Peters JH, Lockwood CJ;
 XX
 XX WPI; 1992-166519/20.
 XX
 XX Predicting toxemia in pregnancy - by detecting elevated levels of
 PT fibronectin having variably included type III repeat region in body fluid
 PT sample.
 XX
 PS Disclosure; Fig 2; 9pp; English.
 XX
 CC The human fibronectin Type III repeat sequence ED2 contains a region
 CC which has little sequence homology with other Type III repeats. Peptides
 CC were synthesized, having a sequence based on the ED2 sequence, which were
 CC used to raise antibodies which will immunoreact with ED2 but not with a
 CC plasma fibronectin monomer. The antibodies can be used for detecting
 CC fibronectin cong. variably included Type III repeats in a sample, thus
 CC determining patients destined to develop toxemia, patic. preeclampsia,
 CC prior to the onset of maternal signs and symptoms of the disease,
 CC allowing for early therapeutic intervention and monitoring. See also
 CC AAR23837-42
 CC
 XX Sequence 91 AA;
 SQ
 Query Match 100.0%; Score 77; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGLEPGIDYDVSIVT 15
 |||||
 DB 61 TGLEPGIDYDVSIVT 75
 |||||
 RESULT 5
 ABG98132
 ID ABG98132 standard; protein; 91 AA.
 XX
 AC ABG98132;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Anti-neovascular preparation associated epitope #87.
 XX
 XX Cell-mediated immunity; cellular immune response; CTL response;
 KM tumour neovascutature; anti-angiogenesis.
 XX
 OS Homo sapiens.
 XX
 XX WO200269907-A2.
 XX
 XX 12-SEP-2002.
 XX
 XX 07-MAR-2002; 2002WO-US007204.
 XX
 XX 07-MAR-2001; 2001US-0274063P.
 XX
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX

PI Simard JLL, Diamond DC;
 XX
 XX WPI; 2002-750433/81.
 DR
 XX
 XX Evaluating cell-mediated immunity, in particular cytotoxic T lymphocyte
 PT responses, by implanting vascular cells, useful for treatment and
 PT research models for directly targeting tumor neovascutature.
 XX
 XX Example 5; Page 25; 73pp; English.
 PS
 CC The invention describes a method of evaluating cell-mediated immunity
 CC comprising implanting vascular cells into an immunodeficient mammal,
 CC establishing an immune response in the mammal, and assaying a
 CC characteristic to determine cell-mediated immunity in the mammal. The
 CC methods and compositions of the present invention are useful for the
 CC generation of a cellular immune response, in particular a CTL response,
 CC for treatment directly against a tumour neovascutature. They can also be
 CC used for making research models targeting tumour neovascutature. The
 CC present invention using the anti-angiogenesis approach takes advantage of
 CC the need of tumours to recruit a blood supply to support their continued
 CC growth. This approach aims to disrupt a tumour's supply of nutrients to
 CC cause it to die or at least limit its growth. This is the amino acid
 CC sequence of a peptide associated with the neo-vasculature preparation
 CC for treatment of cancer described in the invention
 CC
 XX Sequence 91 AA;
 SQ
 Query Match 100.0%; Score 77; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGLEPGIDYDVSIVT 15
 |||||
 DB 61 TGLEPGIDYDVSIVT 75
 |||||
 RESULT 6
 AA017878
 ID AA017878 standard; protein; 91 AA.
 XX
 AC AA017878;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE EDB fibronectin domain binding protein.
 XX
 XX EDB fibronectin domain; EDBFD; angiogenesis; gene therapy; transplant;
 KM implant; receptor molecule interaction.
 XX
 XX Unidentified.
 OS
 XX
 XX WO200220563-A2.
 XX
 XX 14-MAR-2002.
 XX
 XX 30-AUG-2001; 2001WO-EP010016.
 XX
 XX 07-SEP-2000; 2000DE-01045803.
 XX
 XX 02-MAY-2001; 2001DE-01023133.
 XX
 XX (SCHD) SCHERING AG.
 PA (REDL/) REDLITZ A.
 PA (KOPF/) KOPFITZ M.
 PA (EGNE/) EGNER U.
 PA (BAHR/) BAHR I.
 PA (MENR/) MENRAD A.
 XX
 XX Menrad A;
 PI
 XX
 XX WPI; 2002-479458/51.
 DR
 XX
 XX New proteins binding specifically to the ED-b fibronectin domain, are
 PT cell adhesion and proliferation mediators useful e.g. in screening tests.
 PT

CC Invention with high affinity for MHC class I.
 XX
 SQ Sequence 91 AA;

Query Match 100.0%; Score 77; DB 7; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
 |||||
 DB 61 TGLEPGIDYDISVIT 75

RESULT 9
 ADC09565
 ID ADC09565 standard; peptide; 146 AA.
 XX
 AC ADC09565;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Epitope with high affinity for MHC class I #SEQ ID 590.
 XX
 KM Epitope; immunological; vaccine;
 KM major histocompatibility complex class I; MHC class I; cancer;
 KW immunisation.
 XX
 OS Unidentified.
 XX
 PN WO2003008537-A2.
 PD 30-JAN-2003.
 XX
 PF 29-MAR-2002; 2002WO-US010189.
 XX
 PR 06-APR-2001; 2001US-0282211P.
 PR 07-NOV-2001; 2001US-0337017P.
 PR 07-MAR-2002; 2002US-0363210P.
 XX
 PA (CTL-) CTL IMMUNOTHERAPIES CORP.
 XX
 PI Simard JLL, Diamond DC, Liu L, Xie Z,
 XX
 DR WPI; 2003-248010/24.
 XX
 PT Epitope having high affinity for major histocompatibility complex class I
 PT useful for treating an animal, evaluating immunogenicity of a vaccine or
 PT therapeutic composition and for diagnosing a disease.
 PS
 PS Claim 1; SEQ ID NO 590; 239pp; English.

CC The invention relates to an isolated epitope polypeptide that has high
 CC affinity for major histocompatibility complex (MHC) class I, and an
 CC epitope cluster comprising the polypeptide. Also disclosed is a vaccine
 CC or immunotherapeutic composition containing an epitope of the invention.
 CC Compositions of the invention may be used in the treatment of cancer. The
 CC method can be combined with a radiation therapy, chemotherapy,
 CC biochemotherapy or surgery. The composition is also useful for evaluating
 CC immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
 CC-peptide complexes of the invention are useful for determining specific T
 CC cell frequency. This method is useful for evaluating immunological
 CC response, by performing the method prior to and subsequent to an
 CC immunisation step. Compositions of the invention are useful for
 CC diagnosing a disease. The current sequence represents an epitope of the
 CC invention with high affinity for MHC class I.
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 77; DB 7; Length 146;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15

DB 95 TGLEPGIDYDISVIT 109
 |||||
 RESULT 10
 ABG98133
 ID ABG98133 standard; protein; 147 AA.
 XX
 AC ABG98133;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Human fibronectin gene ED-B region.
 XX
 KM Cell-mediated immunity; cellular immune response; CTL response;
 KM tumour neovasculation; anti-angiogenesis.
 XX
 OS Homo sapiens.
 XX
 PN WO200269907-A2.
 PD 12-SEP-2002.
 XX
 PF 07-MAR-2002; 2002WO-US007204.
 XX
 PR 07-MAR-2001; 2001US-0274063P.
 XX
 PA (CTL-) CTL IMMUNOTHERAPIES CORP.
 XX
 PI Simard JLL, Diamond DC;
 XX
 DR WPI; 2002-750433/81.
 DR N-PSDB; ABX03678.
 XX
 PT Evaluating cell-mediated immunity. In particular cytotoxic T lymphocyte
 PT responses, by implanting vascular cells; useful for treatment and
 PT research models for directly targeting tumor neovasculation.
 PS
 PS Example 5; Page 29; 73pp; English.

CC The invention describes a method of evaluating cell-mediated immunity
 CC comprising implanting vascular cells into an immunodeficient mammal,
 CC establishing an immune response in the mammal, and assaying a
 CC characteristic to determine cell-mediated immunity in the mammal. The
 CC methods and compositions of the present invention are useful for the
 CC generation of a cellular immune response, in particular a CTL response,
 CC for treatment directly against a tumour neovasculation. They can also be
 CC used for making research models targeting tumour neovasculation. The
 CC present invention using the anti-angiogenesis approach takes advantage of
 CC the need of tumours to recruit a blood supply to support their continued
 CC growth. This approach aims to disrupt a tumour's supply of nutrients to
 CC cause it to die or at least limit its growth. This is the amino acid
 CC sequence of a protein associated with the neo-vasculature preparation
 CC for treatment of cancer described in the invention
 XX
 SQ Sequence 147 AA;

Query Match 100.0%; Score 77; DB 5; Length 147;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
 |||||
 DB 95 TGLEPGIDYDISVIT 109

RESULT 11
 ABP74706
 ID ABP74706 standard; protein; 147 AA.
 XX
 AC ABP74706;
 XX
 DT 03-FEB-2003 (first entry)

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XX DE Human ED-B domain of fibronectin SEQ ID NO:590.
XX XX Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
XX XX T cell.
XX XX Homo sapiens.
XX OS WO200281646-A2.
XX PN 17-OCT-2002.
XX PD 04-APR-2002; 2002WC-US011101.
XX PE 06-APR-2001; 2001US-0282211P.
XX PR 07-NOV-2001; 2001US-0337017P.
XX PR 07-MAR-2002; 2002US-0363210P.
XX XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX PA Simard JUL, Diamond DC, Liu L, Xie Z,
XX PI WPI; 2003-067518/06.
XX DR Novel epitopes useful as vaccines, comprises peptides or nucleic acid
XX PT encoding the peptides, that are useful epitopes of target-associated
XX PT antigens.
XX PS Claim 1; Page 26; 352pp; English.
XX XX
XX CC The present invention describes an isolated epitope (I) and an epitope
XX CC cluster. Also described is a vaccine or immunotherapeutic composition
XX CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
XX CC treating an animal, by administering to an animal the vaccine or
XX CC immunotherapeutic composition. VC is also useful for evaluating
XX CC immunogenicity of a vaccine or immunotherapeutic composition, by
XX CC administering VC to an HLA-transgenic animal and evaluating
XX CC immunogenicity based on a characteristic of the animal, or by in vitro
XX CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
XX CC useful for determining specific T cell frequency, by contacting T cells
XX CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
XX CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
XX CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
XX CC ABP74713 represent sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 147 AA.
XX
XX Query Match 100.0%; Score 77; DB 6; Length 147;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-05;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISVIT 15
Db 95 TGLEPGIDYDISVIT 109

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OS Homo sapiens.
XX XX Location/Qualifiers
XX FH Key 2..1336
XX FT Domain /label= tissue-binding_domain
XX FT 2..926
XX FT Domain /label= tissue-binding_domain
XX FT 928..1336
XX FT Domain /label= tissue-binding_domain
XX PN WO9416085-A2.
XX PD 21-JUL-1994.
XX PE 30-DEC-1993; 93WO-US012687.
XX PF 30-DEC-1992; 92US-00998271.
XX PR 30-DEC-1992; 92US-00998271.
XX XX (ZYMO) ZYMOGENETICS INC.
XX PA Irani MH;
XX PI WPI; 1994-249231/30.
XX PI N-PSDB; AAQ70007.
XX DR New hybrid proteins for use in tissue sealing and wound healing -
XX PT comprising a tissue-binding domain from a protein covalently linked to a
XX PT crosslinking domain of another protein.
XX PS Disclosure; Page 63-69; 87pp; English.
XX XX
XX CC Hybrid proteins have a tissue-binding domain (TBD) from 1 protein linked
XX CC to a crosslinking domain from another protein. The TBD comprises: aa 2-
XX CC 926, 928-1338 and especially 2-1336 of the sequence given in AAR60019;
XX CC the heparin-binding domain (aa 1812-2171 of AAR60021) of fibronectin; the
XX CC collagen-binding domain (aa 282-608 of AAR60021) of fibronectin; or the
XX CC cell-binding domain (aa 1357-1903 or 1532-1631 of AAR60020) of
XX CC fibronectin. DNA encoding a fibronectin-fibrinogen hybrid is given in
XX CC AAQ70007, and sequences for fibronectin and fibrinogen-alpha in AAQ70008
XX CC and AAQ70009, respectively. (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 1336 AA.
XX
XX Query Match 100.0%; Score 77; DB 2; Length 1336;
XX Best Local Similarity 100.0%; Pred. No. 0.00026;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISVIT 15
Db 349 TGLEPGIDYDISVIT 363

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RESULT 12
AAR60019
ID AAR60019 standard; protein; 1336 AA.
XX
XX AAR60019;
XX
XX 25-MAR-2003 (revised)
XX DT 23-FEB-1995 (first entry)
XX
XX Tissue-binding hybrid protein.
XX
XX Tissue binding; tissue sealing; wound healing; vulnary;
XX tissue-binding domain; TBD; crosslinking domain; fibronectin;
XX fibrinogen-alpha; heparin-binding domain; collagen-binding domain;
XX cell-binding domain; hybrid protein.
XX

```

```

RESULT 13
ABO01289
ID ABO01289 standard; protein; 2220 AA.
XX
XX ABO01289;
XX
XX 06-AUG-2003 (first entry)
XX DT
XX
XX Human protein NOV1b.
XX
XX Human; NOVX; cardiomyopathy; atherosclerosis; hypertension;
XX congenital heart defect; prostate cancer; diabetes; metabolic disorder;
XX neoplasm; graft versus host disease; AIDS; bronchial asthma;
XX Crohn's disease; multiple sclerosis; infectious disease; anorexia;
XX cancer-associated cachexia; neurodegenerative disorder;
XX Alzheimer's disease; Parkinson's disease; immune disorder;
XX hematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy;
XX SNP; single nucleotide polymorphism.
XX
XX Homo sapiens.
XX

```

FH Key Location/Qualifiers
 FT Misc-difference 639
 FT /note= "May be Phe as the result of a single nucleotide polymorphism"
 XX
 XX WO2003023008-A2.
 XX
 XX 20-MAR-2003.
 XX
 XX
 PF 09-SEP-2002; 2002WO-US028596.
 XX
 PR 07-SEP-2001; 2001US-0318120P.
 PR 07-SEP-2001; 2001US-0318130P.
 PR 10-SEP-2001; 2001US-0318430P.
 PR 12-SEP-2001; 2001US-0318765P.
 PR 17-SEP-2001; 2001US-0322781P.
 PR 17-SEP-2001; 2001US-0322816P.
 PR 19-SEP-2001; 2001US-0323519P.
 PR 20-SEP-2001; 2001US-0323631P.
 PR 20-SEP-2001; 2001US-0323636P.
 PR 25-SEP-2001; 2001US-0324969P.
 PR 25-SEP-2001; 2001US-0325031P.
 PR 26-SEP-2001; 2001US-0324990P.
 PR 15-FEB-2002; 2002US-0357303P.
 PR 28-FEB-2002; 2002US-0360973P.
 PR 20-MAR-2002; 2002US-0366131P.
 PR 25-MAR-2002; 2002US-0367753P.
 PR 02-APR-2002; 2002US-0369479P.
 PR 10-MAY-2002; 2002US-0379532P.
 PR 17-MAY-2002; 2002US-0381664P.
 PR 17-MAY-2002; 2002US-0381672P.
 PR 28-MAY-2002; 2002US-0383651P.
 PR 29-MAY-2002; 2002US-0384012P.
 PR 19-JUN-2002; 2002US-0390155P.
 PR 06-SEP-2002; 2002US-00390155.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 PI Zhong M, Li L, Gorman L, Spyrek KA, Kekuda R, Taupier RJ, Anderson DW, Vernet CAM, Catterton E, Miller CE, Shenoy SG, Paltunajan M, Pena CE, Tchervet VT, Padigaru M, Gusev VV, Malyanar UM, Burgess CE, Gerlach VL, Casman SU, Rieger DK, Pi Gossett WM, Smithson G, Peyman JA, Scaring G, Rothenberg ME, Larocelle WJ, Shinkens RA, Crabtree J, Rastelli L, Voss EZ, Pi Boldog FL, Edinger SR, Miller I, Macdougall DR, Ellerman K, Pi Chapoval A;
 PI
 XX WPI; 2003-313246/30.
 DR N-PSDB; AC006170.
 XX
 PT New polypeptides and polynucleotides having properties related to stimulation of biochemical or physiological responses in a cell or tissue, useful for diagnosing or preventing e.g. atherosclerosis, hypertension, prostate cancer.
 PT
 XX
 PS Claim 2; Page 110-111; 849P; English.
 XX
 CC The invention relates to an isolated polypeptide comprising one of 127 sequences (appearing as ABO1288-ABO1414) designated as NOVX, a mature form of NOVX, an amino acid sequence which is at least 95% identical to NOVX or an amino acid sequence comprising one or more conservative substitutions in NOVX. Also included are nucleic acids encoding NOVX proteins, determining the presence or amount of NOVX or NOVX DNA in a sample (by introducing the sample to an antibody that binds immunospecifically to the polypeptide, and determining the presence or amount of antibody bound to the polypeptide), determining the presence or expression of NOVX or NOVX DNA in a first mammalian subject, identifying an agent that binds to NOVX, identifying a potential therapeutic agent for treatment of a pathology related to aberrant expression or aberrant physiological interactions of NOVX, screening for a modulator of activity of or of latency or predisposition to a pathology associated with NOVX, a vector comprising NOVX DNA, a cell comprising the vector (used to produce

CC NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides are useful as a marker for cell or tissue type, and in diagnosing and treating pathologies, diseases, conditions or disorders associated with NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, prostate cancer, diabetes, metabolic disorders, neoplasia, graft versus host disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis, infectious diseases, anorexia, cancer-associated cachexia, neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), immune disorders, hematopoietic disorders, dyslipidemias, and wasting disorders associated with chronic diseases. These may also be used to screen for molecules which inhibit or enhance NOVX activity or function, and for detecting specific cell types. CC These may also be used in chromosome mapping, gene therapy, tissue typing, and in forensic biology. The present sequence represents a NOVX protein
 CC
 SQ Sequence 2220 AA;
 CC
 Query Match 100.0%; Score 77; DB 6; Length 2220;
 Best Local Similarity 100.0%; Pred. NO. 0.00047;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGLERGIYDISVIT 15
 Db 1326 TGLERGIYDISVIT 1340
 RESULT 14
 ID AAR60021 standard; protein; 2446 AA.
 AAR60021;
 AC AAR60021;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-FEB-1995 (first entry)
 XX
 DE Fibrinogen-alpha.
 XX
 KM Tissue binding; tissue sealing; wound healing; vulvarity;
 KM tissue-binding domain; TBD; crosslinking domain; fibronectin;
 KM fibrinogen-alpha; heparin-binding domain; collagen-binding domain;
 KM cell-binding domain; hybrid protein.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Domain 282..608
 FT /label= collagen-binding domain
 FT /note= "acts as tissue-binding domain of hybrid protein"
 FT Domain 1812..2171
 FT /label= heparin-binding domain
 FT /note= "acts as tissue-binding domain of hybrid protein"
 XX
 PN WO9416085-A2.
 XX
 PD 21-JUL-1994.
 XX
 PF 30-DEC-1993; 93WO-US012687.
 XX
 PR 30-DEC-1992; 92US-00998271.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Irant MH;
 XX
 DR WPI; 1994-249231/30.
 DR N-PSDB; AAQ70009.
 XX
 PT New hybrid proteins for use in tissue sealing and wound healing - comprising a tissue-binding domain from a protein covalently linked to a crosslinking domain of another protein.
 PT
 XX
 PS Disclosure; Page 37-48; 87PP; English.

XX Hybrid proteins have a tissue-binding domain (TBD) from 1 protein linked
CC to a crosslinking domain from another protein. The TBD comprises: aa 2-
CC 926, 928-1338 and especially 2-1336 of the sequence given in AAR60019;
CC the heparin-binding domain (aa 1812-2171 of AAR60021) of fibronectin; the
CC collagen-binding domain (aa 282-608 of AAR60021) of fibronectin; or the
CC cell-binding domain (aa 1357-1903 or 1532-1631 of AAR60020) of
CC fibronectin. DNA encoding a fibronectin-fibrinogen hybrid is given in
CC AAQ70007, and sequences for fibronectin and fibrinogen-alpha in AAQ70008
CC and AAQ70009, respectively. (Updated on 25-MAR-2003 to correct FN field.)
XX

SQ Sequence 2446 AA;

Query Match 100.0%; Score 77; DB 2; Length 2446;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
Db 1326 TGLEPGIDYDISVIT 1340

RESULT 15
AAB50377
ID AAB50377 standard; protein; 2446 AA.

AC AAB50377;

DT 12-MAR-2001 (first entry)

DE Human fibronectin.

DE Human fibronectin.

XX Human; FN; fibronectin; prostate cancer; biallelic marker; diagnosis.

XX Homo sapiens.

XX MO200058509-A2.

XX 05-OCT-2000.

XX 28-MAR-2000; 2000WO-1B000431.

XX 29-MAR-1999; 99US-0126780P.

XX (GEST) GENSET.

XX Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A;

XX WPI: 2000-594647/56.

XX N-PSDB; AAC89889.

XX Fibronectin polynucleotide and polypeptide sequences, useful for
XX determining the predisposition of individuals to cancer, such as prostate
XX cancer.

XX Claim 4; Page 185-190; 208pp; English.

XX The present sequence is given in a specification relating to an isolated
XX or purified recombinant polynucleotide comprising a contiguous span of at
XX least 12 nucleotides of a fibronectin (FN) gene. The methods and
XX sequences are useful for determining the predisposition of individuals to
XX cancer such as prostate cancer and for the prognosis/detection of an
XX eventual treatment response to therapeutic agents acting against prostate
XX cancer. Biallelic markers allow association studies to be performed to
XX identify genes involved in complex traits

SQ Sequence 2446 AA;

Query Match 100.0%; Score 77; DB 3; Length 2446;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15

Db 1326 TGLEPGIDYDISVIT 1340

Search completed: September 21, 2004, 05:53:32
Job time : 31.2206 secs

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:49:08; Search time 99.1544 Seconds
(without alignments)
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Title: US-10-676-049-3

Perfect score: 77
Sequence: 1 TGLRPGIDYDISVIT 15

Scoring table: ELOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1342398 segs, 32113274 residues

Total number of hits satisfying chosen parameters: 1342398

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications-AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	77	100.0	15	9 US-09-942-117-3	Sequence 3, Appli
2	77	100.0	91	9 US-09-942-117-4	Sequence 89, Appl
3	77	100.0	91	14 US-10-094-699-89	Sequence 589, App
4	77	100.0	91	15 US-10-117-937-589	Sequence 5, Appl
5	77	100.0	91	16 US-10-450-012-5	Sequence 50, Appl
6	77	100.0	147	14 US-10-094-699-90	Sequence 590, App
7	77	100.0	147	15 US-10-117-937-590	Sequence 4, Appl
8	77	100.0	2220	12 US-10-236-392-4	Sequence 23, Appl
9	64	83.1	15	10 US-09-300-4258-23	Sequence 2, Appl
10	64	83.1	15	14 US-10-321-558-2	Sequence 2, Appl
11	56	72.7	15	9 US-09-942-117-2	Sequence 1591, Ap
12	56	72.7	16	US-10-408-7654-1591	Sequence 102, App
13	51	66.2	1297	12 US-10-187-975-102	Sequence 19, Appl
14	50	64.9	15	9 US-09-942-117-19	Sequence 2, Appl
15	50	64.9	270	16 US-10-240-488-2	

15	50	64.9	271	10	US-09-043-981-1	Sequence 1, Appl
17	50	64.9	271	10	US-09-775-864-1	Sequence 1, Appl
18	50	64.9	457	10	US-09-775-964-22	Sequence 22, Appl
19	50	64.9	545	16	US-10-408-7654-349	Sequence 349, Appl
20	50	64.9	547	10	US-09-775-964-13	Sequence 13, Appl
21	50	64.9	549	10	US-09-775-964-23	Sequence 23, Appl
22	50	64.9	573	10	US-09-775-964-30	Sequence 30, Appl
23	50	64.9	574	10	US-09-775-964-24	Sequence 24, Appl
24	50	64.9	693	16	US-10-741-601-364	Sequence 364, App
25	50	64.9	793	14	US-10-171-811-62	Sequence 62, Appl
26	50	64.9	826	10	US-09-775-964-14	Sequence 14, Appl
27	50	64.9	847	16	US-10-741-601-361	Sequence 361, App
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29	50	64.9	1286	16	US-10-741-601-362	Sequence 362, App
30	50	64.9	1315	16	US-10-741-601-358	Sequence 358, App
31	50	64.9	1341	16	US-10-741-601-355	Sequence 355, App
32	50	64.9	1348	16	US-10-741-601-353	Sequence 353, App
33	50	64.9	2296	16	US-10-741-601-357	Sequence 357, App
34	50	64.9	2320	12	US-10-236-392-2	Sequence 2, Appl
35	50	64.9	2320	14	US-10-279-733-8	Sequence 8, Appl
36	50	64.9	2328	12	US-10-182-935A-98	Sequence 98, Appl
37	50	64.9	2328	14	US-10-171-811-64	Sequence 64, Appl
38	50	64.9	2328	15	US-10-236-031B-70	Sequence 70, Appl
39	50	64.9	2328	15	US-10-374-979-98	Sequence 98, Appl
40	50	64.9	2355	15	US-10-144-194A-104	Sequence 104, App
41	50	64.9	2355	15	US-10-360-101-235	Sequence 235, App
42	50	64.9	2355	16	US-10-447-161-3	Sequence 3, Appl
43	50	64.9	2355	16	US-10-734-564-94	Sequence 94, Appl
44	50	64.9	2355	16	US-10-741-601-357	Sequence 357, App
45	50	64.9	2355	16	US-10-741-601-366	Sequence 366, App

ALIGNMENTS

RESULT 1
US-09-942-117-3
Sequence 3, Application US/09942117
Publication No. US20020197700A1
GENERAL INFORMATION:
APPLICANT: MENRAD, ANDREAS
APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPPLITZ, MARCUS
APPLICANT: EGNER, URSULA
APPLICANT: BARR, INKE
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
FILE REFERENCE: SCH-1832
CURRENT APPLICATION NUMBER: US/09/942,117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-3
Query Match 100.0%; Score 77; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3; 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGLRPGIDYDISVIT 15
DB 1 TGLRPGIDYDISVIT 15

Tue Sep 21 07:04:09 2004

us-10-676-049-3.open.rapp

Page 2

RESULT 2

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US-09-942-117-4
Sequence 4, Application US/09942117
Publication No. US20020197700A1
GENERAL INFORMATION:
APPLICANT: MENRAD, ANDREAS
APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPLLITZ, MARCUS
APPLICANT: EGNER, URSULA
APPLICANT: BAHR, INGE
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
FILE REFERENCE: SCH-1832
CURRENT APPLICATION NUMBER: US/09/942,117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045603.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 91
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-4

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Query Match	100.0%;	Score 77;	DB 9;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 2.7e-05;		
Matches 15; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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Db      61 TGLEPGIDYDISVIT 75
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RESULT 3

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/ Sequence 89, Application US/10094699
/ Publication No. US2003004671A1
/ GENERAL INFORMATION:
/ APPLICANT: SIMAD, John, J.L.
/ APPLICANT: DIAMOND, David, C.
/ TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
/ TITL OF INVENTION: CANCER
/ FILE REFERENCE: CILJIM.015A
/ CURRENT APPLICATION NUMBER: US/10/094,699
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION NUMBER: US 60/274,063
/ PRIOR FILING DATE: 2001-03-07
/ NUMBER OF SEQ ID NOS: 109
/ SOFTWARE: Paetsrq for Windows Version 4.0
/ SEQ ID NO 89
/ LENGTH: 91
/ TYPE: prt
/ ORGANISM: Homo sapien
/ US-10-094-699-89

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Query Match	100.0%;	Score 77;	DB 14;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 2.7e-05;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      1 TLEPGIDYDISVIT 15
        |||||
Db      61 TLEPGIDYDISVIT 75

```

RESULT 4
US-10-117-937-589
; Sequence 589, Application US/10117937
; Publication No. US20030220239A1

```

GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIMOND, David, C.
APPLICANT: Liu, Liping
APPLICANT: Xie, Zhidong
TITLE OF INVENTION: EPTIPOE SEQUENCES
FILE REFERENCE: CTLImm_027A
CURRENT APPLICATION NUMBER: US/10/117,937/2
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 589
LENGTH: 91
TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-937-589

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Query Match	100.0%;	Score 77;	DB 15;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 2.7e-05;		
Matches	15;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Qy	1	TGLEPGIDYDISVIT	15
Db	61	TGLEPGIDYDISVIT	75

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RESULT 5
US-10-450-012-5
; Sequence 5, Application US/10450012
; Publication No. US20040091973A1
;
GENERAL INFORMATION:
; APPLICANT: Giovannoni, Leonardo
; TITLE OF INVENTION: Process for selecting anti-angiogenesis
; TITLE OF INVENTION: antibody fragments, anti-angiogenesis antibody fragments thus
; TITLE OF INVENTION: obtained and their use
; FILE REFERENCE: 0360-P03209U80
; CURRENT APPLICATION NUMBER: US/10/450,012
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/EP01/14330
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: F12000A000247
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 91
; TYPE: prt
; ORGANISM: Homo Sapiens
; US-10-450-012-5

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Query Match	100.0%;	Score 77;	DB 16;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 2.7e-05;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	TGLEPGIDYDISVIT	15
Db	61	TGLEPGIDYDISVIT	75

RESULT 6
US-10-094-699-90
; Sequence 90, Application US/10094699
; Publication No. US20030046714A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J L.
; APPLICANT: DIAMOND, David, C.

```

; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: CTJMM.015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-699-90

Query Match      100.0%; Score 77; DB 14; Length 147;
Best Local Similarity 100.0%; Pred. No. 4,6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGLEPGIDYDISVIT 15
      |||||
Db      95 TGLEPGIDYDISVIT 109

RESULT 7
US-10-117-937-590
; Sequence 590, Application US/10:117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: BRITPO SEQUENCES
; FILE REFERENCE: CTJMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-590

Query Match      100.0%; Score 77; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 4,6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGLEPGIDYDISVIT 15
      |||||
Db      95 TGLEPGIDYDISVIT 109

RESULT 8
US-10-236-392-4
; Sequence 4, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie

```

```

; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Larochele, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Maayanxar, Ofiel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Raetelli, Luca
; APPLICANT: Reiser, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/319,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 4
; LENGTH: 2220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-4

Query Match      100.0%; Score 77; DB 12; Length 2220;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGLEPGIDYDISVIT 15
      |||||
Db      1326 TGLEPGIDYDISVIT 1340

RESULT 9
US-09-300-425B-23
; Sequence 23, Application US/09300425B
; Publication No. US20030045681A1
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TARLI, Lorenzo
; APPLICANT: VITI, Francesca

```

APPLICANT: BIRCHER, Manfred
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: SCH-1733P1
CURRENT APPLICATION NUMBER: US/09/300,425B
CURRENT FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide formula
US-09-300-425B-23

Query Match 83.1%; Score 64; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGLEPGIDYDIS 12
Db 4 TGLEPGIDYDIS 15

RESULT 10
US-10-321-558-2
Sequence 2, Application US/10321558
Publication No. US20030176653A1
GENERAL INFORMATION:
APPLICANT: NERI, DARIO
APPLICANT: TARLI, LORENZO
APPLICANT: VITI, FRANCESCA
APPLICANT: BIRCHER, MANFRED
TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
FILE REFERENCE: NOTAR-1 C1
CURRENT APPLICATION NUMBER: US/10/321,558
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: 09/512,082
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 09/300,425
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/075,338
PRIOR FILING DATE: 1998-05-11
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-321-558-2

Query Match 83.1%; Score 64; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGLEPGIDYDIS 12
Db 4 TGLEPGIDYDIS 15

RESULT 11
US-09-942-117-2
Sequence 2, Application US/09942117
Publication No. US20020197700A1
GENERAL INFORMATION:
APPLICANT: MENRAD, ANDREAS

APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPPLITZ, MARCUS
APPLICANT: EGNER, URSULA
APPLICANT: BAHR, INKE
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
FILE REFERENCE: SCH-1832
CURRENT APPLICATION NUMBER: US/09/342,117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-2

Query Match 72.7%; Score 56; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGLEPGIDYD 10
Db 6 TGLEPGIDYD 15

RESULT 12
US-10-408-765A-1591
Sequence 1591, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faly, Boia D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 66088,465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1591
LENGTH: 1207
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-1591

Query Match 66.2%; Score 51; DB 16; Length 1207;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GLEPGIDYDISV 13
Db 532 GLEPGIDYISV 543

RESULT 13
US-10-187-975-102
Sequence 102, Application US/10187975
Publication No. US20030224982A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Shenoy, Suresh


```

APPLICANT: Patirajan, Meera
APPLICANT: Elletman, Karen
APPLICANT: Gorman, Linda
APPLICANT: Zhong, Wei
APPLICANT: Catterton, Elina
APPLICANT: Spytek, Kimberly
APPLICANT: Miller, Charles
APPLICANT: Edinger, Shionit
APPLICANT: Hjal, Tord
APPLICANT: Gerlach, Valerie
APPLICANT: Shimkets, Richard
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Anderson, David
APPLICANT: Guo, Xiaojia
APPLICANT: Baumgartner, Jason
APPLICANT: Padigaru, Muralidhara
APPLICANT: Peyman, John
APPLICANT: Smithson, Glenda
APPLICANT: Casman, Stacie
APPLICANT: Voss, Edward
APPLICANT: Boldog, Ferenc
APPLICANT: Pena, Carol
APPLICANT: Chapoval, Andrei
APPLICANT: Rastelli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Verne, Corine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: 21402-337A
CURRENT APPLICATION NUMBER: US/10/187, 975
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/303, 046
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/303, 828
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/304, 502
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/305, 011
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/305, 262
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/305, 673
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/306, 085
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 60/307, 536
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/308, 228
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/308, 877
PRIOR FILING DATE: 2001-07-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 288
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 102
LENGTH: 1297
TYPE: PRT
ORGANISM: Homo sapiens
US-10-187-975-102

Query Match      66.2%; Score 51; DB 12; Length 1297;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GLEPGIDYDISV 13
      |||||
Db      532 GLEPGRDYEVSV 543

RESULT 14
US-09-942-117-19
; Sequence 19, Application US/09942117
; Publication No. US20020197700A1

```

```

GENERAL INFORMATION:
APPLICANT: MENRAD, ANDREAS
APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPPLITZ, MARCUS
APPLICANT: ESNER, URSULA
APPLICANT: BAH, INKE
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
FILE REFERENCE: SCH-1832
CURRENT APPLICATION NUMBER: US/09/942, 117
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-19

Query Match      64.9%; Score 50; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GIDYDISVIT 15
      |||||
Db      1 GIDYDISVIT 10

RESULT 15
US-10-240-488-2
; Sequence 2, Application US/10240488
; Publication No. US20040175377A1
GENERAL INFORMATION:
APPLICANT: Peters, Donna M
APPLICANT: Kautman, Paul L
TITLE OF INVENTION: Agent and Method for Reducing Intraocular Pressure
FILE REFERENCE: 960296, 96951
CURRENT APPLICATION NUMBER: US/10/240, 488
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/192942
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 270
TYPE: PRT
ORGANISM: Homo sapiens
US-10-240-488-2

Query Match      64.9%; Score 50; DB 16; Length 270;
Best Local Similarity 71.4%; Pred. No. 3.3;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TELEPGIDYDISVI 14
      |||||
Db      240 TELEPGTEXTIYVI 253

Search completed: September 21, 2004, 06:30:30
Job time : 99.1544 secs

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Blank

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: September 21, 2004, 05:47:40 : Search time 8.60294 Seconds

(without alignments)
90.015 Million cell updates/sec

Title: US-10-676-049-3

Sequence: 1 TGLERGDYDISVIT 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	77	100.0	1336	2	US-08-551-356-6	Sequence 6, Appl1
2	77	100.0	1336	5	PCT-US93-12687-6	Sequence 6, Appl1
3	77	100.0	2446	2	US-08-551-356-2	Sequence 2, Appl1
4	77	100.0	2446	5	PCT-US93-12687-2	Sequence 2, Appl1
5	50	64.9	21	3	US-08-933-1008-8	Sequence 8, Appl1
6	50	64.9	32	3	US-08-933-1008-15	Sequence 15, Appl1
7	50	64.9	271	3	US-08-933-1008-15	Sequence 1, Appl1
8	50	64.9	271	3	US-08-933-1008-14	Sequence 14, Appl1
9	50	64.9	271	4	US-09-366-009-1	Sequence 1, Appl1
10	50	64.9	271	4	US-08-809-156B-1	Sequence 1, Appl1
11	50	64.9	271	4	US-09-043-881-1	Sequence 1, Appl1
12	50	64.9	296	2	US-08-836-854-4	Sequence 4, Appl1
13	50	64.9	368	2	US-08-836-854-17	Sequence 17, Appl1
14	50	64.9	457	2	US-08-836-854-16	Sequence 16, Appl1
15	50	64.9	457	2	US-09-366-009-22	Sequence 22, Appl1
16	50	64.9	457	4	US-08-809-156B-22	Sequence 22, Appl1
17	50	64.9	547	4	US-09-366-009-13	Sequence 13, Appl1
18	50	64.9	547	4	US-08-809-156B-13	Sequence 13, Appl1
19	50	64.9	549	4	US-08-836-854-11	Sequence 11, Appl1
20	50	64.9	549	4	US-09-366-009-23	Sequence 23, Appl1
21	50	64.9	573	4	US-08-809-156B-23	Sequence 23, Appl1
22	50	64.9	573	4	US-09-366-009-30	Sequence 30, Appl1
23	50	64.9	573	4	US-08-809-156B-30	Sequence 30, Appl1
24	50	64.9	574	3	US-08-836-854-21	Sequence 21, Appl1
25	50	64.9	574	3	US-09-463-286-1	Sequence 1, Appl1
26	50	64.9	574	3	US-09-366-009-24	Sequence 24, Appl1
27	50	64.9	574	4	US-08-809-156B-24	Sequence 24, Appl1

28	50	64.9	826	4	US-09-366-009-14	Sequence 14, Appl1
29	50	64.9	826	4	US-08-809-156B-14	Sequence 14, Appl1
30	50	64.9	2231	1	US-08-153-799-16	Sequence 16, Appl1
31	50	64.9	2324	1	US-08-283-857-1	Sequence 1, Appl1
32	50	64.9	2324	5	PCT-US95-09819-1	Sequence 1, Appl1
33	50	64.9	2327	6	US-09-016-366A-12	Sequence 12, Appl1
34	50	64.9	2386	2	US-09-016-366A-12	Sequence 12, Appl1
35	49	63.6	89	1	US-08-241-853-32	Sequence 32, Appl1
36	49	63.6	89	2	US-08-850-917-32	Sequence 32, Appl1
37	49	63.6	94	4	US-08-717-169-8	Sequence 8, Appl1
38	49	63.6	94	4	US-09-638-202A-110	Sequence 110, Appl1
39	49	63.6	94	4	US-09-228-901A-8	Sequence 8, Appl1
40	49	63.6	94	4	US-09-096-749A-110	Sequence 110, Appl1
41	49	63.6	96	4	US-08-638-202A-112	Sequence 112, Appl1
42	49	63.6	96	4	US-09-096-749A-112	Sequence 112, Appl1
43	49	63.6	175	1	US-08-078-683A-34	Sequence 34, Appl1
44	49	63.6	175	4	US-08-471-970A-34	Sequence 34, Appl1
45	49	63.6	256	1	US-07-959-369-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-551-356-6
Sequence 6, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Iran, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,356
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
FILING DATE:
APPLICATION NUMBER: US/07/998,271
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holly, Julie A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-356-6
Query Match 100.0%; Score 77; DB 2; Length 1336;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TGLERGDYDISVIT 15
|||||

DB 349 TGLEPGIDYDISVIT 363

RESULT 2
PCT-US93-12687-6
Sequence 6, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Iranl, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-6

Query Match 100.0%; Score 77; DB 5; Length 1336;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
DB 349 TGLEPGIDYDISVIT 363

RESULT 3
US-08-551-356-2
Sequence 2, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Iranl, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,356
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
FILING DATE:
APPLICATION NUMBER: US/07/998,271
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holly, Julie A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-356-2

Query Match 100.0%; Score 77; DB 2; Length 2446;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
DB 1326 TGLEPGIDYDISVIT 1340

RESULT 4
PCT-US93-12687-2
Sequence 2, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Iranl, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-2

Query Match 100.0%; Score 77; DB 5; Length 2446;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISVT 15
DB 1326 TGLEPGIDYDISVT 1340

RESULT 5
US-08-933-100B-8
Sequence 8, Application US/08933100B
Patent No. 6274704
GENERAL INFORMATION:
APPLICANT: FUKAI, FUMIO
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDE AND CANCER
TITLE OF INVENTION: METASTASIS INHIBITOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,100B
FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PERRY, GLENN
REGISTRATION NUMBER: 28458
REFERENCE/DOCKET NUMBER: 7898/242094
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: Sequence of a part (1835 - 1855) of Heparin binding site
Patent No. 6274704
US-08-933-100B-8
Query Match 64.9%; Score 50; DB 3; Length 21;
Best Local Similarity 71.4%; Pred. No. 0.045;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISVT 14
DB 6 TGLEPGITTYTVI 19
RESULT 6
US-08-933-100B-15
Sequence 15, Application US/08933100B
Patent No. 6274704
GENERAL INFORMATION:
APPLICANT: FUKAI, FUMIO
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDE AND CANCER

TITLE OF INVENTION: METASTASIS INHIBITOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,100B
FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PERRY, GLENN
REGISTRATION NUMBER: 28458
REFERENCE/DOCKET NUMBER: 7898/242094
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 32
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: sequence of a part (1829-1860) of Heparin binding site of
US-08-933-100B-15
Query Match 64.9%; Score 50; DB 3; Length 32;
Best Local Similarity 71.4%; Pred. No. 0.073;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISVT 14
DB 12 TGLEPGTETTYTVI 25

RESULT 7
US-08-536-891A-1
Sequence 1, Application US/08536891A
Patent No. 6033907
GENERAL INFORMATION:
APPLICANT: David A. Williams
TITLE OF INVENTION: Enhanced Virus-Mediated DNA Transfer
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas O. Henry
STREET: Bank One Tower, Suite 3700, 111 Monument Circle
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: COMPAQ
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCIT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/536,891A
FILING DATE: September 29, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03817
FILING DATE: March 27, 1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/218,355
FILING DATE: March 25, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Thomas Q. Henry
REGISTRATION NUMBER: 28,309
REFERENCE/DOCKET NUMBER: 7037-52/1U-33-CIP-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 634-3456
TELEFAX: (317) 637-7561
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein fragment
US-08-536-891A-1

Query Match 64.9%; Score 50; DB 3; Length 271;
Best Local Similarity 71.4%; Pred. No. 0.84;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVT 14
|||||:|||||
Db 241 TGLEPGTEYTYIVY 254

RESULT 8
US-08-933-100B-14
Sequence 14, Application US/08933100B
Patent No. 6274704
GENERAL INFORMATION:
APPLICANT: FUKAI, FUMIO
APPLICANT: KATAYAMA, TAKASHI
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDE AND CANCER
TITLE OF INVENTION: METASTASIS INHIBITOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,100B
FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PERRY, GLENN
REGISTRATION NUMBER: 28458
REFERENCE/DOCKET NUMBER: 7898/242094
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 271
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE: OTHER INFORMATION: sequence of a part (1600-1870) of Heparin binding site
US-08-933-100B-14

Query Match 64.9%; Score 50; DB 3; Length 271;

Best Local Similarity 71.4%; Pred. No. 0.84;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISVT 14
|||||:|||||
Db 241 TGLEPGTEYTYIVY 254

RESULT 9
US-09-366-009-1
Sequence 1, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Ueno, Takashi
Koyama, No. 6426042uro
Hashino, Kimikazu
Kato, Ikunoshita
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-366-009-1

Query Match 64.9%; Score 50; DB 4; Length 271;
Best Local Similarity 71.4%; Pred. No. 0.84;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGLEPGIDYDISVT 14
|||||:|||||
Db 241 TGLEPGTEYTYIVY 254

RESULT 10
US-08-809-156B-1

```

; Sequence 1, Application US/0809156B
; Patent No. 6472204
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; APPLICANT: Uemori, Takashi
; APPLICANT: Koyama, No. 6472204uto
; APPLICANT: Hashino, Kimikazu
; APPLICANT: Kato, Ikumoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; TITLE OF INVENTION: CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; City: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,156B
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/03254
; FILING DATE: 07-NOV-1996
; PRIOR APPLICATION DATA: JP 294382/1995
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977,6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-809-156B-1

Query Match      64.9%; Score 50; DB 4; Length 271;
Best Local Similarity 71.4%; Pred. No. 0.84;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy      1 TGLEPGIDYDISVI 14
        |||||:|:|
Db      241 TGLEPGTEYTYVI 254

RESULT 11
US-09-043-981-1
; Sequence 1, Application US/09043981
; Patent No. 6670177
; GENERAL INFORMATION:
; APPLICANT: Williams, David A.
; TITLE OF INVENTION: METHODS FOR ENHANCED VIRUS MEDIATED DNA TRANSFER USING
; FILE REFERENCE: 7037-297
; CURRENT APPLICATION NUMBER: US/09/043,981
; CURRENT FILING DATE: 1998-06-19

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; EARLIER APPLICATION NUMBER: US96/15712
; EARLIER FILING DATE: 1996-09-30
; EARLIER APPLICATION NUMBER: 08/536,891
; EARLIER FILING DATE: 1995-09-29
; EARLIER APPLICATION NUMBER: 60/024,169
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-043-981-1

Query Match      64.9%; Score 50; DB 4; Length 271;
Best Local Similarity 71.4%; Pred. No. 0.84;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy      1 TGLEPGIDYDISVI 14
        |||||:|:|
Db      241 TGLEPGTEYTYVI 254

RESULT 12
US-08-836-854-4
; Sequence 4, Application US/08836854
; Patent No. 5824547
; GENERAL INFORMATION:
; APPLICANT: HASHINO, Kimikazu
; APPLICANT: KATSUSHITA, Hideyuki
; APPLICANT: KATO, Ikumoshin
; TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/02425
; FILING DATE: 29-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 317721/1994
; FILING DATE: 29-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: HASHINO=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-836-854-4

Query Match      64.9%; Score 50; DB 2; Length 296;
Best Local Similarity 71.4%; Pred. No. 0.92;

```

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGLEPGIDYISVI 14
|||||:|||||
Db 241 TGLEPGTEYTYVI 254

RESULT 13
US-08-836-854-17
; Sequence 17, Application US/08836854
; Patent No. 5824547
; GENERAL INFORMATION:
; APPLICANT: HASHINO, Kimikazu
; APPLICANT: MATSUSHITA, Hideyuki
; APPLICANT: KATO, Ikumoshin
; TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/02425
; FILING DATE: 29-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 317721/1994
; FILING DATE: 29-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: HASHINO=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-836-854-17

Query Match 64.9%; Score 50; DB 2; Length 368;
Best Local Similarity 71.4%; Pred. No. 1.2;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGLEPGIDYISVI 14
|||||:|||||
Db 338 TGLEPGTEYTYVI 351

RESULT 14
US-08-836-854-16
; Sequence 16, Application US/08836854
; Patent No. 5824547
; GENERAL INFORMATION:
; APPLICANT: HASHINO, Kimikazu
; APPLICANT: MATSUSHITA, Hideyuki

NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-16

Query Match 64.9%; Score 50; DB 2; Length 457;
Best Local Similarity 71.4%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGLEPGIDYISVI 14
|||||:|||||
Db 427 TGLEPGTEYTYVI 440

RESULT 15
US-09-366-009-22
; Sequence 22, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, No. 6426042
; Hashino, Kimikazu
; Kato, Ikumoshin

TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/366,009

FILING DATE: 02-Aug-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/809,156

FILING DATE: <Unknown>

APPLICATION NUMBER: JP 294382/1995

FILING DATE: 13-NOV-1995

APPLICATION NUMBER: JP 051847/1996

FILING DATE: 08-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerard J.

REGISTRATION NUMBER: 19,763

REFERENCE/DOCKET NUMBER: 977.6507P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-875-8383

TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-366-009-22

Query Match

64.9%; Score 50; DB 4; Length 457;

Best Local Similarity 71.4%; Pred. NO. 1.5; Mismatches 0; Gaps 0;

Matches 10; Conservative 1; Indels 3; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVI 14

Db 427 TGLEPGREYTIYVI 440

Search completed: September 21, 2004, 06:15:27
Job time : 9.60294 secs

This Page Blank (uspto)

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53; Search time 45.5 Seconds

(without alignments)
192.383 Million cell updates/sec

Title: US-10-676-049-4

Sequence: 1 EVPOLDLSPVDITSSIGL.....SVITLNGESAPPTLTQOT 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	147	2 S00848	fibronectin, trans
2	462	100.0	2477	2 S14428	fibronectin precu
3	457	98.9	90	2 I46162	fibronectin ED-B-
4	422	91.3	1020	2 A29355	fibronectin - chic
5	363	78.6	2481	2 A43908	fibronectin - Afri
6	148.5	32.1	2386	1 FNHU	fibronectin precu
7	147.5	31.9	2265	1 FNBO	fibronectin - bovi
8	128.5	27.8	2273	2 A28512	fibronectin - chic
9	107.5	22.7	1427	2 I51669	tumor suppressor
10	105	22.3	1810	2 A32230	fibronectin - chic
11	104	22.5	189	2 S71465	restictin precurs
12	103	22.3	1353	1 JH0675	collagen alpha 1(V
13	103	22.3	2944	2 A54849	collagen alpha 1(X
14	102	22.1	3124	2 A40020	titin, cardiac mus
15	99	21.4	26926	1 I38344	tenascin - eacern
16	97	21.0	647	2 A43902	protein-tyrosine K
17	97	21.0	1125	1 S57846	cytoactin - chick
18	96.5	20.9	933	2 A31930	fibronectin ED-A-
19	95.5	20.7	89	2 I46161	fibronectin - guin
20	95.5	20.7	123	2 A40790	probable tenascin
21	93.5	20.2	4006	2 T09070	tumor suppressor P
22	93	20.1	1447	2 A54100	type XII collagen
23	92	19.9	929	2 I51027	undulin 1 - human
24	91.5	19.8	843	2 A40970	tenascin-X - bovin
25	91	19.7	4135	2 T42629	protein-tyrosine-P
26	89.5	19.4	440	2 I50213	tenascin precursor
27	89.5	19.4	2019	1 J01322	janusin precursor
28	89	19.3	1356	2 A45445	exo-poly-alpha-gal
29	88.5	19.2	1148	2 S72635	

30	87.5	18.9	2201	2 A32160	tenascin-C - human
31	87	18.8	1122	2 I54237	protein-tyrosine K
32	87	18.8	1123	1 JN0712	protein-tyrosine K
33	87	18.8	1125	1 JH0771	neogemin - chicken
34	87	18.8	1443	2 I50600	tenascin precursor
35	87	18.8	1746	1 A19594	collagen alpha 1(X
36	85	18.4	1747	2 A45974	collagen alpha 1(X
37	85	18.4	531212	2 S31212	collagen alpha 1(X
38	85	18.4	1888	2 S78476	chitinase (EC 3.2.
39	84.5	18.3	597	1 S32039	tenascin-X - mouse
40	84	18.2	660	2 I48839	titin, muscle - ch
41	83.5	18.1	817	2 A48721	hypothetical prote
42	82.5	17.9	725	2 A90255	hypothetical prote
43	82.5	17.9	900	2 T32827	undulin 2 - human
44	82	17.7	445	2 B40970	leukocyte antigen-
45	81.5	17.6	1897	1 T8HDLK	

ALIGNMENTS

RESULT 1

S00848
fibronectin, transformation-associated splice form - human (fragment)

N.Alternate names: fibronectin ED-B

C.Species: Homo sapiens (man)

C.Date: 01-Dec-1989 #sequence revision 01-Dec-1989 #text_change 21-Jul-2000

C.Accession: S00848, I59102; A28347

R.Paoletti, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.

Nucleic Acids Res. 16, 3545-3557, 1988

A.Title: Sequence analysis and in vivo expression show that alternative splicing of ED-

A.Reference number: S00848, MUID:88023940, PMID:3375063

A.Accession: S00848

A.Molecule type: DNA

A.Residues: 1-147 <PAC>

A.Cross-references: EMBL:X07717, NID:G31406, PID:CB52437.1, PID:G5725425

R.Gutman, A.; Kornblith, A.R.

Proc. Natl. Acad. Sci. U.S.A. 84, 7179-7182, 1987

A.Title: Identification of a third region of cell-specific alternative splicing in huma

A.Reference number: I59102, MUID:88041070, PMID:3478690

A.Accession: I59102

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 26-134 <GUT>

A.Cross-references: GB:M8179, NID:G182693, PID:AAA52461.1, PID:G182695

R.Zardi, L.; Cammerella, B.; Stiri, A.; Petersen, T.E.; Paoletti, G.; Bara

EMBO J. 6, 2337-2342, 1987

A>Title: Transformed human cells produce a new fibronectin isoform by preferential alte

A.Reference number: A28347, MUID:88029324, PMID:2822387

A.Accession: A28347

A.Molecule type: protein

A.Residues: 3-146 <ZAR>

C.Genetics:

A.Gene: GDB:FN1

A.Cross-references: GDB:119135, OMIM:135600

A.Map position: 2q34-2q34

A.Introns: 35/1, 126/1

C.Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II rep

F;Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heve

Query Match	100.0%	Score 462;	DB 2;	Length 147;
Best Local Similarity	100.0%	Pred. No. 4,4e-40;		
Matches	91;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;
QY	1	EVPOLDLSPVDITSSIGLRWTPINSSITIGRTTVAAGGPIFPDSDSVGYTV	60	
DB	35	EVPOLDLSPVDITSSIGLRWTPINSSITIGRTTVAAGGPIFPDSDSVGYTV	94	
QY	61	TGLEPGIDYDISVITLNGESAPPTLTQOT	91	
DB	95	TGLEPGIDYDISVITLNGESAPPTLTQOT	125	

RESULT 2

S14428

fibronectin precursor - rat

C|Species: Rattus norvegicus (Norway rat)

C|Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text change 20-Aug-1999

C|Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049

R|Hynes, R.O.

Submitted to the EMBL Data Library, July 1989

A|Reference number: S14428

A|Accession: S14428

A|Molecule type: mRNA

A|Residues: 1-2477 <HYN>

A|Cross-references: EMBL:X15905; NID:956163; PIDN:CAA4020.1; PID:956164

R|Schwarzbauer, U.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.

EMBO J. 6, 2573-2580, 1987

A|Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.

A|Reference number: S12455; PMID:88054951; PMID:2445560

A|Accession: S12455

A|Status: nucleic acid sequence not shown

A|Molecule type: mRNA

A|Residues: 609-1810,'T',1812-2283 <SCH>

A|Cross-references: EMBL:X15906

R|Tankun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.

Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984

A|Title: A single rat fibronectin gene generates three different mRNAs by alternative splicing.

A|Reference number: A22319; PMID:84298097; PMID:6089177

A|Accession: A22319

A|Molecule type: DNA

A|Residues: 2052-2237 <TAM>

R|Falkenberg, C.; Enghild, J.J.; Thøgersen, I.B.; Salvesen, G.; Akerstrøm, B.

Biochem. J. 301, 745-751, 1994

A|Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in

A|Reference number: S46203; PMID:94330948; PMID:7519849

A|Accession: S46203

A|Status: preliminary

A|Molecule type: protein

A|Residues: 1183-1192;'Gln',1268,'P',1270-1271,'D',1273,'CF',1276,'PY',1385-1399 <FAL>

R|Patel, R.S.; Odehmat, E.; Schwarzbauer, J.E.; Hynes, R.O.

EMBO J. 6, 2565-2572, 1987

A|Title: Organization of the fibronectin gene provides evidence for exon shuffling during

A|Reference number: S00459; PMID:88054950; PMID:3119323

A|Accession: S00459

A|Molecule type: DNA

A|Residues: 1-139;2382-2477 <PAT>

A|Cross-references: EMBL:X05831

A|Note: the authors translated the codon CCG for residues 51 and 94 as Ala

R|Schwarzbauer, J.E.; Tankun, J.W.; Lemischka, I.R.; Hynes, R.O.

Cell 35, 421-431, 1983

A|Title: Three different fibronectin mRNAs arise by alternative splicing within the codi

A|Reference number: A27252; PMID:84082067; PMID:6317187

A|Accession: A27252

A|Molecule type: mRNA

A|Residues: 1586-1720,'T',1722,1813-2477 <SC2>

R|Odehmat, E.; Tankun, J.W.; Hynes, R.O.

Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985

A|Title: Repeating modular structure of the fibronectin gene: Relationship to protein st

A|Reference number: I59049; PMID:86016741; PMID:3863113

A|Accession: I59049

A|Status: translated from GB/EMBL/DBJ

A|Molecule type: DNA

A|Residues: 1722-1810 <RES>

A|Cross-references: GB:M11750; NID:9204164; PIDN:AAA1170.1; PID:9554437

C|GeneID:51

A|Intons: 51/1; 94/1; 2416/3; 2454/3

C|Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe

C|Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; dupli

F|1-32/Domain: signal sequence #status predicted <Sig>

F|33-2477/Product: fibronectin #status predicted <Mat>

F|33-86/Domain: fibronectin type I repeat homology <IF1>

F|38-116/Domain: fibronectin type I repeat homology <IF2>

F|187-226/Domain: fibronectin type I repeat homology <IF4>

F|232-271/Domain: fibronectin type I repeat homology <IF5>

F|308-342/Domain: fibronectin type I repeat homology <IF6>

F|360-401/Domain: fibronectin type II repeat homology <2F1>

F|420-461/Domain: fibronectin type II repeat homology <2F2>

F|470-508/Domain: fibronectin type I repeat homology <1F7>

F|518-555/Domain: fibronectin type I repeat homology <1F8>

F|561-599/Domain: fibronectin type I repeat homology <1F9>

F|609-692/Domain: fibronectin type III repeat homology <FN3A>

F|718-800/Domain: fibronectin type III repeat homology <FN3B>

F|809-890/Domain: fibronectin type III repeat homology <FN3C>

F|905-987/Domain: fibronectin type III repeat homology <FN3D>

F|995-1076/Domain: fibronectin type III repeat homology <FN3E>

F|1085-1164/Domain: fibronectin type III repeat homology <FN3F>

F|1172-1257/Domain: fibronectin type III repeat homology <FN3G>

F|1265-1348/Domain: fibronectin type III repeat homology <FN3H>

F|1356-1439/Domain: fibronectin type III repeat homology <FN3I>

F|1447-1529/Domain: fibronectin type III repeat homology <FN3J>

F|1537-1619/Domain: fibronectin type III repeat homology <FN3K>

F|1631-1616/Region: cell attachment (R-G-D) motif

F|1631-1713/Domain: fibronectin type III repeat homology <FN3L>

F|1721-1803/Domain: fibronectin type III repeat homology <FN3M>

F|1811-1893/Domain: fibronectin type III repeat homology <FN3N>

F|1903-1984/Domain: fibronectin type III repeat homology <FN3O>

F|1992-2074/Domain: fibronectin type III repeat homology <FN3P>

F|2181-2183/Region: cell attachment (R-G-D) motif

F|2189-2273/Domain: fibronectin type III repeat homology <FN3Q>

F|2236-2335/Domain: fibronectin type I repeat homology <1F10>

F|2341-2378/Domain: fibronectin type I repeat homology <1F11>

F|2385-2420/Domain: fibronectin type I repeat homology <1F12>

F|53-79, 77-88, 98-126, 124-136, 142-170, 168-180, 187-216, 214-226, 232-261, 259-271, 308-335, 333

368, 2366-2378, 2385-2411, 2409-2420/disulfide bonds: #status predicted

F|2458/disulfide bonds: interchain (to 2462) #status predicted

F|2462/disulfide bonds: interchain (to 2458) #status predicted

Query Match

Best Local Similarity 100.0%; Score 462; DB 2; Length 2477;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 EVPOLTLSPVDITDSSIGLRWPLNSSTIIGRIITVAAGEGPIFEDVDSVGYYTV 60

Db 1265 EVPOLTLSPVDITDSSIGLRWPLNSSTIIGRIITVAAGEGPIFEDVDSVGYYTV 1324

Db 61 TGLRPGIDYISVITTLINGESAPPTLTQQT 91

Db 1325 TGLRPGIDYISVITTLINGESAPPTLTQQT 1355

RESULT 3

146162

fibronectin ED-B - dog (fragment)

C|Species: Canis lupus familiaris (dog)

C|Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999

C|Accession: 146162

R|Zhang, D.W.; Burton-Wurster, N.; Lust, G.

J. Biol. Chem. 270, 1817-1822, 1995

A|Title: Alternative splicing of ED-A and ED-B sequences of fibronectin pre-mRNA differs

A|Reference number: 146161; PMID:95130563; PMID:7829518

A|Accession: 146162

A|Status: preliminary; translated from GB/EMBL/DBJ

A|Molecule type: mRNA

A|Residues: 1-90 <ZHA>

A|Cross-references: EMBL:U16208; NID:9562166; PIDN:AAA67749.1; PID:9562169

C|Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe

Query Match

Best Local Similarity 100.0%; Score 457; DB 2; Length 90;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 VPQTLTDSFVDTIDSSIGLRWPLNSSTIIGRIITVAAGEGPIFEDVDSVGYYTV 61

Db 1 VPQTLTDSFVDTIDSSIGLRWPLNSSTIIGRIITVAAGEGPIFEDVDSVGYYTV 60

```

Qy      62  GLEPGIDYDISVITLLINGESAPTTLTQQT 91
      |||
      61  GLEPGIDYDISVITLLINGESAPTTLTQQT 90

RESULT 4
A29355
  fibronectin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #ext_change 12-Feb-1999
C:Accession: A29355
R:Norton, P.A.; Hynes, R.O.
Mol. Cell. Biol. 7, 4297-4307, 1987
A>Title: Alternative splicing of chicken fibronectin in embryos and in normal and trans
A:Reference number: A29355; MUID:88142820; PMID:2830487
A:Molecule type: mRNA
A:Residues: 1-1020 <NOR>
C:Genetics: 176/3
A:Intons: 176/3
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter
F:1-86/Domain: fibronectin type III repeat homology <FN3H>
F:92-177/Domain: fibronectin type III repeat homology <FN3I>
F:180-262/Domain: fibronectin type III repeat homology <FN3J>
F:257-259/Region: cell attachment (R-G-D) motif
F:274-356/Domain: fibronectin type III repeat homology <FN3K>
F:364-446/Domain: fibronectin type III repeat homology <FN3L>
F:454-536/Domain: fibronectin type III repeat homology <FN3M>
F:546-628/Domain: fibronectin type III repeat homology <FN3N>
F:636-718/Domain: fibronectin type III repeat homology <FN3O>
F:837-917/Domain: fibronectin type III repeat homology <FN3P>
F:940-979/Domain: fibronectin type I repeat homology <1F10>
F:940-969,967-979,985-1012/Disulfide bonds: #status predicted

Query Match      91.3%; Score 422; DB 2; Length 1020;
Best Local Similarity 93.2%; Pred. No. 5.1e-35;
Matches 82; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1  EVPOLTLSPVDITDSSIGLRMPPLNSITIGRTVVAAGEGIPFEDFVDSVGYTV 60
      |||
      94  EVPOLTLSPVDITDSSIGLRMPPLNSITIGRTVVAAGEGIPFEDFVDSVGYTV 153
      |||

Db      61  TGLEPGIDYDISVITLLINGESAPTTLT 88
      |||
      154  TGLEPGIDYDISVITLLINGESAPTTVS 181
      |||

RESULT 5
A43908
  fibronectin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #ext_change 12-Feb-1999
C:Accession: A43908
R:Desimone, D.W.; Norton, P.A.; Hynes, R.O.
Dev. Biol. 149, 357-369, 1992
A>Title: Identification and characterization of alternatively spliced fibronectin mRNAs
A:Reference number: A43908; MUID:92111942; PMID:1730390
A:Accession: A43908
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2481 <DES>
A:Cross-references: GB:M77820
A>Note: sequence extracted from NCBI backbone (NCBIP:77473)
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C:Keywords: duplication; extracellular matrix; glycoprotein; heterodimer
F:35-90/Domain: fibronectin type I repeat homology <1F1>
F:100-138/Domain: fibronectin type I repeat homology <1F2>
F:144-182/Domain: fibronectin type I repeat homology <1F3>
F:189-228/Domain: fibronectin type I repeat homology <1F4>
F:234-273/Domain: fibronectin type I repeat homology <1F5>
F:309-343/Domain: fibronectin type I repeat homology <1F6>
F:361-402/Domain: fibronectin type II repeat homology <2F1>

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F:421-462/Domain: fibronectin type II repeat homology <2F2>
F:471-509/Domain: fibronectin type I repeat homology <1F7>
F:519-556/Domain: fibronectin type I repeat homology <1F8>
F:562-600/Domain: fibronectin type I repeat homology <1F9>
F:610-693/Domain: fibronectin type III repeat homology <FN3A>
F:719-801/Domain: fibronectin type III repeat homology <FN3B>
F:810-891/Domain: fibronectin type III repeat homology <FN3C>
F:906-988/Domain: fibronectin type III repeat homology <FN3D>
F:996-1077/Domain: fibronectin type III repeat homology <FN3E>
F:1086-1165/Domain: fibronectin type III repeat homology <FN3F>
F:1173-1258/Domain: fibronectin type III repeat homology <FN3G>
F:1266-1349/Domain: fibronectin type III repeat homology <FN3H>
F:1357-1440/Domain: fibronectin type III repeat homology <FN3I>
F:1448-1530/Domain: fibronectin type III repeat homology <FN3J>
F:1538-1620/Domain: fibronectin type III repeat homology <FN3K>
F:1615-1617/Region: cell attachment (R-G-D) motif
F:1632-1714/Domain: fibronectin type III repeat homology <FN3L>
F:1722-1804/Domain: fibronectin type III repeat homology <FN3M>
F:1812-1894/Domain: fibronectin type III repeat homology <FN3N>
F:1994-1985/Domain: fibronectin type III repeat homology <FN3O>
F:1993-2075/Domain: fibronectin type III repeat homology <FN3P>
F:2197-2277/Domain: fibronectin type III repeat homology <FN3Q>
F:2301-2340/Domain: fibronectin type I repeat homology <1F10>
F:2346-2383/Domain: fibronectin type I repeat homology <1F11>
F:2390-2425/Domain: fibronectin type I repeat homology <1F12>
F:55-81,79-90,100-128,126-139,144-172,170-182,189-218,216-228,234-263,261-273,309-336,3
273,237-2383,2390-2416,2414-2425/Disulfide bonds: #status predicted
F:2465/Disulfide bonds: interchain (to 2463) #status predicted
F:2463/Disulfide bonds: interchain (to 2459) #status predicted

Query Match      78.6%; Score 363; DB 2; Length 2481;
Best Local Similarity 73.6%; Pred. No. 1.5e-28;
Matches 67; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

Qy      1  EVPOLTLSPVDITDSSIGLRMPPLNSITIGRTVVAAGEGIPFEDFVDSVGYTV 60
      |||
      1266  ELPOLTLSPVDITDSSIGLRMPPLNSITIGRTVVAAGEGIPFEDFVDSVGYTV 1325
      |||

Db      61  TGLEPGIDYDISVITLLINGESAPTTLTQQT 91
      |||
      1326  SLEPGIDYDISVITLLINGESAPTTIQT 1356
      |||

RESULT 6
FNUH
  fibronectin precursor [validated] - human
N:Alternate names: fibronectin splice form ED-A
C:Species: Homo sapiens (man)
C>Date: 27-Nov-1985 #sequence_revision 31-Mar-1993 #ext_change 08-Dec-2000
C:Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A2
R:Dean, D.C.; Bowlin, C.L.; Bourgeois, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A>Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A:Reference number: A26460; MUID:87175578; PMID:3031656
A:Accession: A26460
A:Molecule type: DNA
A:Residues: 1-49 <DEA>
A:Cross-references: GB:M15801; NID:9182686; PIDN:AAA53376.1; PID:9553293
R:Oldberg, A.; Ruoslahti, E.
J. Biol. Chem. 261, 2113-2116, 1986
A>Title: Evolution of the fibronectin gene.
A:Reference number: A26284; MUID:86111901; PMID:3003095
A:Accession: A26284
A:Molecule type: DNA
A:Residues: 1447-1540 <OLD>
A:Cross-references: GB:M12549; NID:9182688
A>Note: the authors translated the codon TTC for residue 1494 as Glu
Nucleic Acids Res. 16, 3545-3557, 1988
A>Title: Sequence analysis and in vivo expression show that alternative splicing of Ed-
A:Reference number: S00848; MUID:88233940; PMID:3375063
A:Accession: S03917
A:Molecule type: DNA

```

A:Residues: 1594-1767, 'V', 1769-1783 <PAO>
A:Cross-references: EMBL:X07718; NID:931402
A:Note: the authors translated the codon AAC for residue 1631 as Asp
R:Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986
A:Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:
A:Reference number: A24854; MUID:87030929; PMID:3770201
A:Accession: A24854
A:Molecule type: DNA
A:Residues: 1992-2147 <VTB>
A:Cross-references: GB:X045530; NID:931436
R:Gutman, A.; Yamada, K.M.; Kornblith, A.
FEBS Lett. 207, 145-148, 1986
A:Title: Human fibronectin is synthesized as a pre-propolypeptide.
A:Reference number: A24476; MUID:87030890; PMID:3770189
A:Accession: A24476
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-14, 'Q', 16-38 <GUT>
R:Kornblith, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985
A:Title: Primary structure of human fibronectin: differential splicing may generate at l
A:Reference number: A91008; MUID:85284965; PMID:2992939
A:Accession: A91008
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 32-1344, 1346-2080, 2112-2386 <KOR>
A:Cross-references: GB:X02761
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5868, 1984
A:Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A:Reference number: A93529; MUID:84272256; PMID:6462919
A:Accession: A93529
A:Molecule type: mRNA
A:Residues: 973-2080, 2112-2386 <KO2>
A:Cross-references: GB:X00739
R:Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A:Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a
A:Reference number: A21011; MUID:83290929; PMID:6688418
A:Accession: A21011
A:Molecule type: mRNA
A:Residues: 1434-1537 <OL2>
A:Cross-references: GB:X00055; NID:9182680; PIDN:AAA52459.1; PID:9182683
R:Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A:Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra
A:Reference number: A90495; MUID:85280409; PMID:292573
A:Accession: A90495
A:Molecule type: mRNA
A:Residues: 1594-2386 <BER>
A:Cross-references: GB:110905; NID:9182696; PIDN:AAA52462.1; PID:9182697
R:Umezawa, K.; Kornblith, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A:Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A:Reference number: A22245; MUID:85231203; PMID:2989004
A:Accession: A22245
A:Molecule type: mRNA
A:Residues: 1948-2067 <UME>
A:Cross-references: GB:M27569; NID:9182705; PIDN:AAA52465.1; PID:9182706
A:Accession: B22245
A:Molecule type: mRNA
A:Residues: 1975-1991, 2017-2039 <UM2>
A:Cross-references: GB:M27590
R:Seikiuchi, K.; Kios, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A:Title: Human liver fibronectin complementary DNAs: identification of two different mes
A:Reference number: 152294; MUID:87026578; PMID:3021206
A:Accession: 165273
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 <SEX>
A:Cross-references: GB:M14060; NID:9182701; PIDN:AAA52464.1; PID:9182704

R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectins
A:Reference number: A21165; MUID:83221567; PMID:6304699
A:Accession: A21165
A:Molecule type: mRNA
A:Residues: 2291-2386 <KO3>
A:Cross-references: GB:X00729; NID:9182681; PIDN:AAA52460.1; PID:9182684
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 259, 12670-12674, 1983
A:Title: Primary structure of human plasma fibronectin.
A:Reference number: A52398; MUID:84032463; PMID:6630202
A:Accession: A52398
A:Molecule type: protein
A:Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>
R:Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A:Title: Further characterization of the binding of fibronectin to gelatin reveals the p
A:Reference number: S34791; MUID:93312001; PMID:8323285
A:Accession: S34791
A:Molecule type: protein
A:Residues: 291-300, 551-560 <GAR2>
R:Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A:Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A:Reference number: A60904; MUID:87019725; PMID:352418
A:Accession: A60904
A:Molecule type: protein
A:Residues: 293-301 <GRI>
R:Calaycay, J.; Pandey, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A:Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pl
A:Reference number: A23901; MUID:8608277; PMID:3900070
A:Accession: A23901
A:Molecule type: protein
A:Residues: 616-677, 'Q', 679-703, 'PT' <CAL>
R:Pierschbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A:Title: The cell attachment domain of fibronectin. Determination of the primary structu
A:Reference number: A92386; MUID:82265604; PMID:7050098
A:Accession: A92386
A:Molecule type: protein
A:Residues: 1441-1548 <PIE>
A:Note: residues 1524-1527 are responsible for the cell-binding activity
R:Garcia-Pardo, A.; Rosagnolo, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A:Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dom
A:Reference number: A32517; MUID:87241275; PMID:3593230
A:Accession: A32517
A:Molecule type: protein
A:Residues: 1589-1630, 'T', 1722-2058 <GAR3>
R:Trüssel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pand
Biochem. J. 274, 731-738, 1991
A:Title: Human plasma fibronectin. Demonstration of structural differences between the A
A:Reference number: S14357; MUID:91190085; PMID:2012601
A:Accession: S14357
A:Molecule type: protein
A:Residues: 1614-1630, 'T', 1722-2081, 2113-2244 <TRE>
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A:Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dal
A:Reference number: A23891; MUID:85261459; PMID:4019516
A:Accession: A23891
A:Molecule type: protein
A:Residues: 2071-2080, 2112-2356 <GAR4>
C:Comment: The extra domain and connecting strand 3 are subject to developmental and tis
C:Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
tion, and transformation.
C:Genetics:
A:Gene: GDB:FNI
A:Cross-references: GDB:119135; OMIM:135600
A:Map position: 2934-2934
A:Introns: 49/3, 1266/1, 1357/1, 1447/1, 1487/1, 1541/1, 1631/1, 1721/1, 1991/1, 2145/1

C:\Superfamily.fibronectin; fibronectin type I repeat homology; fibronectin type II repeat
C:\Kewords: acute phase, alternative splicing; cell adhesion; collagen binding; duplicat
F_1-26/Domain: signal sequence #status predicted <SIG>
F_27-31/Domain: propeptide #status predicted <PRO>
F_32-2386/Product: fibronectin #status experimental <MAT>
F_52-272/Domain: fibrin and heparin binding <FBH>
F_97-115/Domain: fibronectin type I repeat homology <IF1>
F_141-119/Domain: fibronectin type I repeat homology <IF2>
F_166-225/Domain: fibronectin type I repeat homology <IF3>
F_231-270/Domain: fibronectin type I repeat homology <IF4>
F_308-608/Domain: collagen binding <CBR>
F_360-401/Domain: fibronectin type I repeat homology <IF6>
F_420-461/Domain: fibronectin type II repeat homology <2F1>
F_470-508/Domain: fibronectin type II repeat homology <2F2>
F_518-555/Domain: fibronectin type I repeat homology <1F8>
F_561-559/Domain: fibronectin type I repeat homology <1F9>
F_609-692/Domain: fibronectin type III repeat homology <3FA>
F_716-706/Domain: heparin binding <HPB>
F_719-801/Domain: fibronectin type III repeat homology <3FB>
F_810-891/Domain: fibronectin type III repeat homology <3FC>
F_906-988/Domain: fibronectin type III repeat homology <3FD>
F_996-1077/Domain: fibronectin type III repeat homology <2FE>
F_1086-1164/Domain: fibronectin type III repeat homology <3FG>
F_1173-1258/Domain: fibronectin type III repeat homology <3FH>
F_1266-1349/Domain: fibronectin type III repeat homology <3FI>

Query March 32.1%; Score 148.5; DB 1; Length 2386;
Best Local Similarity 36.5%; Pred. No.1.2e-05;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

Oy 2 VPQLDISFYDITDSIGLRWTPUNSSFTLCGRATVVA-----GGGIPFFEDFYDVSV 55
Db 907 VPSRDIDGFVEVDVKTKIMWT--PESAVGTYRVDPVLPGHGQRLEP-----SRN 959

Oy 56 GYTVTGLEPCIDYDISVTILINGESAPFLTLTOOT 91
Db 960 TFAEVTGLSPGVTTYFKYFAVSHGRESKPRLAQOTT 995

RESULT 7
FNBO
fibronectin - bovine
C:\Species: Bos primigenius taurus (cattle)
C:\Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text change 20-Oct-2000
A:\Accession: A26452; B21165; A23292
R:\Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.
Eur. J. Biochem. 161, 441-453, 1986
A:\Title: Complete primary structure of bovine plasma fibronectin.
A:\Reference number: A26452; MUID:87054047; PMID:3780752
A:\Accession: A26452
A:\Molecule type: PROTEIN
A:\Residues: 1-2265 <SKO>
R:\Xorbnlight, A.R.; Viibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A:\Title: Isolation and characterization of cDNA clones for human and bovine fibronectins
A:\Reference number: A21165; MUID:83221567; PMID:6304699
A:\Accession: B21165
A:\Molecule type: mRNA
A:\Residues: 2170-2265 <KOR>
A:\Cross-references: GG:K00800; NID:G163055; PID:NAAA30521.2; PID:G5713323
R:\Peterson, T.E.; Thøgersen, H.C.; Skorstengaard, K.; Viibe-Pedersen, K.; Sahl, P.; Søttrup,
Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983
A:\Title: Partial primary structure of bovine plasma fibronectin: three types of internal
A:\Reference number: A23292; MUID:83117805; PMID:6218503
A:\Accession: A23292
A:\Molecule type: protein
A:\Residues: 1-16,'C',18-20,'S',22-432;447-463;1367-1517;1567-1673;2062-2176,'N',2178-2262
C:\Comment: Cys-1201 and Cys-2015 have free sulfhydryl groups.
C:\Comment: The plasma fibronectin molecule consists of two chains, which are connected b
ating, and maintenance of cell shape.

C:Comment: Plasma fibronectin is synthesized by hepatocytes
C:Superfamily: fibronectin, fibronectin type I repeat homology; fibronectin type II rep
C:Keywords: acute phase; alternative splicing; collagen binding; duplication; extracell
F:21-241/Domain: fibrin and heparin binding <FB>
F:21-56/Domain: fibronectin type I repeat homology <1F1>
F:66-104/Domain: fibronectin type I repeat homology <1F2>
F:110-148/Domain: fibronectin type I repeat homology <1F3>
F:155-154/Domain: fibronectin type I repeat homology <1F4>
F:200-239/Domain: fibronectin type I repeat homology <1F5>
F:277-577/Domain: collagen binding <CB>
F:277-311/Domain: fibronectin type II repeat homology <1F6>
F:329-370/Domain: fibronectin type II repeat homology <2F1>
F:389-430/Domain: fibronectin type II repeat homology <2F2>
F:439-477/Domain: fibronectin type I repeat homology <1F7>
F:487-524/Domain: fibronectin type I repeat homology <1F8>
F:530-568/Domain: fibronectin type I repeat homology <1F9>
F:578-661/Domain: fibronectin type III repeat homology <FN3A>
F:668-770/Domain: fibronectin type III repeat homology <FN3B>
F:779-860/Domain: fibronectin type III repeat homology <FN3C>
F:875-957/Domain: fibronectin type III repeat homology <FN3D>
F:965-1046/Domain: fibronectin type III repeat homology <FN3E>
F:1055-1134/Domain: fibronectin type III repeat homology <FN3F>
F:1142-1227/Domain: fibronectin type III repeat homology <FN3G>
F:1235-1318/Domain: fibronectin type III repeat homology <FN3H>
F:1336-1404/Domain: fibronectin type III repeat homology <GN3I>
F:1410-1511/Domain: cell attachment <CAD>
F:1416-1502/Domain: fibronectin type III repeat homology <FN3J>
F:1493-1495/Domain: cell attachment (R-G-D) motif
F:1510-1592/Domain: fibronectin type III repeat homology <FN3K>
F:1600-1870/Domain: heparin binding <HB2>
F:1600-1682/Domain: fibronectin type III repeat homology <FN3L>
F:1692-1773/Domain: fibronectin type III repeat homology <FN3M>
F:1761-1863/Domain: fibronectin type III repeat homology <FN3N>
F:1970-1972/Region: cell attachment (R-G-D) motif
F:1982-2062/Domain: fibronectin type III repeat homology <FN3O>
F:1985-2216/Domain: fibrin binding <FB2>
F:2085-2124/Domain: fibronectin type I repeat homology <1F10>
F:2130-2167/Domain: fibronectin type I repeat homology <1F11>
F:2174-2209/Domain: fibronectin type I repeat homology <1F12>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Cross-link: isopeptide (Gln) (interchain) to Lys N6-amino of fibrin) #status experim
F:21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,302-
7,2155-2167,2174-2200,2198-2209/disulfide bonds: #status predicted
F:1309,497,511,846,976,1213,1987/Binding site: carbohydrate (Asn) (covalent) #status exp
F:1205,1692/Binding site: carbohydrate (Asn) (covalent) #status absent
F:11943,1944/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:12246/disulfide bonds: interchain (to 2250) #status predicted
F:12250/disulfide bonds: interchain (to 2246) #status predicted
F:12263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 31.3%; Score 147.5; DB 1; Length 2265;
Best local Similarity 36.1%; Pred. No. 1.4e-06;
Matches 35; Conservative 13; Mismatches 36; Indels 13; Gaps 3;

QY 1 EVPOLTLSPVDITDSSIGLRMPPLNSITIGRITVAA-----GEGIPFEDVDDSS 54
DB 875 KVPEPRDLQFVETVDVITIMTP-PESPVTGVRVDVIVPNLPGHGORLPV-----SR 927
QY 55 VGYYTVGLPEGIDYDVSITLLINGSGSAPITLTQCT 91
DB 928 NTFAEVWTGLSPGVTHKVFVAVNGRSEKPLTAQAT 964

RESULT 8
A28512
fibronectin - chicken (fragment)
C:Species: Gallus gallus (Chicken)
C>Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text change 20-Aug-1999
C:Accession: A28512
R:Kubomura, S.; Osara, M.; Karsaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi,
Biochim. Biophys. Acta 910, 171-181, 1987
Article: Genetic analysis of the cell binding domain region of the chicken fibronectin
A:Reference number: A28512; MUID:86050950; PMID:2823899

A:Accession: A28512
A:Molecule type: DNA
A:Residues: 1-273 <K0B>
A:Cross-references: GS:X06533, NID:g63393, PIDD:CA29781.1, PID:g295716
A:Note: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C:Genetics:
A:Insertions: 90/1; 129/1; 184/1; 236/1
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat homology; fibronectin type III repeat homology <FN3K>
C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heterotetramer; fibronectin type III repeat homology (fragment) <FN3f>
F:90-172/Domain: fibronectin type III repeat homology <FN3J>
F:167-169/Region: cell attachment (R-G-D) motif
F:184-266/Domain: fibronectin type III repeat homology <FN3K>

Query March	27.8%	Score 128.5;	DB 2;	Length 273;
Best Local Similarity	35.9%	Pred. No. 1e-05;		
Matches 33;	Conservative 13;	Mismatches 43;	Indels 3;	Gaps 3
Cy	1	EVDPQLDLSFVITLSTGICRTPLNSTIIGYITV-AAGGICPIFDEFVSSGYGT	59	
Db	184	ELITSPMQVTDQNDISIRMLP-SSSPGVGHVIAPEKKGHG-PIKTRVPPDQTVT	241	
Cy	60	VTLGEPGIDYDISVITLLNGESAPITLITQOT	91	
Db	242	IQGLEPTEVYRWVSVAQNONGSELELVETAAVT	273	

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RESULT 9
151669
Tumor suppressor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C/Accession: 151669
R/Physically, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, E.R.
Dev. Biol. 166, 654-665, 1994
A/Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the
A/Reference number: 151668; MUID:95113183; PMID:7813784
A/Accession: 151669
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1427 >PTE>
A/Cross-references: EMBL:U10986; NID:G606873; PIDN:AAA70168.1; PID:G606874
C/Genetics:
;Gene: XDCCA

```

Query Match	23.1%;	Score 107.5;	DB 2;	Length 1427;
Best Local Similarity	35.1%;	Pred. No. 0.0038		
Matches	134;	Conservative	12;	Mismatches 40;
			Indels	11;
			Gaps	5

QY	1	EVPQLDLSFVDTLTDSSIGLRMT-PINSGII-GYRIVMAAGEIPFEDF-WDSVGY	57
	::	:::::	::::
Db	724	QVDDQSSSLHRLPLTISIMSTPPLNPIVVRG---IIKGVSPIAETVRDSCRY	780
QY	58	YTVTGEPEGIDYDISVITLLINGESAP-----TTLTQ	89
	::	:::::	::::
Db	781	YSIENLEPSSHYVISKAPNNAGEGVLYESATTSQ	817

```

RESULT 10
A32230
tenascin precursor - chicken
N/Alternate names: cytotactin; hexabrachion
N/Contains: tenascin 190K; tenascin 200K
C/Species: Gallus gallus (chicken)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C/Accession: A32230, B32230, A33379, B33379, C33379, S01292, A30903
R/Notes: F.S.; Hoffman, S.; Cunningham, B.A.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1909, 1989
A/Title: A detailed structural model of cytotactin: protein homologies, alternative RNA
A/Reference number: A32230; MUID:89184536; PMID:2467292
A/Accession: A32230
A/Status: preliminary
A/Molecule type: DNA

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A:Residues: 1-1810 <ON>
A:Cross-references: GB:U04519; NID:g211717; PIDN:AAA48745.1; PID:g211718
A:Accession: B32230
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1044,1318-1810 <O2>
A:Cross-references: GB:U04519
R:Sprang, J., Beck, K., Chiquet-Ehrismann, R.
Cell 59, 325-334, 1989
A:Title: Two contrary functions of tenascin: dissection of the active sites by recombina
A:Reference number: A33379; MUID:50030407; PMID:247825
A:Accession: A33379
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-5-
A:Cross-references: GB:M23121; NID:g212746; PIDN:AAA4086.1; PID:g212749
A:Accession: B33379
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-5-
A:Cross-references: GB:M23121
R:Pearson, C.A., Pearson, D., Shibahara, S., Hoffsteenge, J., Chiquet-Ehrismann, R.
EMBO J. 7, 2977-2982, 1988
A:Title: Tenascin: cDNA cloning and induction by TGF-beta.
A:Reference number: S01292; MUID:89030589; PMID:2460335
A:Accession: S01292
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 27-181,'R',183-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-
A:Cross-references: EMBL:X08030
A:Note: part of this sequence was confirmed by protein sequencing
C:Superfamily: tenascin; EGF homology; fibronogen beta/gamma homology; fibronectin type
C:Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell
F:1-22/Domain: signal sequence #status predicted <Sig>
F:23-33/Domain: propeptide #status predicted <Pro>
F:34-1810/Product: tenascin 230k #status predicted <Mat>
F:222-249/Domain: EGF homology <EGF1>
F:318-342/Domain: EGF homology <EGF>
F:592-673/Domain: fibronectin type III repeat homology <FN3A>
F:681-765/Domain: fibronectin type III repeat homology <FN3B>
F:773-857/Domain: fibronectin type III repeat homology <FN3C>
F:865-949/Domain: fibronectin type III repeat homology <FN3D>
F:957-1037/Domain: fibronectin type III repeat homology <FN3E>
F:1046-1128/Domain: fibronectin type III repeat homology <FN3F>
F:1137-1219/Domain: fibronectin type III repeat homology <FN3G>
F:1228-1310/Domain: fibronectin type III repeat homology <FN3H>
F:1318-1399/Domain: fibronectin type III repeat homology <FN3I>
F:1407-1487/Domain: fibronectin type III repeat homology <FN3J>
F:1495-1575/Domain: fibronectin type III repeat homology <FN3K>
F:1590-1799/Domain: fibronogen beta/gamma homology <EBG>
F:1734-1747/Domain: calcium binding #status predicted <CMB>

```

Query Match Similarity      22.7%; Score 105; DB 1; Length 1810;
Best Local Similarity      35.1%; Pred. No. 0.023;
Matches      27; Conservative      15; Mismatches      33; Indels      2; Gaps      2.

QY      8 LSFVDITDSSIGLRWPTLINSSTLIGYRITVVAAGEGPIFDEFVDSVGYVTGTLEPGI 67
      :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1325 IFSFDITENSAKVSWTP-PRSRVDSYRVSVYPITGTGPNVVT-VDGSKTRTKLVLVEGV 1382
      :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      68 DYDISVITTLINGESAP 84
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      1383 DYNVNINISVKGFESEEP 1399
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
S71465
fibronectin - chicken (fragment)
;Species: Gallus gallus (chicken)

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C>Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #ext_change 21-Jan-2000
 C/Accession: S71465
 R/Gehris, A.L.; Brandl, D.W.; Lewis, S.D.; Bennett, V.D.
 Biochim. Biophys. Acta 1311, 5-12, 1996
 A/Title: The exon encoding the fibronectin type III-9 repeat is constitutively included
 A/Reference number: S71465; MUID:96183658; PMID:8603103
 A/Accession: S71465
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-189 <GB>
 A/Cross-references: EMBL:U20386; NID:g1323735; PIDN:AA01062.1; PID:g1323736
 A/Note: the authors translated the codon AAG for residue 50 as Asn and AAG for residue 1
 C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
 F:100-183/Domain: fibronectin type II repeat homology <3FR>

Query Match 22.5%; Score 104; DB 2; Length 189;
 Best Local Similarity 39.1%; Pred. No. 0.0022;
 Matches 34; Conservative 11; Mismatches 38; Indels 4; Gaps 4;

Db 105 TGDFDITANSFTVMI-APRATITGKRRHHPGVGRP-KEDRVPSRSITITNL 162
 65 PGIDYDISVITLINGSBAPTITTOQT 91
 Db 163 PGTEYVVSITA-VNGRESEVPLVGQOT 188

RESULT 12
 JH0675
 restrictin precursor - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 10-Sep-1999
 C/Accession: JH0675; PS0385; S23254
 R/Norenberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
 Neuron 8, 849-863, 1992
 A/Title: The chicken neuronal extracellular matrix molecule restrictin: similarity with EG
 A/Reference number: JH0675; MUID:92265298; PMID:1375037
 A/Accession: JH0675
 A/Molecule type: mRNA
 A/Residues: 1-1353 <NOE>
 A/Cross-references: GB:X64649; NID:g63613; PIDN:CAA45920.1; PID:g63614
 A/Experimental source: Brain
 A/Accession: PS0385
 A/Molecule type: protein
 A/Residues: 579-586;827-840 <NOE1>
 C/Comment: This protein is a neural extracellular matrix protein implicated in neural ce
 C/Superfamily: restrictin; EGF homology; fibronectin beta/gamma homology; fibronectin typ
 C/Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycoprot
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:34-1353/Product: restrictin #status predicted <MAT>
 F:203-229/Domain: EGF homology <EG1>
 F:234-260/Domain: EGF homology <EG2>
 F:265-291/Domain: EGF homology <EG3>
 F:296-322/Domain: EGF homology <EG4>
 F:324-405/Domain: fibronectin type III repeat homology <FN1>
 F:413-494/Domain: fibronectin type III repeat homology <FN2>
 F:502-584/Domain: fibronectin type III repeat homology <FN3>
 F:592-676/Domain: fibronectin type III repeat homology <FN4>
 F:684-764/Domain: fibronectin type III repeat homology <FN5>
 F:772-853/Domain: fibronectin type III repeat homology <FN6>
 F:861-941/Domain: fibronectin type III repeat homology <FN7>
 F:949-1027/Domain: fibronectin type III repeat homology <FN8>
 F:1035-1115/Domain: fibronectin type III repeat homology <FN9>
 F:1130-1338/Domain: fibronectin beta/gamma homology <FBG>
 F:1272-1286/Region: calcium binding #status predicted
 F:53,197,277,391,469,580,734,790,960,1031,1041,1256,1342/Binding site: carbohydrate (Asn

Query Match 22.3%; Score 103; DB 1; Length 135;
 Best Local Similarity 32.5%; Pred. No. 0.027;
 Matches 26; Conservative 15; Mismatches 37; Indels 2; Gaps 1;

Qy 7 DLSPVDITDSIGLRMTPLNNSITIGRITVAAGSIPFEDFVDSVGVTGTEPG 66

Db 330 NLRVGTGSDGIELANSLGAT--EYVVSQPGPGSGQRCQVPCDWNITITTELEPG 387
 Qy 67 IDYDISVITLINGSBAPT 86
 Db 388 VAVNVSIVAVISDVLSFPT 407

RESULT 13
 A54849
 collagen alpha 1(VII) chain precursor - human
 N/Alternate names: procollagen alpha 1(VII) chain
 C/Species: Homo sapiens (man)
 C/Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #ext_change 15-Sep-2003
 R/Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
 U.Biol. Chem. 269, 20256-20262, 1994
 A/Title: Cloning of human type VII collagen. Complete primary sequence of the alpha1(VI
 A/Reference number: A54849; MUID:94327588; PMID:8051117
 A/Accession: A54849
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-2944 <CHR>
 A/Cross-references: GB:L02870; NID:g987124; PIDN:AAA75438.1; PID:g987125
 R/Tanaka, T.; Takahashi, K.; Furukawa, F.; Yamura, S.
 Biochem. Biophys. Res. Commun. 183, 958-963, 1992
 A/Title: Molecular cloning and characterization of type VII collagen cDNA.
 A/Reference number: PH0844; MUID:92231902; PMID:1567409
 A/Accession: PH0844
 A/Molecule type: mRNA
 A/Residues: 'ERR',340-475,'RALSSTASSTLCNATRWKPCNRGSHWTRACPCNRPASHRAAPAC',524-528,'C'
 A/Residues: 'ERR',340-475,'RALSSTASSTLCNATRWKPCNRGSHWTRACPCNRPASHRAAPAC',524-528,'C'
 A/Cross-references: DDBJ:D11152; DDBJ:D13694; NID:g453598; PIDN:BA02853.1; PID:g453599
 A/Experimental source: keratinocyte
 A/Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
 R/Parente, M.G.; Chung, L.C.; Rymaszewski, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Ma
 Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
 A/Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
 A/Reference number: S16316; MUID:91334380; PMID:1871109
 A/Accession: S16316
 A/Molecule type: mRNA
 A/Residues: 815-892,'E',894-1439 <PAR>
 A/Residues: 815-892,'E',894-1439 <PAR>
 A/Cross-references: GB:M65188; GB:949017; NID:g180914; PIDN:AAA96439.1; PID:g180915
 A/Experimental source: keratinocyte
 R/Gammon, W.R.; Abernethy, M.L.; Pedilla, K.M.; Pilsavanh, P.S.; Cook, M.E.; Wright, J.
 J. Invest. Dermatol. 99, 691-696, 1992
 A/Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion pro
 A/Reference number: S16328; MUID:93107742; PMID:1469284
 A/Accession: S16328
 A/Status: translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 'ERR',372-517,'DV',520-540,'W',542-1255 <RES>
 A/Residues: 'ERR',372-517,'DV',520-540,'W',542-1255 <RES>
 A/Cross-references: GB:S51236; NID:g262308; PIDN:AA24637.1; PID:g262309
 R/Setlzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Granville, R.W.; Burgess, R.E
 J. Biol. Chem. 264, 3822-3826, 1989
 A/Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagen
 A/Reference number: A30296; MUID:89139437; PMID:2537292
 A/Accession: A30296
 A/Molecule type: protein
 A/Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E',1203,'C',2034-2041;
 A/Note: two reported peptides cannot be reliably located
 R/Greenspan, D.S.
 Hum. Mol. Genet. 2, 273-278, 1993
 A/Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
 A/Reference number: I8103; MUID:93271985; PMID:8499916
 A/Accession: I8103
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 2395-2871,'S',2873-2944 <RE2>
 A/Cross-references: GB:L06862; NID:g388713; PIDN:AAA89196.1; PID:g388714
 R/Christiano, A.M.; Rymaszewski, M.; Uitto, J.
 Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
 A/Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser sub
 A/Reference number: A55255; MUID:94224777; PMID:8170945

A:Contents: annotation
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Genetics:
A:Gene: GDB:COL7A1; EBR1; EBD1; EB
A:Cross-references: GDB:128750; OMIM:120120
A:Map position: 3p21.3-3p21.3
A>Note: defects in this gene can result in dominant and recessive dystrophic epidermolysis
C:Note: there are 118 introns
C:Complex: type VII collagen is probably a homotrimer
C:Function:
A:Description: structural component of extracellular polymer associated with anchoring
F:Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproline
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
F:17-1253/Domain: amino-terminal nonhelical #status predicted <NC1>
F:36-201/Domain: von Willebrand factor type A repeat homology <VMA1>
F:231-318/Domain: fibronectin type III repeat homology <FN1>
F:327-413/Domain: fibronectin type III repeat homology <FN2>
F:414-502/Domain: fibronectin type III repeat homology <FN3>
F:508-593/Domain: fibronectin type III repeat homology <FN4>
F:598-683/Domain: fibronectin type III repeat homology <FN5>
F:686-771/Domain: fibronectin type III repeat homology <FN6>
F:776-862/Domain: fibronectin type III repeat homology <FN7>
F:864-952/Domain: fibronectin type III repeat homology <FN8>
F:954-1045/Domain: fibronectin type III repeat homology <FN9>
F:1052-1219/Domain: von Willebrand factor type A repeat homology <VMA2>
F:1170-1172/Region: cell attachment (R-G-D) motif
F:1189-1251/Region: cysteine/proline-rich
F:1254-2783/Region: interrupted helical
F:1334-1336/Region: cell attachment (R-G-D) motif
F:2008-2010/Region: cell attachment (R-G-D) motif
F:2553-2555/Region: cell attachment (R-G-D) motif
F:2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F:2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:337-786/109/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:2167-2176-2185-2189-2664-2667-2673/Modified site: 4-hydroxyproline (Pro) #status exper
F:2625-2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F:2625-2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
F:2634-2802-2804/Disulfide bonds: interchain #status predicted

Query Match 22.3%; Score 103; DB 2; Length 2944;
Best Local Similarity 31.1%; Pred. No. 0.065;
Matches 28; Conservative 19; Mismatches 39; Indels 4; Gaps 3;

QY 2 VPQTLDSFVDTISSIGLRWPLN--SSTIGCRITVVAAGEGIPFEDFVDSVGYT 59
DB 957 VPSI-EHRVVDNISIDVTLLMTVPVSRASSYILSMR-PLRGPGQEVGSPQTLPGIASSQR 1014
QY 60 VTGLEPGIDVDISVITLLNGESAPPTLNO 69
DB 1015 VTGLEPVSITFSLRPLVDSVRGPEASVQ 1044

RESULT 14
A40020
collagen alpha 1(XII) chain precursor - chicken
N/AlternateNames: fibronectin
C/Species: Gallus gallus (chicken)
C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #ext_change 15-Sep-2003
C/Accession: A40020; A34485; B34485; A28037; S22254; S28811
R/Yamada, M.; Yamada, K.M.; Yamada, S.S.; Shikimura, T.; Tanaka, H.; Nishida, Y.; Obata
J. Cell Biol. 115, 209-221, 1991
A>Title: The complete primary structure of type XII collagen shows a chimeric molecule w
nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A:Reference number: A40020; MUID:92011862; PMID:1918137
A:Accession: A40020
A:Molecule type: mRNA
A:Residues: 1-3124 <YAM>
A:Cross-references: GB:000624; NID:9222810; PIDN:BA00701.1; PID:9222811
A>Note: in the authors' translation, residues 1216-1219 are shown after residue 1235 and
R/Gordon, M.K.; Gerecke, D.R.; Dubler, B.; van der Rest, M.; Olsen, B.R.

A>Title: Type XII collagen. A large multidomain molecule with partial homology to type I
A:Reference number: A34485; MUID:90062079; PMID:2584192
A:Accession: A34485
A:Molecule type: mRNA
A:Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
A:Cross-references: EMBL:J05137; NID:9211284; PIDN:AAA48635.1; PID:9211285
A:Accession: B34485
A:Molecule type: protein
A:Residues: 2772-2792/2846-2873 <GOR2>
R/Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A>Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA c
A:Reference number: A28037; MUID:87317590; PMID:3476925
A:Accession: A28037
A:Molecule type: mRNA
A:Residues: 2960-2976, 'F', 2978-3074, 'AG' <GOR3>
A:Cross-references: EMBL:M1375; NID:9211649; PIDN:AAA48718.1; PID:9211650
A>Note: this sequence has been revised in reference A34485
R/Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Biochem. 207, 847-856, 1992
A>Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of
A:Reference number: S23814; MUID:92366621; PMID:1333460
A:Accession: S23814
A:Molecule type: protein
A:Residues: 'X', 1333, 'Q', 1335-1347, 1914-1928, 2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-2517 <
J. Biol. Chem. 267, 17724-17727, 1992
R/Dubler, B.; van der Rest, M.
A>Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-
A:Reference number: S22254; MUID:88087065; PMID:3121603
A:Accession: S22254
A:Molecule type: protein
A:Residues: 2831-2832, 'T', 2834, 'R', 2836-2843, 3002-3014 <DUB>
R/Trieb, U.; Trieb, B.
Biochim. Biophys. Acta 1171, 97-98, 1992
A>Title: The two splice variants of collagen XII share a common 5' end.
A:Reference number: S28811; MUID:93042014; PMID:1420368
A:Accession: S28811
A:Molecule type: preliminary
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-24, 1189-1257, 'S', 1259-1263, 'E', 1265-1280 <TRU>
A:Cross-references: EMBL:X67327
C:Genetics:
A:Introns: 2845/3, 2863/3, 2887/3, 2899/3, 2922/1, 2985/1, 3008/1, 3065/1
C/Keywords: alternative splicing; cell binding; coiled coil; connective tissue; disulfid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-3124/Product: collagen alpha 1(XII) chain #status predicted <MAT>
F:24-1189-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted
F:24-118/Domain: IIR #status predicted <IIR>
F:24-105/Domain: fibronectin type III repeat homology <FN3A>
F:137-301/Domain: von Willebrand factor type A repeat homology <VMA1>
F:332-425/Domain: IIRB #status predicted <IIRB>
F:437-601/Domain: von Willebrand factor type A repeat homology <VMA2>
F:629-1178/Domain: IIR #status predicted <IIR>
F:630-711/Domain: fibronectin type III repeat homology <FN3C>
F:721-802/Domain: fibronectin type III repeat homology <FN3D>
F:812-885/Domain: fibronectin type III repeat homology <FN3E>
F:905-986/Domain: fibronectin type III repeat homology <FN3F>
F:996-1076/Domain: fibronectin type III repeat homology <FN3G>
F:1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F:1197-1361/Domain: von Willebrand factor type A repeat homology <VMA3>
F:1384-2299/Domain: IIR #status predicted <IIR>
F:1384-1465/Domain: fibronectin type III repeat homology <FN3I>
F:1474-1557/Domain: fibronectin type III repeat homology <FN3J>
F:1566-1647/Domain: fibronectin type III repeat homology <FN3K>
F:1655-1738/Domain: fibronectin type III repeat homology <FN3L>
F:1756-1838/Domain: fibronectin type III repeat homology <FN3M>
F:1847-1928/Domain: fibronectin type III repeat homology <FN3N>
F:1937-2019/Domain: fibronectin type III repeat homology <FN3O>
F:2028-2110/Domain: fibronectin type III repeat homology <FN3P>
F:2119-2199/Domain: fibronectin type III repeat homology <FN3Q>
F:2207-2298/Domain: fibronectin type III repeat homology <FN3R>

F,2338-2440/Region: cell adhesion #status predicted
F,2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted
F,2751-2902/Domain: collagenous COL2 #status predicted <COL2>
F,2899-2901/Region: cell attachment (R-G-D) motif
F,2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F,2946-3048/Domain: collagenous COL1 #status predicted <COL1>
F,3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F,32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate (asn) (cov
F,2280,2789,2836,2842,2860,2866,3004,3007/Modified site: hydroxyproline (Pro) #stat

Query Match 22.1%; Score 102; DB 2; Length 3124;
Best Local Similarity 31.0%; Pred. No. 0.089;
Matches 27; Conservative 12; Mismatches 28; Indels 20; Gaps 3;

QY 7 DLSFVDTSSIGLRMTPLNSITIGRTVVAAGGIPFEDFVDSVGYTYT----- 60
DB 911 NLTTTITDTTTLVLSWTPA-PGTNNYRI-----VWMSLYDTMGKRVPGNTWD 959
QY 61 ---TGLEPGIDYDISVITLNGESAP 84
DB 960 AVLDGLEPRTKRIKSIYAAVSGSGDP 986

RESULT 15
138344
titin, cardiac muscle [validated] - human
N:Alternate names: connectin
N:Contents: serine/threonine-specific protein kinase (EC 2.7.1.1-)
C/Species: Homo sapiens (man)
C/Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #ext. change 15-Sep-2000
C/Accession: I38344; I38345; S20898; S20897; S6365; S37393
R:Label: S.; Kollermerer, B.
Science 270, 293-296, 1995
A>Title: titins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330; PMID:7569978
A:Accession: I38344
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A:Molecule type: mRNA
A:Residues: 1-26926 <LAB1>
A/Cross-references: EMBL:X90568; NID:91017424; PID:91017425
R:Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
Biochemistry 34, 553-561, 1995
A>Title: Dissecting titin into its structural motifs: identification of an alpha-helix
A:Accession: I38345
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1977-2014 <MUS>
A/Cross-references: EMBL:X83270; NID:9602579; PID:CA458243.1; PID:9602580
A>Note: conformation and properties are reported for a synthetic peptide corresponding
R:Label: S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A>Title: Towards a molecular understanding of titin.
A:Reference number: S20897; MUID:92258380; PMID:1582406
A:Accession: S20898
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 13597-14200, 'I', 14202-14696 <LAB2>
A/Cross-references: EMBL:X64698; NID:937192; PID:CA445939.1; PID:937193
A:Accession: S20897
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 16330-16382, 'S', 16384-16756, 'F', 16758-16860 <LAB3>
A/Cross-references: EMBL:X64699; NID:937190; PID:CA445940.1; PID:937191
A:Accession: S20899
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 'P', 22278-22431, 'R', 22433-22448, 'G', 22450-22453, 'Q', 22455-22480, 'TR', 22483-2
A/Cross-references: EMBL:X64697; NID:937190; PID:CA445938.1; PID:937195
R:Kollermerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labelle, S.
J. Mol. Biol. 256, 556-563, 1996
A>Title: Genomic organization of M line titin and its tissue-specific expression in two
A:Reference number: S6365; MUID:96177761; PMID:8604138

A:Accession: S6365
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 26729-26825 <COL>
A/Cross-references: EMBL:X92412; NID:91236761
R:Gautel, M.; Leonard, K.; Labelle, S.
EMBO J. 12, 3827-3834, 1993
A>Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differentia
A:Reference number: S37393; MUID:94008990; PMID:8404852
A:Accession: S37393
A:Molecule type: mRNA
A:Residues: 26831-26926 <GAD>
R:Impero, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A:Reference number: A66736; PDB:1RTT
A:Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
R:Plut, W.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66201; PDB:1NCT
A:Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
C/Genetics:
A:Gene: GDB:TTN
A/Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q32
C/Function:
A:Description: structural protein forming filaments in striated muscle
C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; pr
C:Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glyco
structural protein
F,24752-25008/Domain: protein kinase homology <KIN>
F,84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3437,3628,3772,4068
98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,
tetus predicted
F,16780,16976,17579,17602,17657,17681,17845,17899,18121,18188,18209,18336,18670,18680,1
F,1900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,24
F,26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 21.4%; Score 99; DB 1; Length 26926;
Best Local Similarity 34.6%; Pred. No. 2.2;
Matches 27; Conservative 11; Mismatches 36; Indels 4; Gaps 2;

QY 10 FVDITSSIGLRMTPLNSITIGRTVVAAGGIPFEDFVDSVGYTYTGLPBG 66
DB 21366 YIDVREITTLKMPPLDGGSKIVGYSIEKRGNER-VACNFTDVSQCQYTVGLSPG 21424
QY 67 IDYDISVITLNGESAP 84
DB 21425 DRYEFRIIRNAVGTISP 21442

Search completed: September 21, 2004, 05:48:44
Job time : 46.75 secs

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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:37 / Search time 26.0956 Seconds
(without alignments)
181.578 Million cell updates/sec

Title: US-10-676-049-4

Sequence: 1 EVFQTLDSFVDTSSIGL.....SVITLNGESAPTLTQOT 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	2477	1	FINC MOUSE
2	462	100.0	2477	1	FINC RAT
3	452	97.8	1256	1	FINC CHICK
4	363	78.6	2481	1	FINC XENLA
5	348	75.3	1328	1	FINC PLUMA
6	148.5	32.1	2386	1	FINC HUMAN
7	147.5	31.9	2265	1	FINC BOVIN
8	120	26.0	522	1	FINC HORSE
9	116	25.1	522	1	FINC CANFA
10	105	22.7	1808	1	TENA CHICK
11	103	22.3	2944	1	CA17 HUMAN
12	102	22.1	3124	1	CA1C CHICK
13	97.5	21.1	1119	1	CA1C MOUSE
14	97.5	21.0	1125	1	TIE2 BOVIN
15	96.5	20.9	3063	1	CA1C HUMAN
16	93	20.1	1447	1	DOC HUMAN
17	93	20.1	1447	1	DOC MOUSE
18	92	19.9	929	1	CA1C NOTVI
19	89	19.3	1329	1	KP10 HUMAN
20	87.5	18.9	2201	1	TENA HUMAN
21	87	18.8	1122	1	TIE2 MOUSE
22	87	18.8	1377	1	NEOI RAT
23	87	18.8	1443	1	NEOI CHICK
24	87	18.8	1461	1	NEOI HUMAN
25	87	18.8	1493	1	NEOI MOUSE
26	87	18.8	1746	1	TENA PIG
27	85	18.4	1888	1	CA1E CHICK
28	84.5	18.3	597	1	CHIX STROI
29	84.5	18.3	4289	1	TENX HUMAN
30	83.5	18.1	1294	1	TENN HUMAN
31	82.5	17.9	725	1	YA33 SUISO
32	82	17.7	765	1	KP10 MOUSE
33	81.5	17.6	1560	1	TENN MOUSE

34	81.5	17.6	1897	1	PTPE HUMAN
35	80	17.3	1124	1	TIE2 HUMAN
36	78.5	17.0	639	1	CA1C RABIT
37	78	16.9	1238	1	PTPJ MOUSE
38	77	16.7	2029	1	LAR DROME
39	74.5	16.1	2554	1	TLES DROME
40	73.5	15.9	1241	1	NEPN HUMAN
41	73	15.8	880	1	GN4 THEFU
42	71.5	15.5	1010	1	CONT CHICK
43	71.5	15.5	1197	1	CAMI BRAE
44	71.5	15.5	1240	1	NPAS HUMAN
45	71	15.4	149	1	YCCA_ECOLI

ALIGNMENTS

RESULT 1	FINC_MOUSE	STANDARD	PRT: 2477 AA.
ID	P11276; Q61567; Q61568; Q61569; Q64233; Q80U14;		
AC	01-JUL-1989 (Rel. 11, Created)		
DT	15-MAR-2004 (Rel. 43, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Fibronectin precursor (FN).		
GN	FN1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE OF 1-920 FROM N.A.		
RC	STRAIN=FVB/N-3; TISSUE=breast tumor;		
RX	MEDLINE=22188257; PubMed=12477932;		
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diachenko L., Marusina K., Farmer A.A., Rudin G.M., Hong L.,		
RA	Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshynki S., Carinici P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosch S.A., McEwan P.J., McKernan K.J., Gay L.J., Hulik S.W.,		
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faney J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,		
RA	Scherer A., Schein J.E., Jones S.J.M., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length		
RT	human and mouse cDNA sequences."		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	SEQUENCE OF 1-28 FROM N.A.		
RC	TISSUE=Liver;		
RX	MEDLINE=9413113; PubMed=8299972;		
RA	Polly P., Nicholson R.C.,		
RA	"Sequence of the mouse fibronectin-encoding gene promoter region."		
RA	Gene 137:353-354 (1993).		
RN	[3]		
RP	SEQUENCE OF 562-834 FROM N.A.		
RC	STRAIN=NMRI;		
RX	MEDLINE=95403556; PubMed=7673336;		
RA	Tails V.F., Weller A., Timpl R., Ekblom M., Ekblom P.,		
RA	"Regulation of mesenchymal extracellular matrix protein synthesis by		
RA	transforming growth factor-beta and glucocorticoids in tumor		
RA	stroma."		
RA	J. Cell Sci. 108:2153-2162 (1995).		
RN	[4]		
RP	SEQUENCE OF 899-2376 FROM N.A.		
RA	Gorski G., Aros M., Norton P.,		

Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

15) SEQUENCE OF 2375-2477 FROM N.A.
MEDLINE=88124987; PubMed=3124113;
Blatti S.P., Foster D.N., Ranganathan G., Moses H.T., Getz M.J.;
"Induction of fibronectin gene transcription and mRNA is a primary
RT response to growth-factor stimulation of A9-2B cells.";
Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).
16) SEQUENCE OF 2375-2477 FROM N.A.
TISSUE=Kidney;
MEDLINE=93011702; PubMed=1327855;
Rahmandjian B.W., Salomon C., Leonard N., Tremblay S., Turler H.;
"Fibronectin gene expression in proliferating, quiescent, and SV40-
RT infected mouse kidney cells.";
Exp. Cell Res. 202:464-470(1992).
17) STRUCTURE BY NMR OF 1447-1630.
MEDLINE=98202578; PubMed=9533887;
Cople V., Tomita Y., Akiyama S.K., Acta S., Yamada K.M., Venable R.M.,
RA Pastor R.W., Krueger S., Torchia D.A.;
"Solution structure and dynamics of linked cell attachment modules of
RT mouse fibronectin containing the RGD and synergy regions: comparison
RT with the human fibronectin crystal structure.";
J Mol. Biol. 277:663-682(1998).
18) DOWN-REGULATION BY GLUCOCORTICOID.
MEDLINE=21600963; PubMed=11737251;
Gu Y.-C., Tates J.F., Gullberg D., Timpi R., Ekblom M.;
RT "Glucocorticoids down-regulate the extracellular matrix proteins
RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
Eur. J. Haematol. 67:176-184(2001).
19) FUNCTION: Fibronectins bind cell surfaces and various compounds
including collagen, fibrin, heparin, DNA, and actin. Fibronectins
are involved in cell adhesion, cell motility, opsonization, wound
healing, and maintenance of cell shape.
20) SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
variants, connected by 2 disulfide bonds near the carboxyl ends;
to a lesser extend homodimers. Interacts with FBLN1 (By
similarity).
21) SUBCELLULAR LOCATION: Secreted; extracellular matrix.
22) ALTERNATIVE PRODUCTS:
23) Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced. Each of the "extra
domain" and the connecting strand 3 are present in some forms of
fibronectin and absent in others;
Name=1;
24) IsoId=PI1276-1; Sequence=Displayed.
25) TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
forms), made by fibroblasts, epithelial and other cell types, is
deposited as fibrils in the extracellular matrix.
26) INDUCTION: Glucocorticoids suppressed mRNA expression and protein
synthesis.
27) PTM: Sulfated (By similarity).
28) SIMILARITY: Contains 12 fibronectin type I domains.
29) SIMILARITY: Contains 2 fibronectin type II domains.
30) SIMILARITY: Contains 17 fibronectin type III domains.

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DR EMBL; BC051083; AAH51082.1; -
DR EMBL; Z22729; CAA80422.1; -
DR EMBL; X82467; CAA57796.1; -
DR EMBL; X93162; CAA63564.1; -
DR EMBL; M18194; AAA37636.1; -

[illegible]

Query Match 100.0%; Score 462; DB 1; Length 2477;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYVQDLSEFVDTSSIGLRTPLNSSTIGRIYVVAAGCPIFEFDVSSVGYTV 60
 DB 1265 EYVQDLSEFVDTSSIGLRTPLNSSTIGRIYVVAAGCPIFEFDVSSVGYTV 1324

QY 61 TGLEPGIDYDISYITLINGSASAFTLLTQOT 91
 DB 1325 TGLEPGIDYDISYITLINGSASAFTLLTQOT 1355

RESULT 2
 FINE_RAT STANDARD; PRT; 2477 AA.

AC P04937;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin precursor (FN).
 GN FN1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer; TISSUE=Liver;
 RA MEDLINE=88054951; PubMed=2445560;
 RA Schwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;
 RT "Multiple sites of alternative splicing of the rat fibronectin gene transcript";
 RL EMBO J. 6:2573-2580(1987).
 RN [2]
 RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.
 RC STRAIN=Fischer; TISSUE=Liver;
 RA MEDLINE=88054950; PubMed=3119323;
 RA Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.;
 RT "Organization of the fibronectin gene provides evidence for exon shuffling during evolution";
 RL EMBO J. 6:2565-2572(1987).
 RN [3]
 RP SEQUENCE OF 1586-2477 FROM N.A.
 RC STRAIN=Fischer; TISSUE=Liver;
 RA Schwarzbauer J.E., Tankun J.W., Lemischka I.R., Hynes R.O.;
 RT "Three different fibronectin mRNAs arise by alternative splicing within the coding region";
 RL Cell 35:421-431(1983).
 CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape.
 CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS; TO A LESSER EXTENT HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Comment=Each of the "extra domain" and the connecting strand 3 are present in some forms of fibronectin and absent in others;
 CC Name=1; IsoId=P04937-1; Sequence=Displayed;
 CC Name=2; Synonyms=FNII-13-less;
 CC IsoId=P04937-2; Sequence=VSP_003258;
 CC Name=3; Synonyms=Lambda-RLR4-5;
 CC IsoId=P04937-3; Sequence=VSP_003259;
 CC Name=4; Synonyms=Lambda-RLR5;
 CC IsoId=P04937-4; Sequence=VSP_003260;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted by hepatocytes. Cellular FN (dimeric or cross-linked multimeric forms), made by fibroblasts, epithelial and other cell types, is

CC deposited as fibrils in the extracellular matrix.
 CC -1- PTM: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
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 CC -----
 CC EMBL; X15906; CAA34020.1; -;
 CC EMBL; L29191; AAA41166.1; -;
 CC EMBL; L29191; AAA41166.1; JOINED.
 CC EMBL; L29191; AAA41167.1; -;
 CC EMBL; L29191; AAA41167.1; JOINED.
 CC EMBL; L29191; AAA41168.1; -;
 CC EMBL; L29191; AAA41168.1; JOINED.
 CC EMBL; X05832; CAA29278.1; -;
 CC EMBL; X05832; CAA29279.1; -;
 CC EMBL; X05833; CAA29280.1; -;
 CC EMBL; X05834; CAA29281.1; -;
 CC PIR; S14428; S14428.
 CC HSSP; P02751; IFR.
 CC Interpro; IPR006029; EGF like.
 CC Interpro; IPR000083; Fibnctnl.
 CC Interpro; IPR008857; FN_III-like.
 CC Interpro; IPR003961; FN_III.
 CC Interpro; IPR000562; FN_Type_II.
 CC Interpro; IPR003962; FNII_subd.
 CC Pfam; PF00039; fn1; 12.
 CC Pfam; PF00040; fn2; 2.
 CC Pfam; PF00041; fn3; 17.
 CC PRINTS; PR00013; FNTYPEII.
 CC PRINTS; PR00014; FNTYPEIII.
 CC PRODOM; PD00095; FN_Type_II; 2.
 CC SMART; SM00058; FN1; 12.
 CC SMART; SM00059; FN2; 2.
 CC SMART; SM00060; FN3; 13.
 CC PROSITE; PS00022; EGF_1; 2.
 CC PROSITE; PS00023; FIBRONECTIN_2; 2.
 CC PROSITE; PS01253; FIBRONECTIN_1; 12.
 CC KEGG; Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation; Signal.
 CC KEGG; Cell adhesion; Repeat; Alternative splicing; Signal.
 CC FT 1
 CC FT 32
 CC FT 33 2477 FIBRONECTIN.
 CC FT 53 273 FIBRIN- AND HEPARIN-BINDING 1.
 CC FT 308 608 COLLAGEN-BINDING.
 CC FT 906 1171
 CC FT 1357 1630 CELL-ATTACHMENT.
 CC FT 1811 2081 HEPARIN-BINDING 2.
 CC FT 2295 2427 FIBRIN-BINDING 2.
 CC FT 51 91 FIBRONECTIN TYPE-I 1.
 CC FT 96 139 FIBRONECTIN TYPE-I 2.
 CC FT 140 183 FIBRONECTIN TYPE-I 3.
 CC FT 185 229 FIBRONECTIN TYPE-I 4.
 CC FT 230 274 FIBRONECTIN TYPE-I 5.
 CC FT 306 345 FIBRONECTIN TYPE-I 6.
 CC FT 345 404 FIBRONECTIN TYPE-II 1.
 CC FT 405 469 FIBRONECTIN TYPE-II 2.
 CC FT 468 511 FIBRONECTIN TYPE-I 7.
 CC FT 516 558 FIBRONECTIN TYPE-I 8.
 CC FT 559 602 FIBRONECTIN TYPE-I 9.
 CC FT 609 706 FIBRONECTIN TYPE-III 1.
 CC FT 707 808 FIBRONECTIN TYPE-III 2.
 CC FT 809 903 FIBRONECTIN TYPE-III 3.
 CC FT 904 994 FIBRONECTIN TYPE-III 4.
 CC FT 995 1084 FIBRONECTIN TYPE-III 5.
 CC FT 1085 1172 FIBRONECTIN TYPE-III 6.
 CC FT 1173 1264 FIBRONECTIN TYPE-III 7.


```

Oy      61  TGLEPGJDIYDVSITTLINGESAPPTLTQOT  91
Db      204  TGLEPGJDIYDVSITTLINGESAPPTLTQOT  234

RESULT 4
FINC_XENIA          STANDARD;          PRT;  2481 AA.
AC  091740;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Fibronectin precursor.
GN  FN1.
OS  Xenopus laevis (African clawed frog) .
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
   [1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=92111942; PubMed=170390;
RA  Desjone D W., Norton P.A., Hynes R.O.;
RT  "Identification and characterization of alternatively spliced
RT  fibronectin mRNAs expressed in early Xenopus embryos.";
RL  Dev. Biol. 149:357-369(1992) .
CC  -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC  including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC  are involved in cell adhesion, cell motility, opsonization, wound
CC  healing, and maintenance of cell shape (by similarity) .
CC  -1- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
CC  CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
CC  SIMILARITY) .
CC  -1- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=1;
CC  Comment=A number of isoforms are produced. Each of the "extra
CC  domain" and the connecting strand 3 are present in some forms of
CC  fibronectin and absent in others;
CC  Name=1;
CC  IsoId=Q91740-1; Sequence=Displayed;
CC  -1- TISSUE SPECIFICITY: IN EARLY XENOPUS EMBRYO, CELLULAR FORMS OF
CC  FIBROECTIN PRECIPITATE WHICH INCLUDE BOTH EXTRA DOMAIN. IN
CC  FIBROECTIN OF EMBRYONIC AND ADULT LIVER THE CONNECTING STRAND 3
CC  CAN BE EITHER COMPLETELY EXCLUDED OR INCLUDED.
CC  -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC  -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC  -1- SIMILARITY: Contains 17 fibronectin type III domains.
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL, M77820, AAA49707.1, -.
DR  HSSP, P02751, ZEN2.
DR  InterPro: IPR006209, EGF_1like.
DR  InterPro: IPR000083, Fibrinctn.
DR  InterPro: IPR008957, FN_III_1like.
DR  InterPro: IPR003961, FN_III.
DR  InterPro: IPR000562, FN_Type_II.
DR  Pfam, PF00039, FN1_12.
DR  Pfam, PF00040, FN2_2.
DR  Pfam, PF00041, FN3_17.
DR  PRINTS, PR00013, FNTYPEII.
DR  ProDom, PD000995, FN_Type_II, 2.
DR  SMART, SM00058, FN1_12.
DR  SMART, SM00059, FN2_2.
DR  SMART, SM00060, FN3_17.
DR  PROSITE, PS00022, EGF_1, 2.
DR  PROSITE, PS01253, FIBRONECTIN_1, 11.

```


RA MEDLINE=85280409; PubMed=2925273;
RA Bernard M.P., Kolbe M., Weil D., Chu M.-L.;
RT "Human cellular fibronectin: comparison of the carboxyl-terminal
RT portion with rat identifies primary structural domains separated by
RT hypervariable regions.";
RL Biochemistry 24:2698-2704(1985).
RN [14]
RP SEQUENCE OF 1712-1739 FROM N.A.
RX MEDLINE=87026578; PubMed=3021206;
RA Sekiguchi K., Kios A.M., Kurachi K., Yoshitake S., Hakomori S.;
RT "Human liver fibronectin complementary DNAs: identification of two
RT different messenger RNAs possibly encoding the alpha and beta
RT subunits of plasma fibronectin.";
RL Biochemistry 25:4936-4941(1986).
RN [15]
RP SEQUENCE OF 1788-2386 FROM N.A. (ISOFORMS 4; 5 AND 6).
RC TISSUE=Cartilage; PubMed=12127832;
RX MEDLINE=22126816; PubMed=12127832;
RA Parker A.E., Boutell U., Carr A., Maciewicz R.A.;
RT "Novel cartilage-specific splice variants of fibronectin.";
RL Osteoarthritis Cartilage 10:528-534(2002).
RN [16]
RP SEQUENCE OF 32-290.
RX MEDLINE=84032463; PubMed=6630202;
RA Garcia-Pardo A., Pearlstein E., Frangione B.;
RT "Primary structure of human plasma fibronectin. The 29,000-dalton
RT NH2-terminal domain.";
RL J. Biol. Chem. 258:12670-12674(1983).
RN [17]
RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
RX MEDLINE=87080265; PubMed=3024962;
RA Owens R.V., Baralle F.E.;
RT "Mapping the collagen-binding site of human fibronectin by expression
RT in Escherichia coli.";
RL EMBO J. 5:2825-2830(1986).
RN [18]
RP SUBFATION.
RX MEDLINE=86042625; PubMed=2414772;
RA Liu M.C., Yu S., Sy U., Redman C.M., Lipmann F.;
RT "Tyrosine sulfation of proteins from the human hepatoma cell line
RT HepG2.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
RN [19]
RP O-GLYCOSYLATION OF THR-2064.
RX MEDLINE=81190085; PubMed=2012601;
RA Tresselt T., McCarthy J.B., Calaycay J., Lee T.D., Legesse K.,
RA Shively J.E., Pande H.;
RT "Human plasma fibronectin. Demonstration of structural differences
RT between the A- and B-chains in the III CS region.";
RL Biochem. J. 274:731-738(1991).
RN [20]
RP PEIN-BINDING SITE
RX MEDLINE=93015879; PubMed=1400330;
RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,
RA Argaves W.S.;
RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding
RT region of fibronectin.";
RL J. Biol. Chem. 267:20120-20125(1992).
RN [21]
RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
RX MEDLINE=95081153; PubMed=7989369;
RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
RT "Further characterization of the NH2-terminal fibrin-binding site on
RT fibronectin.";
RL J. Biol. Chem. 269:31938-31945(1994).
RN [22]
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=92162710; PubMed=1311202;
RA Baron M., Main A.D., Driscoll P.C., Mardon H.J., Boyd J.,
RA Campbell I.D.;
RT "1H NMR assignment and secondary structure of the cell adhesion type
RT III module of fibronectin."

RN [23]
RP STRUCTURE BY NMR OF 1447-1540
RX MEDLINE=93046665; PubMed=1423622;
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;
RT "The three-dimensional structure of the tenth type III module of
RT fibronectin: an insight into RGD-mediated interactions.";
RL Cell 71:671-678(1992).
RN [24]
RP STRUCTURE BY NMR OF 182-275.
RX MEDLINE=94141923; PubMed=8308892;
RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,
RA Campbell I.D.;
RT "Solution structure of a pair of fibronectin type I modules with
RT fibrin binding activity.";
RL J. Mol. Biol. 235:1302-1311(1994).
RN [25]
RP STRUCTURE BY NMR OF 32-92.
RX MEDLINE=96069779; PubMed=7583666;
RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;
RT "High-resolution structural studies of the factor XIIIa crosslinking
RT site and the first type I module of fibronectin.";
RL Nat. Struct. Biol. 2:946-950(1995).
RN [26]
RP STRUCTURE BY NMR OF 406-464.
RX MEDLINE=98179558; PubMed=9514732;
RA Sticht H., Pickford A.R., Potts J.R., Campbell I.D.;
RT "Solution structure of the glycosylated second type 2 module of
RT fibronectin.";
RL J. Mol. Biol. 276:177-187(1998).
RN [27]
RP STRUCTURE BY NMR OF EXTRA ED-B DOMAIN FROM ISOFORM 7.
Query Match 32.1%; Score 148.5; DB 1; Length 2386;
Best Local Similarity 36.5%; Pred. No. 4.6e-07;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;
QY 2 VPOQLTDSFVIDIDSSGLAMTFLNLSSTITGRTVVA-----GEGIFEDFDSSV 55
DB 907 VPSPRDQFVENVDDVKITMTWP-PESAVRGVVDVLPVNLPEHGQRLPI-----SRN 959
QY 56 GYVTVGLFPGIDYDISVITLNGGESAPPTLQQT 91
DB 960 TFAVTLSPGVTVYFVKFVAVSGRESKPLTAQQT 995
RESULT 7
FNC BOVIN STANDARD; PRT; 2265 AA.
ID FNC BOVIN
AC P07589;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin (FN).
GN FNI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE.
RP MEDLINE=87054047; PubMed=3780752;
RX Skorstengaard K., Jensen M.S., Sahl P., Petersen T.B., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin.";
RL Eur. J. Biochem. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=93117805; PubMed=6218503;
RA Petersen T.E., Thorgeresen H.C., Skorstengaard K., Vibe-Pedersen K.,
RA Sahl P., Sottrup-Jensen L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
RT of internal homologs."

Best Local Similarity 36.1%; Pred. No. 5.5e-07;
Matches 35; Conservative 13; Mismatches 36; Indels 13; Gaps 3;
Db 1 EVPOLDISFVIDSSIGLRMTPLNSSTIGRITVAA-----GEGIPREDVDS 54
875 KVPBRRLQFVEVDVATTMTTP-PSPTGIRVDVPPNLPCHGGRUPLV-----SR 927
55 VGYVTVTGLEPDIYDISVITLLNGSGSAPTTLTQQT 91
928 NTFALVTGLSPGVYHFKVFVAVNGRSEKTLTAQAT 964

RESULT 8
FINC_HORSE STANDARD; PRT; 522 AA.
AC Q28377; Q28378; 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin (FN) (Fragment).
GN FN1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Liver;
RX MEDLINE=96324983; PubMed=8702559;
RA MacLeod J.N., Burton-Wurster N., Gu D.N., Lust G.;
RT "Fibronectin mRNA splice variant in articular cartilage lacks bases
RT encoding the V, III-15, and I-10 protein segments.",
RL J. Biol. Chem. 271:18954-18960(1996).
CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC are involved in cell adhesion, cell motility, opsonization, wound
CC healing, and maintenance of cell shape.
CC -1- FUNCTION: Isoform 2 is probably involved in matrix organization of
CC cartilage.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS,
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC Name=2; Sequence=Displayed;
CC Name=2; Synonyms=(V+C)-;
CC Name=2; IsoId=Q28377-2; Sequence=VSP_003253; VSP_003254;
CC Note=Backs repeat 15 of fibronectin type-III, repeat 10 of
CC fibronectin type-I, and the connecting strand 3;
CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
CC forms), made by fibroblasts, epithelial and other cell types, is
CC deposited as fibrils in the extracellular matrix. Isoform 2 is the
CC major transcript in articular cartilage; very low levels in lymph
CC node, bone, aorta, and skin; absent from liver, spleen, placenta,
CC cardiac muscle, skeletal muscle, stomach, small intestine, and
CC kidney.
CC -1- PTM: Sulfated (By similarity).
CC -1- SIMILARITY: Contains at least 4 fibronectin type III domains.
CC -1- SIMILARITY: Contains at least 3 fibronectin type I domains.
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CC -----
DR EMBL, U52107; AAC48613.1; -.
DR EMBL, U52108; AAC48614.1; -.
DR HSSP, P02751, 1ENVH.
DR InterPro, IPR000083; Fibnctn1.
DR InterPro, IPR008957; FN_III-like.
DR InterPro, IPR003961; FN_III.
DR InterPro, IPR003962; FNIII_subd.
DR Pfam, PF00039; FN1; 3.
DR Pfam, PF00041; FN3; 3.
DR PRINTS, PR00014; FNTPR11.
DR SMART, SM00058; FN1; 2.
DR SMART, SM00060; FN3; 3.
DR PROSITE, PS01253; FIBRONECTIN_1; 2.
KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
KW Repeat; Sulfation; Alternative splicing.
FT NON TER 1 1
FT DOMAIN 1 204
FT 325 3522
FT DOMAIN 1 25
FT DOMAIN 26 114
FT DOMAIN 115 204
FT DOMAIN 205 315
FT DOMAIN 316 395
FT DOMAIN 417 461
FT 462 504
FT 506 522
FT DOMAIN 304 306
FT SITE 419 448
FT DISULFID 446 458
FT DISULFID 446 491
FT DISULFID 489 501
FT MOD RES 515 515
FT CARBOHYD 321 321
FT CARBOHYD 277 277
FT CARBOHYD 278 278
FT VASPLIC 205 205
FT 462 462
FT VASPLIC 206 462
FT NON TER 522 522
FT SEQUENCE 522 AA; 57577 MW; 893E8AC95864D41 CRC64;
SQ
Query Match 26.0%; Score 120; DB 1; Length 522;
Best Local Similarity 33.8%; Pred. No. 7.3e-05;
Matches 27; Conservative 16; Mismatches 35; Indels 2; Gaps 2;
Db 12 DIYDSIGLRMTPLNSSTIGRITVAAEGGIPREDVDSVGYVTVTGLEPGIDYDI 71
37 DAEFTTITISMR-TKETITGFOVDVPA-NQGPPIQRTIKPVRVSRTIGLQPGIDYKI 94
72 SVITLLNGSGSAPTTLTQQT 91
95 YLYTLNDNRRSPVITDAGT 114

RESULT 9
FINC_CANFA STANDARD; PRT; 522 AA.
AC Q28275; Q28276; 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin (FN) (Fragment).
GN FN1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2)

RA MacLeod J.N., Burton-Wurster N., Gu D.N., Lust G.,
 RT "Fibronectin mRNA splice variant in articular cartilage lacks bases
 encoding the V, III-15, and I-10 protein segments.",
 RL J. Biol. Chem. 271:18954-18960(1996).
 CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
 including collagen, fibrin, heparin, DNA, and actin. Fibronectins
 are involved in cell adhesion, cell motility, opsonization, wound
 healing, and maintenance of cell shape.
 CC -1- FUNCTION: Isoform 2 is probably involved in matrix organization of
 cartilage.
 CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
 variants, connected by 2 disulfide bonds near the carboxyl ends;
 to a lesser extent homodimers.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Each of the "extra domain" and the connecting strand 3
 CC are present in some forms of fibronectin and absent in others;
 CC Name=1;
 CC IsoId=Q28275-1; Sequence=Displayed;
 CC Name=2; Synonyms=(V+C)-;
 CC IsoId=Q28275-2; Sequence=VSP_003251, VSP_003252;
 CC Note=Lacks repeat 15 of fibronectin type-III, repeat 10 of
 CC fibronectin type-I, and the connecting strand 3;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 CC forms), made by fibroblasts, epithelial and other cell types, is
 CC deposited as fibrils in the extracellular matrix. Isoform 2 is the
 CC major transcript in articular cartilage, but it is absent from
 CC liver.
 CC -1- PTM: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains at least 4 fibronectin type III domains.
 CC -1- SIMILARITY: Contains at least 3 fibronectin type I domains.
 CC -----
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 CC -----
 CC EMBL: U52106; AAC48612.1; -;
 CC DR EMBL: U52105; AAC48611.1; -;
 CC DR HSSP: P02751; IFNH.
 CC DR InterPro: IPR000083; Fibnrcn1.
 CC DR InterPro: IPR008957; FN_III-like.
 CC DR InterPro: IPR003961; FN_III.
 CC DR InterPro: IPR003962; FnIII_subd.
 CC DR Pfam: PF00039; fn1; 3.
 CC DR Pfam: PF00041; fn3; 3.
 CC DR PRINTS: PR00014; ENTPR11.
 CC DR SMART: SMO0058; FN1; 2.
 CC DR SMART: SMO0060; FN3; 3.
 CC DR PROSITE: PS01253; FIBRONECTIN_1; 2.
 CC KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
 CC Repeat; Sulfation; Alternative splicing.
 CC FT NON TER 1 1
 CC FT DOMAIN <1 204 HEPARIN-BINDING 2 (BY SIMILARITY).
 CC FT DOMAIN 325 >522 FIBRIN-BINDING 2 (BY SIMILARITY).
 CC FT DOMAIN <1 25 FIBRONECTIN TYPE-III 13.
 CC FT DOMAIN 26 114 FIBRONECTIN TYPE-III 14.
 CC FT DOMAIN 115 204 FIBRONECTIN TYPE-III 15.
 CC FT DOMAIN 205 315 CONNECTING STRAND 3 (CS-3) (V REGION).
 CC FT DOMAIN 316 395 FIBRONECTIN TYPE-III 16.
 CC FT DOMAIN 417 461 FIBRONECTIN TYPE-I 10.
 CC FT DOMAIN 462 504 FIBRONECTIN TYPE-I 11.
 CC FT DOMAIN FIBRONECTIN TYPE-I 12.
 CC SITE 506 >522 CELL ATTACHMENT SITE (POTENTIAL).
 CC SITE 304 306
 CC FT DISULFID 419 448 BY SIMILARITY.
 CC FT DISULFID 446 458 BY SIMILARITY.
 CC FT DISULFID 464 491 BY SIMILARITY.
 CC FT DISULFID 489 501 BY SIMILARITY.

FT DISULFID 508 >522 BY SIMILARITY.
 FT MOD_RES 509 SUPRATON (POTENTIAL). (BY SIMILARITY).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 277 277 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 278 278 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT VARSPLIC 205 205 D-> E (in isoform 2).
 FT VARSPLIC /Frid=VSP_003251.
 FT VARSPLIC 206 462 Missing (in isoform 2).
 FT NON_TER 522 522 /Frid=VSP_003252.
 SQ SEQUENCE 522 AA; 57700 MW; DB1D9A54C2BD4E26 CRC64;
 Query Match 25.1%; Score 116; DB 1; Length 522;
 Best Local Similarity 32.5%; Pred. No. 0.00019;
 Matches 26; Conservative 17; Mismatches 35; Indels 2; Gaps 2;
 QY 12 DITDSIGLAWTPNLSHTIGRYITVAAGEGIPEDFVDSVGYVTTGLEPGIYDI 71
 DB 37 DATEITITISWR-ETKETEITGFQVDALPANGQNP1-ORTIRPDVRSYITGLQPGTDYKI 94
 QY 72 SVITLINGSAPPTLIQOT 91
 DB 95 YLYTLINDNARSSPVVIDAST 114
 RESULT 10
 ID TENA_CHICK STANDARD; PRT; 1808 AA.
 AC P10039; O73584; O73585; P21313;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tenascin precursor (TN) (Hexabrachion) (Cytoectin) (Neuronectin)
 DE (GMM) (J1) (Mlotendinous antigen) (Glioma-associated-extracellular
 DE matrix antigen) (GP 150-225).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RX MEDLINE=90030407; PubMed=2478295;
 RA Spring J., Beck K., Chiquet-Ehrismann R.;
 RT "Two contrary functions of tenascin: dissection of the active sites
 RT by recombinant tenascin fragments";
 RL Cell 59:325-334(1989).
 RN [2]
 RP SEQUENCE OF 27-722 FROM N.A., AND SEQUENCE OF 79-96.
 RC TISSUE=Fibroblast;
 RX MEDLINE=89030589; PubMed=2460335;
 RA Pearson C.A., Pearson D., Shibahara S., Hofsteenge J.,
 RT Chiquet-Ehrismann R.;
 RL "Tenascin: cDNA cloning and induction by TGF-beta.";
 RL EMBO J. 7:12977-12982(1988).
 RN [3]
 RP SEQUENCE OF 464-1018 AND 1412-1661 FROM N.A., AND SEQUENCE OF 852-868.
 RC TISSUE=embryo;
 RX MEDLINE=88176910; PubMed=2451243;
 RA Jones F.S., Burgeon M.P., Hoffman S., Crossin K.L., Cunningham B.A.,
 RT Edelman G.M.;
 RT "A cDNA clone for cytoectin contains sequences similar to epidermal
 RT growth factor-like repeats and segments of fibronectin and
 RT fibronectin";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2186-2190(1988).
 CC -1- FUNCTION: SAM (substrate-adhesion molecule) that appears to
 CC inhibit cell migration. May play a role in supporting the growth
 CC of epithelial tumors. Ligand for integrins alpha-8/beta-1,
 CC alpha-9/beta-1, alpha-V/beta-3 and alpha-V/beta-6.
 CC -1- SUBUNIT: Hexameric. A homotrimer may be formed in the triple
 CC coiled-coil region and may be stabilized by disulfide rings at
 CC both ends. Two of such half-hexabrachions may be disulfide linked

CC	-1- SUBCELLULAR LOCATION:	Secreted; extracellular matrix.
CC	-1- ALTERNATIVE PRODUCTS:	Event=Alternative splicing; Named isoforms=3;
CC	Comment=Isoforms are produced in a tissue- and time-specific manner during development;	
CC	Name=1; Synonyms=230 kDa;	
CC	IsoId=P10039-1; Sequence=Displayed;	
CC	Name=2; Synonyms=200 kDa;	
CC	IsoId=P10039-2; Sequence=VSP_001410;	
CC	Name=3; Synonyms=190 kDa;	
CC	IsoId=P10039-3; Sequence=VSP_001411;	
CC	-1- INDUCTION:	By TGF-beta.
CC	-1- SIMILARITY:	Contains 14 EGF-like domains.
CC	-1- SIMILARITY:	Contains 11 fibronectin type III domains.
CC	-1- SIMILARITY:	Contains 1 fibronectin C-terminal domain.
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CC	EMBL; M23121; AAA49086.1; .	
DR	EMBL; X08031; CAB40811.1; .	
DR	EMBL; X08030; CAB30824.1; ALT_TERM.	
DR	EMBL; J03641; AAA48748.1; ALT_SEQ.	
DR	EMBL; M20816; AAA48749.1; ALT_SEQ.	
DR	PIR; A31930; A31930.	
DR	PDB; 1QR4; 29-DEC-99.	
DR	InterPro; IPR006209; EGF like.	
DR	InterPro; IPR002181; Fibritogen_C.	
DR	InterPro; IPR008957; FN_IIT-like.	
DR	InterPro; IPR003961; FN_IIT.	
DR	InterPro; IPR006210; IEGF.	
DR	InterPro; IPR002049; Lamlnn_EGF.	
DR	Pfam; PF00008; EGF; 11.	
DR	Pfam; PF00147; fibrinogen_C; 1.	
DR	Pfam; PFC00043; fn3; 11.	
DR	PRINTS; PR00041; EGF/LAMININ.	
DR	SMART; SM00181; EGF; 10.	
DR	SMART; SM00186; FBG; 1.	
DR	SMART; SMO0060; FN3; 9.	
DR	PROSITE; PS00022; EGF_1; 14.	
DR	PROSITE; PS01186; EGF_2; 14.	
DR	PROSITE; PS50026; EGF_3; 5.	
KM	Glycoprotein; Cell adhesion; Repeat; EGF-like domain; Coiled coil; Extracellular matrix; Signal; Alternative splicing; 3D-structure.	
FT	SIGNAL	1
FT	PROPEP	23
FT	CHAIN	34
FT	DOMAIN	118
FT	DOMAIN	142
FT	DOMAIN	176
FT	DOMAIN	188
FT	DOMAIN	219
FT	DOMAIN	250
FT	DOMAIN	281
FT	DOMAIN	312
FT	DOMAIN	343
FT	DOMAIN	374
FT	DOMAIN	405
FT	DOMAIN	436
FT	DOMAIN	467
FT	DOMAIN	498
FT	DOMAIN	529
FT	DOMAIN	560
FT	DOMAIN	591
FT	DOMAIN	680
FT	DOMAIN	771
FT	DOMAIN	862
FT	DOMAIN	954
FT	DOMAIN	1042
FT	DOMAIN	1042
FT	DOMAIN	1043
FT	DOMAIN	1133
FT	DOMAIN	1224
FT	DOMAIN	1315
FT	DOMAIN	1405
FT	DOMAIN	1493
FT	DOMAIN	1589
FT	DOMAIN	1808
FT	DISULFID	64
FT	DISULFID	192
FT	DISULFID	196
FT	DISULFID	207
FT	DISULFID	218
FT	DISULFID	223
FT	DISULFID	227
FT	DISULFID	238
FT	DISULFID	249
FT	DISULFID	254
FT	DISULFID	264
FT	DISULFID	269
FT	DISULFID	271
FT	DISULFID	280
FT	DISULFID	285
FT	DISULFID	289
FT	DISULFID	302
FT	DISULFID	311
FT	DISULFID	316
FT	DISULFID	320
FT	DISULFID	333
FT	DISULFID	347
FT	DISULFID	357
FT	DISULFID	362
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FT	DISULFID	373
FT	DISULFID	378
FT	DISULFID	388
FT	DISULFID	393
FT	DISULFID	404
FT	DISULFID	409
FT	DISULFID	419
FT	DISULFID	424
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FT	DISULFID	455
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FT	DISULFID	471
FT	DISULFID	475
FT	DISULFID	488
FT	DISULFID	497
FT	DISULFID	502
FT	DISULFID	512
FT	DISULFID	506
FT	DISULFID	519
FT	DISULFID	533
FT	DISULFID	537
FT	DISULFID	548
FT	DISULFID	550
FT	DISULFID	554
FT	DISULFID	568
FT	DISULFID	579
FT	DISULFID	581
FT	CARBOHYD	38
FT	CARBOHYD	168
FT	CARBOHYD	186
FT	CARBOHYD	186
FT	CARBOHYD	328
FT	CARBOHYD	603
FT	CARBOHY	

SQ SEQUENCE 1808 AA; 198858 MW; B924A06CF9EFD6DE CRC64;

Query Match 22.7%; Score 105; DB 1; Length 1808;
 Best Local Similarity 35.1%; Pred. No. 0.01; Indels 2; Gaps 2;
 Matches 27; Conservative 15; Mismatches 33; Indels 2; Gaps 2;

QY 8 LSFVDITDSIGKRWTPPLNSSTIIIGRTVVAAGSEPIFEFDVDSVGYTVTGLEPCI 67
 DB 1323 ISFSDITENSATSWTF-PRSRDYSRVSVYVITGTPMNVV-VDSKRTRTLVLVPGCV 1380
 QY 68 DYDISVITLINGSAP 84
 DB 1381 DYNWNIISVKGFESESEP 1397

RESULT 11
 CA17_HUMAN STANDARD; PRT; 2944 AA.
 ID Q02388; Q14054; Q16507;
 AC Q02388; Q14054; Q16507;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE collagen alpha 1(VII) chain precursor (long-chain collagen) (LC
 collagen).
 GN COL7A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94327588; PubMed=8051117;
 RA Cristiano A.M., Greenspan D.S., Lee S., Uitto J.;
 RT "Cloning of human type VII collagen. Complete primary sequence of the
 alpha 1(VII) chain and identification of intragenic polymorphisms.";
 J. Biol. Chem. 269:20256-20262(1994).
 RN [2]
 RP SEQUENCE OF 128-1493 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=9338437; PubMed=1307247;
 RA Cristiano A.M., Rosenbaum L.M., Chung-Honet L.C., Parente M.G.,
 Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Burgess R.E.,
 Uitto J.;
 RT "The large non-collagenous domain (NC-1) of type VII collagen is
 amino-terminal and chimeric. Homology to cartilage matrix protein,
 the type III domains of fibronectin and the A domains of von
 Willebrand factor.";
 Hum. Mol. Genet. 1:475-481(1992).
 RN [3]
 RP SEQUENCE OF 815-1439 FROM N.A.
 RX MEDLINE=91334380; PubMed=1871109;
 RA Parente M.G., Chung L.C., Rymaenen J., Woodley D.T., Wynn K.W.,
 Bajer E.A., Mattei M.-G., Chu M.-L., Uitto J.;
 RT "Human type VII collagen: cDNA cloning and chromosomal mapping of the
 gene.";
 Proc. Natl. Acad. Sci. U.S.A. 88:6931-6935(1991).
 RN [4]
 RP SEQUENCE OF 369-1255 FROM N.A.
 RX MEDLINE=93107742; PubMed=1469284;
 RA Gannon W.R., Abernethy M.L., Padilla K.M., Prisyanyan P.S.,
 Cook M.E., Wright J., Briggman R.A., Hunt S.W. III;
 RT "Noncollagenous (NC1) domain of collagen VII resembles multidomain
 adhesion proteins involved in tissue-specific organization of
 extracellular matrix.";
 J. Invest. Dermatol. 99:691-696(1992).
 RN [5]
 RP SEQUENCE OF 340-675 FROM N.A.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=92231902; PubMed=1567409;
 RA Tanaka T., Takahashi K., Furukawa F., Imanura S.;
 RT "Molecular cloning and characterization of type VII collagen cDNA.";
 Biochem. Biophys. Res. Commun. 183:958-963(1992).
 RN [6]
 RP SEQUENCE OF 2395-2944 FROM N.A.

RX MEDLINE=93271985; PubMed=8499916;
 RA Greenspan D.S.;
 RT "The carboxyl-terminal half of type VII collagen, including the non-
 collagenous NC-2 domain and intron/exon organization of the
 corresponding region of the COL7A1 gene.";
 Hum. Mol. Genet. 2:273-278(1993).
 RN [7]
 RP SEQUENCE OF 1-87 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94375010; PubMed=8088784;
 RA Cristiano A.M., Hoffman G.G., Chung-Honet L.C., Lee S., Cheng W.,
 Uitto J., Greenspan D.S.;
 RT "Structural organization of the human type VII collagen gene (COL7A1),
 composed of more exons than any previously characterized gene.";
 Genomics 21:169-179(1994).
 RN [8]
 RP VARIANT EBDSC ARG-2034.
 RX MEDLINE=89227237; PubMed=2653224;
 RA Fine J.D., Johnson L., Wright T.;
 RT "Epidermolysis bullosa simplex superficialis. A new variant of
 epidermolysis bullosa characterized by subcorneal skin cleavage
 mimicking peeling skin syndrome.";
 Arch. Dermatol. 125:633-638(1989).
 RN [9]
 RP REVIEW ON DEB VARIANTS.
 RX MEDLINE=96041696; PubMed=9375848;
 RA Jaevikailio A., Pulkkinen L., Uitto J.;
 RT "Molecular basis of dystrophic epidermolysis bullosa: mutations in
 the type VII collagen gene (COL7A1).";
 Hum. Mutat. 10:338-347(1997).
 RN [10]
 RP VARIANT DEB LYS-2798.
 RX MEDLINE=93291877; PubMed=8513326;
 RA Cristiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y.,
 Lin A.N., Dietz H.C., Hovnanian A., Uitto J.;
 RT "A missense mutation in type VII collagen in two affected siblings
 with recessive dystrophic epidermolysis bullosa.";
 Nat. Genet. 4:62-66(1993).
 RN [11]
 RP VARIANT DEB SER-2040.
 RX MEDLINE=94224777; PubMed=8170945;
 RA Cristiano A.M., Rymaenen M., Uitto J.;
 RT "Dominant dystrophic epidermolysis bullosa: identification of a
 gly--Ser substitution in the triple-helical domain of type VII
 collagen.";
 Proc. Natl. Acad. Sci. U.S.A. 91:3549-3553(1994).
 RN [12]
 RP VARIANT DEB CYS-2623.
 RX MEDLINE=96081220; PubMed=8541842;
 RA Cristiano A.M., Lee J.Y.-Y., Chen W.J., Laforgia S., Uitto J.;
 RT "Periapical epidermolysis bullosa: genetic linkage to COL7A1 and
 identification of a glycine-to-cysteine substitution in the triple-
 helical domain of type VII collagen.";
 Hum. Mol. Genet. 4:1579-1583(1995).
 RN [13]
 RP VARIANT DEB ARG-2043.
 RX MEDLINE=95164985; PubMed=7861014;
 RA Cristiano A.M., Morricone A., Paradisi M., Angelo C., Mazzanti C.,
 Cavaliere R., Uitto J.;
 RT "A glycine-to-arginine substitution in the triple-helical domain of
 type VII collagen in a family with dominant dystrophic epidermolysis
 bullosa.";
 J. Invest. Dermatol. 104:438-440(1995).
 RN [14]
 RP VARIANTS DEB.
 RX MEDLINE=96220218; PubMed=8644729;
 RA Cristiano A.M., McGrath J.A., Tan K.C., Uitto J.;
 RT "Glycine substitutions in the triple-helical region of type VII
 collagen result in a spectrum of dystrophic epidermolysis bullosa
 phenotypes and patterns of inheritance.";
 Am. J. Hum. Genet. 58:671-681(1996).
 RN [15]
 RP VARIANT DEB ARG-2575.

EX MEDLINE=96154068; PubMed=8592061;
RA Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., Utito J.;
RT "Molecular basis of recessive dystrophic epidermolysis bullosa:
RT genotype/phenotype correlation in a case of moderate clinical
RT severity.";
RL J. Invest. Dermatol. 106:119-124(1996).
RN [16]
RP VARIANT DEB ARG-1782.
RX MEDLINE=96183562; PubMed=8618018;
RA Christiano A.M., McGrath J.A., Utito J.;
RT "Influence of the second COL7A1 mutation in determining the
RT phenotypic severity of recessive dystrophic epidermolysis bullosa.";
RL J. Invest. Dermatol. 106:766-770(1996).
RN [17]
RP VARIANT DEB ASP-2073.
RX MEDLINE=96310789; PubMed=8757758;
RA Dunnill M.G.S., McGrath J.A., Richards A.J., Christiano A.M.,
RA Utito J., Pope F.M., Bady R.A.J.;
RT "Clinicopathological correlations of compound heterozygous COL7A1
RT mutations in recessive dystrophic epidermolysis bullosa.";
RL J. Invest. Dermatol. 107:171-177(1996).
RN [18]
RP VARIANTS DEB TRP-1982; GLY-2008; ALA-2025; GLU-2049; TRP-2063 AND
RP ARG-2575.
RX MEDLINE=97465605; PubMed=9326325;
RA Hovnanian A., Rochat A., Bodemer C., Petit E., Rivers C.A., Prost C.,
RA Freitag S., Christiano A.M., Utito J., Lathrop M., Barrandon Y.,
RA de Prost Y.;
RT "Characterization of 18 new mutations in COL7A1 in recessive
RT dystrophic epidermolysis bullosa provides evidence for distinct
RT molecular mechanisms underlying defective anchoring fibril
RT formation.";
RL Am. J. Hum. Genet. 61:599-610(1997).
RN [19]
RP VARIANT DEB ARG-1652.
RX MEDLINE=98106792; PubMed=9444387;
RA Cserhalmi-Friedman P.B., Karpatt S., Horvath A., Christiano A.M.;
RT "Identification of a glycine substitution and a splice site mutation
RT in the type VII collagen gene in a proband with milds recessive
RT dystrophic epidermolysis bullosa.";
RL Arch. Dermatol. Res. 289:640-645(1997).
RN [20]
RP VARIANTS DEB ARG-2009 AND ARG-2043.
RX MEDLINE=97358588; PubMed=9215684;
RA Winberg J.-O., Hammami-Hausasli N., Nilsen O., Anton-Lamprecht I.,
RA Naylor S.L., Kerbacher K., Zimmermann B., Krajci P.,
RA Gedde-Dahl T. Jr., Bruckner-Tuderman L.;
RT "Modulation of disease severity of dystrophic epidermolysis bullosa by
RT a splice site mutation in combination with a missense mutation in the
RT COL7A1 gene.";
RL Hum. Mol. Genet. 6:1125-1135(1997).
RN [21]
RP VARIANTS DEB ASP-1519; ASP-2006; GLU-2015 AND ARG-2034.
RX MEDLINE=98334662; PubMed=9668111;
RA Hammami-Hausasli N., Schumann H., Raghunath M., Kilgus O., Luecht U.,
RA Jünger T., Bruckner-Tuderman L.;
RT "Some, but not all, glycine substitution mutations in COL7A1 result in
RT intracellular accumulation of collagen VII, loss of anchoring
RT fibrils, and skin blistering.";
RL J. Biol. Chem. 273:19228-19234(1998).
RN [22]
RP VARIANTS DEB CYS-2008; ARG-2207 AND SER-2775.
RX MEDLINE=98410969; PubMed=9740253;
RA Kom A., Pulkkinen L., Ishida-Yamamoto A., Hashimoto I., Utito J.;
RT "Novel COL7A1 mutations in dystrophic forms of epidermolysis
RT bullosa.";
RL J. Invest. Dermatol. 111:534-537(1998).
RN [23]
RP VARIANT DEB ARG-1347.
RX MEDLINE=99019477; PubMed=9804332;
RA Terecina M., Poserato P., Schubert M., Sonego G., Azorzi F.,
RA Query Match

Best Local Similarity 31.1%, Pred. No. 0.028;
Matches 28; Conservative 19; Mismatches 39; Indels 4; Gaps 3;
QY 2 VPQIDLSFVDITSSIGLRWTPLN--SRTIGYRTVAAGSGIPFEDFDSVGYYT 59
DB 957 VPSI-ELAVDTSIDSVTLATPVSRASSYILSR-PLRGCGVPSQPCTLPETSSQR 1014
QY 60 VTGLEPGIDYDISVTLINGESAPTTLTQ 89
DB 1015 VTGLEPGVSYIFSLTPVLDGCGPEASVTQ 1044
RESULT 12
CALC_CHICK STANDARD, PRT, 3124 AA.
AC P13944; Q04509;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Collagen alpha 1(XII) chain precursor (Fibrochimerin).
GN COL12A1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn;
RX MEDLINE=92011862; PubMed=1918137;
RA Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H.,
RA Nishida Y., Obara M., Kimata K.;
RT "The complete primary structure of type XII collagen shows a chimeric
RT molecule with reiterated fibronectin type IIR motifs, von Willebrand
RT factor A motifs, a domain homologous to a noncollagenous region of
RT type IX collagen, and short collagenous domains with an Arg-Gly-Asp
RT site.";
RL J. Cell Biol. 115:209-221(1991).
RN [2]
RP SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
RP 2846-2873
RX MEDLINE=9062079; PubMed=2584192;
RA Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.;
RT "Type XII collagen. A large multidomain molecule with partial
RT homology to type IX collagen.";
RL J. Biol. Chem. 264:19772-19778(1989).
RN [3]
RP SEQUENCE OF 2960-3076 FROM N.A.
RX MEDLINE=87317590; PubMed=3476925;
RA Gordon M.K., Gerecke D.R., Olsen B.R.;
RT "Type XII collagen: distinct extracellular matrix component
RT discovered by cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
RN [4]
RP SEQUENCE OF 1-1283 FROM N.A. (ISOFORM SHORT), AND ALTERNATIVE
RP SPLICING.
RC TISSUE=Embryo;
RX MEDLINE=93042014; PubMed=1420368;
RA Trueb J., Trueb B.;
RT "The two splice variants of collagen XII share a common 5' end.";
RL Biochim. Biophys. Acta 1171:97-98(1992).
RN [5]
RP ALTERNATIVE SPLICING.
RX MEDLINE=95370352; PubMed=7642694;
RA Koch M., Bohmann B., Mathison M., Hagios C., Trueb B., Chiquet M.;
RT "Large and small splice variants of collagen XII: differential
RT expression and ligand binding.";
RL J. Cell Biol. 130:1005-1014(1995).
CC -1- FUNCTION: Type XII collagen interacts with type I collagen-
CC containing fibrils, the COL1 domain could be associated with the
CC surface of the fibrils, and the COL2 and NC3 domains may be
CC localized in the pericellular matrix.
CC -1- SUBUNIT: Trimer of identical chains each containing 190 kDa of

FT	DOMAIN	1199	1371	1473	1565	1654	1755	1846	1937	2027	2118	2206	2295	2500	2716	2750	2902	2945	3048	3124	3123	2440	2901	32	32	797	890	890	981	981	1006	1032	1032	1066	1258	1258	1264	2759	2803	2977	3075	3124	340578	MM; 094285AF7F346CF	CRC64;	Sequence	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;	Query Match	Best Local Similarity	22.18;	Score 102;	DB 1;	Length 3124;	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;	Query Match	Best Local Similarity	22.18;	Score 102;	DB 1;	Length 3124;	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;
FT	DOMAIN	1199	1371	1473	1565	1654	1755	1846	1937	2027	2118	2206	2295	2500	2716	2750	2902	2945	3048	3124	3123	2440	2901	32	32	797	890	890	981	981	1006	1032	1032	1066	1258	1258	1264	2759	2803	2977	3075	3124	340578	MM; 094285AF7F346CF	CRC64;	Sequence	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;	Query Match	Best Local Similarity	22.18;	Score 102;	DB 1;	Length 3124;	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;																
FT	DOMAIN	1199	1371	1473	1565	1654	1755	1846	1937	2027	2118	2206	2295	2500	2716	2750	2902	2945	3048	3124	3123	2440	2901	32	32	797	890	890	981	981	1006	1032	1032	1066	1258	1258	1264	2759	2803	2977	3075	3124	340578	MM; 094285AF7F346CF	CRC64;	Sequence	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;	Query Match	Best Local Similarity	22.18;	Score 102;	DB 1;	Length 3124;	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;																
FT	DOMAIN	1199	1371	1473	1565	1654	1755	1846	1937	2027	2118	2206	2295	2500	2716	2750	2902	2945	3048	3124	3123	2440	2901	32	32	797	890	890	981	981	1006	1032	1032	1066	1258	1258	1264	2759	2803	2977	3075	3124	340578	MM; 094285AF7F346CF	CRC64;	Sequence	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;	Query Match	Best Local Similarity	22.18;	Score 102;	DB 1;	Length 3124;	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;																
FT	DOMAIN	1199	1371	1473	1565	1654	1755	1846	1937	2027	2118	2206	2295	2500	2716	2750	2902	2945	3048	3124	3123	2440	2901	32	32	797	890	890	981	981	1006	1032	1032	1066	1258	1258	1264	2759	2803	2977	3075	3124	340578	MM; 094285AF7F346CF	CRC64;	Sequence	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;	Query Match	Best Local Similarity	22.18;	Score 102;	DB 1;	Length 3124;	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;																
FT	DOMAIN	1199	1371	1473	1565	1654	1755	1846	1937	2027	2118	2206	2295	2500	2716	2750	2902	2945	3048	3124	3123	2440	2901	32	32	797	890	890	981	981	1006	1032	1032	1066	1258	1258	1264	2759	2803	2977	3075	3124	340578	MM; 094285AF7F346CF	CRC64;	Sequence	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;	Query Match	Best Local Similarity	22.18;	Score 102;	DB 1;	Length 3124;	Matches	27;	Conservative	12;	Mismatches	28;	Indels	20;	Gaps	3;																
FT	DOMAIN	1199	1371	1473	1565	1654	1755	1846	1937	2027	2118	2206	2295	2500	2716	2750	2902	2945	3048	3124	3123	2440	2901	32	32	797	890	890	981	981	1006	10																																																								


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FT CARBOHYD 893 893 O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
FT CARBOHYD 985 985 O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
FT CARBOHYD 1769 1769 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 2212 2212 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 2533 2533 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 2684 2684 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT VARSPLIC 25 1190 Missing (in isoform X11B-1 and isoform
FT VARSPLIC 3062 3064 /FTID=VSP 001150.
FT VARSPLIC 3064 3064 X11B-2).
FT VARSPLIC 3065 3119 /FTID=VSP 001151.
FT VARSPLIC 3065 3119 Missing (in isoform X11A-2 and isoform
FT VARSPLIC 3065 3119 X11B-2).
SQ SEQUENCE 3119 AA; 340239 MW; 981F939C686AB3251 CRC64;

Query Match 21.1%; Score 97.5; DB 1; Length 3119;
Best Local Similarity 32.0%; Pred. No. 0.11;
Matches 24; Conservative 12; Mismatches 38; Indels 1; Gaps 1;

QY 12 DITDSSIGLWPEPLNSTIGRIYVVAAGEGIPFEDVDSVGYVTGLEPGIDYDI 71
Db 919 DITDSSIGAWTSA-PGMWGRGVSKSLYDIEAGETLNGDAHTMENIQPTKTKI 977
QY 72 SVITLLNGESAFT 86
Db 978 SVFATYSSGEGEPT 992

RESULT 14
TIE2_BOVIN STANDARD; PRT; 1125 AA.
AC Q06807;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Angiopoietin 1 receptor precursor (EC 2.7.1.112) (tyrosine-protein
kinase receptor TIE-2).
GN TEK OR TIE2 OR TIE-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=94022374; PubMed=8415706;
RA Sato T.N., Qin Y., Kozak C.A., Andus K.L.;
RT "Tie-1 and Tie-2 define another class of putative receptor tyrosine
kinase genes expressed in early embryonic vascular system.";
RT Proc. Natl. Acad. Sci. U.S.A. 90:9355-9358(1993).
CC -1- FUNCTION: This protein is a protein tyrosine-kinase transmembrane
receptor for angiopoietin 1. It may constitute the earliest
mammalian endothelial cell lineage marker. Probably regulates
endothelial cell proliferation, differentiation and guides the
proper patterning of endothelial cells during blood vessel
formation.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Specifically expressed in developing vascular
endothelial cells.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Tie
subfamily.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 3 fibronectin type III domains.
CC -1- SIMILARITY: Contains 3 EGF-like domains.
CC -----
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; X71424; CA50555.1; --
DR PIR; S57846; S57846.
DR HSSP; P13362; IFGK.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR002043; laminin_EGF.
DR InterPro; IPR007019; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00041; fn3_3.
DR Pfam; PF00063; Kinase_1.
DR PRINTS; PR00011; EGFAMININ.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00180; EGF_Lam; 1.
DR SMART; SM00060; FN3_3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50835; IG_Like; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding;
KW Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain;
KW Glycoprotein; Phosphorylation; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 1125
FT DOMAIN 19 746
FT TRANSMEM 747 771
FT DOMAIN 772 1125
FT DOMAIN 44 123
FT DOMAIN 210 252
FT DOMAIN 254 299
FT DOMAIN 301 341
FT DOMAIN 350 440
FT DOMAIN 444 538
FT DOMAIN 541 635
FT DOMAIN 639 730
FT DOMAIN 825 1097
FT NP_BIND 831 839
FT BINDING 856 856
FT ACT_SITE 965 965
FT MOD_RES 993 993
FT CARBOHYD 158 158
SQ SEQUENCE 1125 AA; 125927 MW; 015F1320AB85B7F CRC64;

Query Match 21.0%; Score 97; DB 1; Length 1125;
Best Local Similarity 31.2%; Pred. No. 0.039;
Matches 29; Conservative 16; Mismatches 42; Indels 6; Gaps 2;

QY 3 PQLDLSVVDITDSIGRWPLN---STIIIGRIYVVAAGEGIPFEDVDSVGY 58
Db 641 POPENIKIFNITDSAVSWITLDQYSISAIIRK-VQKNEQHDIVKIKVATTIY 698
QY 59 TYTGLEPGIDYDISVITLLNGESAFTLTQOT 91
Db 699 CLKGLEPQTVQVDLFAENNISSNPTSHSLT 731

RESULT 15
CAIC_HUMAN

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FT  VARSP LIC 25 1188 Missing (in isoform short).
FT  SEQUENCE 3063 AA; 333189 MW; 75FEA78FA8E48293 CRC64;
SQ
Query Match 20.9%; Score 96.5; DB 1; Length 3063;
Best Local Similarity 32.1%; Pred. No. 0.13; Mismatches 3; Gaps 2;
Matches 27; Conservative 12; Indels 42;
QY 3 PQLTDLSPVDITDSSIGLRMTPLNSSTIGRITVVAAGEGIFPEDFVDSVGYYTVTG 62
DB 908 PQ--DIVTKDITDTSIGAYMTSA-PGMVRGYRVSWKSLYDVTGTGKNLFEADAHMTIEN 964
QY 63 LERGIIDYDISVTLLINGESAPTT 86
DB 965 LQPETKXRIISVPATYSSGESEPLT 988

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Search completed: September 21, 2004, 05:47:32
 Job time : 27.0956 secs

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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53 Search time 143.191 Seconds
(without alignments)
200.516 Million cell updates/sec

Title: US-10-676-049-4

Sequence: 1 EVFQTLDSFVDITDSSIGL.....SVTLINGESAPFTLTQOT 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

SPTRMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_tvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	457	98.9	90	Q28253	Q28253 canis faml1
2	432	93.5	134	Q9M232	Q9M232 bos taurus
3	327	70.8	2478	Q93406	Q93406 brachydanio
4	123.5	26.7	293	Q9XSG0	Q9XSG0 oryctolagus
5	120	26.0	354	Q9UCS6	Q9UCS6 homo sapien
6	120	26.0	379	Q95617	Q95617 homo sapien
7	119	25.8	320	Q9SKY4	Q9SKY4 bos taurus
8	119	25.8	347	Q9SKY5	Q9SKY5 bos taurus
9	119	25.8	810	Q8R3F3	Q8R3F3 mus musculus
10	114.5	24.8	1253	Q7LOK8	Q7LOK8 ambystoma m
11	112	24.2	1253	Q97566	Q97566 canis faml1
12	111.5	24.1	2944	Q63870	Q63870 mus musculus
13	107.5	23.3	1427	Q91562	Q91562 xenopus lae
14	107	23.2	4039	Q7Z246	Q7Z246 brachydanio
15	107	23.2	18412	Q7Z261	Q7Z261 brachydanio
16	106	22.9	2936	Q7YKX8	Q7YKX8 canis faml1

17	105	22.7	1532	13	Q90994	Q90994 gallus gall
18	105	22.7	1714	13	Q90995	Q90995 gallus gall
19	105	22.7	1810	13	Q90824	Q90824 gallus gall
20	103	22.3	1353	13	Q00546	Q00546 gallus gall
21	99	21.4	1358	4	Q92752	Q92752 homo sapien
22	99	21.4	1358	4	Q15568	Q15568 homo sapien
23	99	21.4	26926	4	Q8W2B3	Q8W2B3 homo sapien
24	99	21.4	26926	4	Q10466	Q10466 homo sapien
25	99	21.4	34350	4	Q8W242	Q8W242 homo sapien
26	96	20.8	1358	11	Q8BYI9	Q8BYI9 mus musculus
27	95.5	20.7	89	6	Q28252	Q28252 canis faml1
28	95	20.6	920	11	Q80UI4	Q80UI4 mus musculus
29	94.5	20.5	206	6	Q86527	Q86527 bos taurus
30	93.5	20.2	4006	11	Q35452	Q35452 mus musculus
31	93.5	20.2	4114	11	Q54796	Q54796 mus musculus
32	93	20.1	1445	11	Q63155	Q63155 rattus norv
33	92	19.9	974	2	Q08166	Q08166 thermomons
34	91.5	19.8	843	4	Q05707	Q05707 homo sapien
35	91.5	19.8	1216	11	Q62884	Q62884 rattus norv
36	91	19.7	426	4	Q9NEK8	Q9NEK8 homo sapien
37	91	19.7	1350	13	Q7T3T6	Q7T3T6 brachydanio
38	91	19.7	1797	11	Q80X19	Q80X19 mus musculus
39	91	19.7	4135	6	Q18977	Q18977 bos taurus
40	89.5	19.4	440	13	Q90816	Q90816 gallus gall
41	89.5	19.4	2019	11	Q64706	Q64706 mus musculus
42	89.5	19.4	2019	11	Q80YX2	Q80YX2 mus musculus
43	89.5	19.4	2110	11	Q80YX1	Q80YX1 mus musculus
44	89	19.3	614	13	Q90484	Q90484 brachydanio
45	89	19.3	932	13	Q57587	Q57587 brachydanio

ALIGNMENTS

RESULT 1

Q28253 PRELIMINARY; PRT; 90 AA.

AC Q28253: MEDLINE=95130563; PubMed=7829518;
DT 01-NOV-1996 (TRENDEL. 01, Last sequence update)
DT 01-NOV-1996 (TRENDEL. 01, Last sequence update)
DT 01-OCT-2003 (TRENDEL. 25, Last annotation update)
DE Fibronectin ED-B (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95130563; PubMed=7829518;
RA Zhang D.W., Burton-Wurster N., Lust G.;
RT "Alternative splicing of ED-A and ED-B sequences of fibronectin pre-
RT mRNA differs in chondrocytes from different cartilaginous tissues and
RT can be modulated by biological factors.";
RL J. Biol. Chem. 270:1817-1822(1995).
DR EMBL; U16208; AAA67749.1; .
DR PIR; I46162; I46162.
DR HSP; P02751; ITRF.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR00857; FN_III-like.
DR Pfam; PF00411; FN3; 1.
DR SMART; SM00060; FN3; 1.
FT NON TER 1
FT NON TER 90
SQ SEQUENCE 90 AA; 9585 MW; 766781BDF8511848 CRC64;

Query Match 98.9%; Score 457; DB 6; Length 90;

Best Local Similarity 100.0%; Pred. NO. 1.7e-40; Indels 0; Gaps 0;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VFQTLDSFVDITDSSIGLRTPLNSSTIIIGYRTVVAAGGCIPIFEDFVDSVGYVT 61
Db 1 VQQLDLSFVDITDSSIGLRTPLNSSTIIIGYRTVVAAGGCIPIFEDFVDSVGYVT 60

QY 62 GLEPGIDYDVSITLLINGESAPITLTOOT 91
 DB 61 GLEPGIDYDVSITLLINGESAPITLTOOT 90

RESULT 2

O9M232 PRELIMINARY; PRT; 134 AA.

AC O9M232.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Fibronectin ED-B+ region (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA De Candia L.M., Rodgers R.J.
 RT "Characterization of the expression of the alternative splicing of ED-
 B, ED-B and V regions of fibronectin mRNA in bovine ovarian follicles
 and corpora lutea."
 RL Reprod. Fertil. Dev. 0:0-0(2000).
 DR EMBL; AF260304; AAF91380.1; -.
 DR HSSP; P02751; 1FNH.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR Pfam; PF00041; FN3; 1.
 DR SMART; SMO0060; FN3; 1.
 FT NON_TER 1 1
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 14408 MW; 820971B2619A48A5 CRC64;

Query Match 93.5%; Score 432; DB 6; Length 134;
 Best Local Similarity 94.5%; Pred. No. 1.2e-37;
 Matches 86; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVFQTLDSFVDTDSIGLRMTPLNSSTIGRIITVAAGGIPFEDFVDSVGYTV 60
 DB 29 EVFQTLDSFVDTDSIGLRMTPLNSSTIGRIITVAAGGIPFEDFVDSVGYTV 88
 QY 61 TGLEPGIDYDVSITLLINGESAPITLTOOT 91
 DB 89 TGLEPGIDYDVSITLLINGESAPITLTOOT 119

RESULT 3

O93406 PRELIMINARY; PRT; 2478 AA.

AC O93406.
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Fibronectin.
 GN FN1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhao Q., Collodi P.
 RT "Characterization and expression of zebrafish fibronectin."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF081128; AAC31947.1; -.
 DR HSSP; P02751; 1FNH.
 DR ZFIN; ZDB-GENE-000426-1; fn1.
 DR GO; GO:0005576; C;extracellular; IEA.

DR InterPro; IPR000083; Fibnctn1.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR000562; FN_Type_II.
 DR Pfam; PF00039; fn1; 12.
 DR Pfam; PF00040; fn2; 2.
 DR Pfam; PF00041; fn3; 17.
 DR PRINTS; PR00013; FNTYPEII.
 DR ProDom; PD000995; FN_Type_II; 2.
 DR SMART; SMO0058; FN1; 12.
 DR SMART; SMO0059; FN2; 2.
 DR SMART; SMO0060; FN3; 14.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 11.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 SQ SEQUENCE 2478 AA; 271652 MW; A03475C55A385750 CRC64;

Query Match 70.8%; Score 327; DB 13; Length 2478;
 Best Local Similarity 62.6%; Pred. No. 4.7e-25;
 Matches 57; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 EVFQTLDSFVDTDSIGLRMTPLNSSTIGRIITVAAGGIPFEDFVDSVGYTV 60
 DB 1264 DVFKITLDSFVDTDSIGLRMTPLNSSTIGRIITVAAGGIPFEDFVDSVGYTV 1263
 QY 61 TGLEPGIDYDVSITLLINGESAPITLTOOT 91
 DB 1324 TGLEPGIDYDVSITLLINGESAPITLTOOT 1354

RESULT 4

O9XSGO PRELIMINARY; PRT; 293 AA.

AC O9XSGO.
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Fibronectin (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NC NCB1_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aortic smooth muscle;
 RA Reichenberg S., Plenz G., Breithardt G.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF135404; AAD24483.1; -.
 DR HSSP; P02751; 1FNH.
 DR GO; GO:0016491; F;oxidoreductase activity; IEA.
 DR GO; GO:0008152; P;metabolism; IEA.
 DR InterPro; IPR002086; Aldehyde dehydr.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR Pfam; PF00041; FN3; 4.
 DR PRINTS; PR00014; FNTYPEIII.
 DR SMART; SMO0060; FN3; 3.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 DR Repeat.
 FT NON_TER 1 1
 FT NON_TER 293 293
 SQ SEQUENCE 293 AA; 31537 MW; F0252D9AE853061 CRC64;

Query Match 26.7%; Score 123.5; DB 6; Length 293;
 Best Local Similarity 30.8%; Pred. No. 8.7e-05;
 Matches 28; Conservative 15; Mismatches 47; Indels 1; Gaps 1;

QY 1 EVFQTLDSFVDTDSIGLRMTPLNSSTIGRIITVAAGGIPFEDFVDSVGYTV 60
 DB 80 EIDKPSQMOVTYQDNISISRWLP-SSSPVTGYRTTPKNGAGPTKTACAPDQTEMTI 138

DR PRINTS; PRO0014; ENTTYPE11.
DR SMART; SMO0060; FN3; 2.
DR NOT PRINT

SQ SEQUENCE 379 AA; 41370 MW; 7E1CA4B9428AC7C2 CRC64;

Best Local Similarity	33.8%;	Pred. No. 0.00028;
Matches	37:	Conservative 16: Mismatches 35: Indels 2: Gaps 2:

12 DTDDSSIGLRWTP LNSSTII GYRITVVAAGEGIP IFEDFVDSVGYT VTGLEPGIDYDI 71

0Y 72 SVITLINGGESAPTTLTQOT 91

DD T/S IIII IINNNAKBSFVVI DAAOI 1974

Q95KV4

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DE Fibronectin (Fragment) .

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC

OX NCBI_TaxID=9913;
BN [1]

RC TISSUE=Cartilage;
Parker A E Boulet J Carr A Maciejewicz B A ;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 EMBL: AJ320529; CAC86917.1; -
 D3

DR InterPro; IPR000083; F1DINCH1.
DR InterPro; IPR003962; F1III subd.

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DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00039; fn1; 3.
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DR FALINIS; FROOOO1; FNI1FEL11.
DR SMART; SM00058; FN1; 2.

Repeat.

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SQ      SEQUENCE      320 AA;      35485 MW;      93E2F4AF2ACF2F0E CRC64;

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Best Local Similarity 32.5%; Pred. No. 0.00029;

12 DITDSSIGLRWTPPLNSSTIIIGYRITVVAAGEGIPIFEDFVDSSVGYYTVTGLEPGIDYDI 71

72 SVITI.TNGGESAPTTI.TOOT 91

D5 95 HLYTLNDNARSSPVVIDAST 114

RESULT 8
095KV5

AC Q95KV5;

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DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibronectin (Fragment).
GN FN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9113;
RN [1]
RP SEQUENCE FROM N.A.
RA Parker A.E., Boutell J., Carr A., Maciewicz R.A.;
RT "Novel Cartilage-Specific Splice Variants of Fibronectin.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ120528; CAC6818.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR InterPro: IPR000083; Fibnrcnl.
DR InterPro: IPR003962; FNII_subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00039; fnl_2.
DR Pfam: PF00041; fnl_3.
DR PRINTS: PR00012; FNYPEI.
DR PRINTS: PR00014; FNYPEIII.
DR SMART: SM00058; FN1; 1.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01253; FIBRONECTIN_1; 1.
KM Repeat.
FT NON_TER 1 1
FT NON_TER 347 347
SQ SEQUENCE 347 AA; 38344 MW; 3DCA85910BEA461 CRC64;

Query Match
Best Local Similarity 25.8%; Score 119; DB 6; Length 347;
Matches 26; Conservative 17; Mismatches 35; Indels 2; Gaps 2;

QY 12 DITDSSIGLRWTPLNSTIIIGYRITVVAAGEGIPEDFVDSVGYVTVTGLEPGIDYDI 71
DB 37 DATETTTTISWR-TKTEITTFQVDAIPANGQFPI-QRTIRPDVRSYTTIGLPQFTDYKI 94
QY 72 SVITLINGESAPFTLTQCT 91
DB 95 HLYTLNDNARSSPVVIDAST 114

RESULT 9
ID Q8R3F3 PRELIMINARY; PRT; 810 AA.
AC Q8R3F3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN FN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC025521; AAH25521.1; -.
DR MGD; MGI:95566; FN1.
DR GO: GO:0007155; P:cell adhesion; IDA.
DR InterPro: IPR006209; EGF_1like.
DR InterPro: IPR000083; Fibnrcnl.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR Pfam: PF00039; fnl_3.
OX NCBI_TaxID=9113;
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DR SMART: SM00060; FN3; 6.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01253; FIBRONECTIN_1; 3.
KM Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 349 349
SQ SEQUENCE 810 AA; 89228 MW; 9A7A4DD0ED3437F CRC64;

Query Match
Best Local Similarity 25.8%; Score 119; DB 11; Length 810;
Matches 25; Conservative 18; Mismatches 35; Indels 2; Gaps 2;

QY 12 DITDSSIGLRWTPLNSTIIIGYRITVVAAGEGIPEDFVDSVGYVTVTGLEPGIDYDI 71
DB 272 DATETTTTISWR-TKTEITTFQVDAIPANGQFPI-QRTISPDVRSYTTIGLPQFTDYKI 329
QY 72 SVITLINGESAPFTLTQCT 91
DB 330 HLYTLNDNARSSPVVIDAST 349

RESULT 10
ID Q7TOK8 PRELIMINARY; PRT; 215 AA.
AC Q7TOK8;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibronectin (Fragment).
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomacidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
RN [1]
RP SEQUENCE FROM N.A.
RA Saffi R., Bertrand S., De Luze A., Vanacker J.M., Marchand O.,
RA Carregui A., Demeneix B., Laudet V.;
RT "Thyroid Hormone Response in A Neogenic Amphibian, The Axolotl
( Ambystoma mexicanum ).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY139973; AAN37600.1; -.
FT NON_TER 1 1
FT NON_TER 215 215
SQ SEQUENCE 215 AA; 23438 MW; 5207871B67C64CA3 CRC64;

Query Match
Best Local Similarity 24.8%; Score 114.5; DB 13; Length 215;
Matches 23; Conservative 21; Mismatches 23; Indels 7; Gaps 3;

QY 3 PQLTDLSPVDITDSSIGLRWTPLNSTIIIGYRITVVAAGEGIPEDFVDSVGYVTVTGLE 62
DB 148 PRVT-----VTEITVITWR-TKTEITTFQVDAIPANGQFPI-QRTISPDIRITTTIG 200
QY 63 LEFGIDYDISVITL 76
DB 201 LQPGTDYKININIVTL 214

RESULT 11
ID O97566 PRELIMINARY; PRT; 1253 AA.
AC O97566;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Alpha-1 type VII collagen non-collagenous domain (Fragment).
GN COL7A1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
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RX MEDLINE=99002915; PubMed=9784596;
 RA Xu L., Chen M., Peng J., O'Toole E.A., Woodley D.T., Chan L.S.;
 RT "Molecular cloning and characterization of a cDNA encoding canine type
 RT VII collagen non-collagenous (NC1) domain, the target antigen of
 RT autoimmune disease epidermolysis bullosa acquisita (EBA).";
 RL Biochim. Biophys. Acta 1408:25-34(1998).
 DR EMBL; AF042093; AAC72024.1; -.
 DR HSSP; P02751; 1FAA.
 DR InterPro; IPR003961; FN_III-like.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF00041; fn3; 9.
 DR Pfam; PF00092; vwa; 2.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00060; FN3; 9.
 DR SMART; SM00327; VWA; 2.
 DR PROSITE; PS50234; VWF_A; 2.
 KM Collagen.
 FT NON_TER.
 SQ SEQUENCE 1253 1253
 Query Match 24.2%; Score 112; DB 6; Length 1253;
 Best Local Similarity 35.2%; Pred. No. 0.0084;
 Matches 32; Conservative 15; Mismatches 40; Indels 4; Gaps 3;
 QY 2 VPQTLDSFVDITDSIGLRWTFPLN--STTIIGRTTVVAAEGIPFEDFVDSVGYT 59
 DB 957 VPS-SGLRVVDTSVDSVTLMTFVSVSSYILSWR-PLGRFGQDIPGASQTLPGISG 1014
 QY 60 VTGLEPGIDYDITVITLINGSAPTLTQ 90
 DB 1015 VTGLEPGISTFTSLTPIRGVGRPEASLTQK 1045
 RESULT 12
 ID 063870 PRELIMINARY; PRT; 2944 AA.
 AC 063870;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1998 (TrEMBLrel. 09, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Type VII collagen.
 GN COL7A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93315168; PubMed=8325648;
 RA Li K., Cristiano A.M., Copeland N.G., Gilbert D.J., Chu M.L.,
 RA Jenkins N.A., Utto J.;
 RT "cDNA cloning and chromosomal mapping of the mouse type VII collagen
 RT gene (Col7a1): evidence for rapid evolutionary divergence of the
 RT gene.";
 RL Genomics 16:733-739(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96275720; PubMed=8752674;
 RA Kivirikko S., Li K., Cristiano A.M., Utto J.;
 RT "Cloning of mouse type VII collagen reveals evolutionary conservation
 RT of functional protein domains and genomic organization.";
 RL J. Invest. Dermatol. 106:1300-1306(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kivirikko S., Li K., Cristiano A.M., Utto J.;
 RT Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U32107; AAB6593.1; -.
 DR EMBL; S63654; AAB27492.1; -.
 DR PIR; A45748; A45748.
 DR HSSP; P12111; 2KNT.
 DR HSSP; MCI.88462; Col7a1.
 GO; GO:0004867; F:serine protease inhibitor activity; IEA.

DR InterPro; IPR008161; Clg_helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF01391; Collagen_24.
 DR Pfam; PF00041; fn3; 9.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF00092; vwa; 2.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR ProDom; PD000007; Clg_helix; 6.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00060; FN3; 9.
 DR SMART; SM00327; VWA; 2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS50234; VWF_A; 2.
 KM Collagen, Protease inhibitor, Serine protease inhibitor.
 SQ SEQUENCE 2944 AA; 295116 MW; 596FA507BC6C02C2 CRC64;
 Query Match 24.1%; Score 111.5; DB 11; Length 2944;
 Best Local Similarity 32.6%; Pred. No. 0.027;
 Matches 28; Conservative 19; Mismatches 36; Indels 3; Gaps 2;
 QY 6 TDLSPVDITDSIGLRWTFPLN--STTIIGRTTVVAAEGIPFEDFVDSVGYT 63
 DB 961 TELRVVDTSVDSVTLMTFVSVSSYILSWR-PLGRFGQDIPGASQTLPGISG 1019
 QY 64 EPQIDYDITVITLINGSAPTLTQ 89
 DB 1020 EPGISYVPSLTPIRGVGRPEASLTQK 1045
 RESULT 13
 ID 091562 PRELIMINARY; PRT; 1427 AA.
 AC 091562;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1998 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tumor suppressor.
 GN XDCCA.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95113183; PubMed=7813784;
 RA Pierceall W.E., Reale M.A., Candia A.F., Wright C.V., Cho K.R.,
 RA Pearson E.R.;
 RT "Expression of a homologue of the deleted in colorectal cancer (DCC)
 RT gene in the nervous system of developing Xenopus embryos.";
 RL Dev. Biol. 166:654-665(1994).
 DR EMBL; U10986; AAA70168.1; -.
 DR PIR; I51659; I51659.
 DR HSSP; P40189; 1BCU.
 DR InterPro; IPR003562; FN_III subd.
 DR InterPro; IPR003561; FN_III-like.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00041; fn3; 6.
 DR Pfam; PF00047; ig; 4.
 DR PRINTS; PR00014; FNTPYELII.
 DR SMART; SM00060; FN3; 6.
 DR SMART; SM00408; IGC2; 3.
 DR PROSITE; PS50835; IG_LIKE; 4.
 KM Immunoglobulin domain; Repeat.
 SQ SEQUENCE 1427 AA; 156533 MW; 61FEA12C8A674972 CRC64;

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Query Match      23.3%; Score 107.5; DB 13; Length 1427;
Best Local Similarity 35.1%; Pred. No. 0.029;
Matches 34; Conservative 12; Mismatches 40; Indels 11; Gaps 5;

QY 1 EVPLTDLSTFVDTSSIGLRWTP--PLNSSTII-GYRTVVAAGEGPIFEDFVDSVGV 57
DB 724 QVPEQPSLHVRLPLTTSILMSWTPPLNPIVARGY--IIYGVGSPVAETVAVDSKORY 780
QY 58 YTVTGLEPGIDYDISVITLLINGESAP-----TTLTQ 89
DB 781 YSEINLEPSSHVYISLKAENNAEGVPLVESATTRSQ 817
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RESULT 14
Q72246 PRELIMINARY; PRT; 4039 AA.
ID Q72246
AC Q72246;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE S1:D2249N21.1.3 (Novel protein similar to human titin (TTN))
DE (Fragment).
GN S1:D2249N21.1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Garner P.;
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL732421; CAD61247.1; -.
DR InterPro; IPR003962; Fhili_subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 16.
DR Pfam; PF00047; Ig; 10.
DR PRINTS; PR00014; FNTPHIII.
DR SMART; SM00060; FN3; 16.
DR SMART; SM00408; IG; 25.
DR SMART; SM00409; IG2; 15.
DR PROSITE; PSS0835; IG-LIKE; 13.
DR PROSITE; PSS0835; IG-LIKE; 13.
FT NON_TER 1 1
FT NON_TER 4039 4039
SQ SEQUENCE 4039 AA; 451611 MW; 7C54CB67CADA1A8D CRC64;

Query Match      23.2%; Score 107; DB 13; Length 4039;
Best Local Similarity 31.9%; Pred. No. 0.12;
Matches 29; Conservative 15; Mismatches 29; Indels 18; Gaps 4;
```

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QY 2 VPOLTLDSFVDTSSIGLRWTP--LNSSTIIGYRTVVAAGEGPIFEDFVDSV-- 55
DB 3915 VPKI-----VDVNTITIDISWCPPLNNGGEILGYHVERCLVGE-----KDWVRCRTEPRC 3964
QY 56 --GYTVTGLEPGIDYDISVITLLINGESAP 84
DB 3965 KDRKTYVTGLTBGADYNLRVAVNBSGGHAP 3995

RESULT 15
Q72261 PRELIMINARY; PRT; 18412 AA.
ID Q72261
AC Q72261;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE S1:Q2167C3.1 (Novel protein similar to human titin (TTN))
```

```
GN D2249N21.1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Corby N.;
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL714003; CAD60685.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000875; C:cytochrome.
DR InterPro; IPR00282; Cytochrome c oxidase.
DR InterPro; IPR003962; Fhili_subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR007119; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR001245; Tyr kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00041; fn3; 119.
DR Pfam; PF00047; Ig; 17.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00014; FNTPHIII.
DR PRODOM; PD000001; Prot kinase; 1.
DR SMART; SM00060; FN3; 119.
DR SMART; SM00409; IG; 55.
DR SMART; SM00408; IG2; 49.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS00268; CECROPIIN; 1.
DR PROSITE; PS00690; DEAH ATP HELICASE; 1.
DR PROSITE; PSS0835; IG-LIKE; 46.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PSS0109; PROTEIN_KINASE_TYR; 1.
FT NON_TER 1 1
FT NON_TER 2035627 MW; 91708CP443715B60 CRC64;

SQ SEQUENCE 18412 AA; 2035627 MW; 91708CP443715B60 CRC64;
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Query Match      23.2%; Score 107; DB 13; Length 18412;
Best Local Similarity 31.9%; Pred. No. 0.77;
Matches 29; Conservative 15; Mismatches 29; Indels 18; Gaps 4;

QY 2 VPOLTLDSFVDTSSIGLRWTP--LNSSTIIGYRTVVAAGEGPIFEDFVDSV-- 55
DB 310 VPKI-----VDVNTITIDISWCPPLNNGGEILGYHVERCLVGE-----KDWVRCRTEPRC 359
QY 56 --GYTVTGLEPGIDYDISVITLLINGESAP 84
DB 360 KDRKTYVTGLTBGADYNLRVAVNBSGGHAP 390
```

Search completed: September 21, 2004, 05:57:08
Job time : 144.191 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 05:46:53; Search time 183.338 Seconds
(without alignments)
140.243 Million cell updates/sec

Title: US-10-676-049-4

Perfect score: 462
Sequence: 1 EVPPQJLDSFVDITDSIGL.....SVTLINGESAPITLTQOT 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Ganc4:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	91	5	ABG98132 Anti-neov
2	462	100.0	91	5	AAO17878 EDB fibro
3	462	100.0	91	6	ABP74705 Human ED-
4	462	100.0	91	7	ADCO9564 Epitope w
5	462	100.0	147	5	ABG98133 Human fib
6	462	100.0	147	5	ABP74706 Human ED-
7	462	100.0	2220	6	ABO01289 Human pro
8	462	100.0	2446	3	AAW50377 Human fib
9	462	100.0	2477	2	AAW95955 Human fib
10	462	100.0	2477	7	ADG63323 Rat Prote
11	459	99.4	91	2	AAW25405 ED-B. 1/1
12	453	98.1	1336	2	AAW60019 Tissue-bi
13	453	98.1	2446	2	AAW60021 Fibrinoge
14	447.5	96.9	1446	7	ADCO9565 Epitope w
15	447	96.8	91	2	AAW23838 The ED2 d
16	447	96.8	31	5	AAW79568 Epitope #
17	447	96.8	31	5	AAW79567 Epitope #
18	447	96.8	31	5	AAW79566 Epitope #
19	447	96.8	31	5	AAW21987 IL14-Ti16
20	447	96.8	269	2	AAW21987 Cathepsin
21	447	96.8	993	4	AAW08039 Novel hum
22	447	96.8	1173	4	ABG22275 AAM3647
23	447	96.8	2265	4	AAW3647 Human pol
24	447	96.8	2320	6	AAW37107 Human fib
25	447	96.8	2320	6	ABR42588 Human fib
26	447	96.8	2320	6	ABO01288 Human pro

26	148.5	32.1	2324	2	AAW92778
27	148.5	32.1	2324	5	AAU74674
28	148.5	32.1	2324	5	AAE23651
29	148.5	32.1	2327	1	AAW70373
30	148.5	32.1	2327	2	AAW15468
31	148.5	32.1	2328	4	AAW68182
32	148.5	32.1	2328	6	ABU07485
33	148.5	32.1	2328	6	ABR41106
34	148.5	32.1	2328	6	ABR92078
35	148.5	32.1	2328	7	ABD970378
36	148.5	32.1	2328	7	ABD98726
37	148.5	32.1	2328	7	ADG63322
38	148.5	32.1	2330	4	AAW36649
39	148.5	32.1	2335	4	AAW36649
40	148.5	32.1	2335	4	ABR58335
41	148.5	32.1	2386	2	AAW61371
42	148.5	32.1	2386	4	AAW36648
43	148.5	32.1	2386	5	AAO17353
44	148.5	32.1	2386	6	ABR81866
45	148.5	32.1	2386	7	ADD18770

ALIGNMENTS

RESULT 1
ABG98132 standard; protein, 91 AA.

ABG98132; 08-JAN-2003 (first entry)

Anti-neovascular preparation associated epitope #87.

Cell-mediated immunity; cellular immune response; CTL response; tumor neovascularization; anti-angiogenesis.

Homo sapiens.

MO200269907-AA.

12-SEP-2002.

07-MAR-2002; 2002WO-US007204.

07-MAR-2001; 2001US-0274063P.

(CTLI-) CTL IMMUNOTHERAPIES CORP.

Simard JTL, Diamond DC;

WPI; 2002-750433/81.

Evaluating cell-mediated immunity, in particular cytotoxic T lymphocyte responses, by implanting vascular cells, useful for treatment and research models for directly targeting tumor neovascularization.

Example 5; Page 25; 73pp; English.

The invention describes a method of evaluating cell-mediated immunity comprising implanting vascular cells into an immunodeficient mammal, establishing an immune response in the mammal, and assaying a characteristic to determine cell-mediated immunity in the mammal. The methods and compositions of the present invention are useful for the generation of a cellular immune response, in particular a CTL response, for treatment directly against a tumor neovascularization. They can also be used for making research models targeting tumor neovascularization. The present invention using the anti-angiogenesis approach takes advantage of the need of tumors to recruit a blood supply to support their continued growth. This approach aims to disrupt a tumor's supply of nutrients to cause it to die or at least limit its growth. This is the amino acid sequence of a peptide associated with the neo-vascularization preparation

CC for treatment of cancer described in the invention
 XX
 SQ Sequence 91 AA;

Query Match 100.0%; Score 462; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.8e-44;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPOLTDLSFVDITDSSIGLRWTPNLSSTIIGYRITVAAGEGPIPEDFVDSVGYYTV 60
 DB 1 EVPQITDLSFVDITDSSIGLRWTPNLSSTIIGYRITVAAGEGPIPEDFVDSVGYYTV 60
 QY 61 TGLEPGIDYDISVITTLINGESAPPTLTQQT 91
 DB 61 TGLEPGIDYDISVITTLINGESAPPTLTQQT 91

RESULT 2

AA017878
 ID AA017878 standard; protein; 91 AA.

AC AA017878;

DT 20-AUG-2002 (first entry)

DE EDB fibronectin domain binding protein.

KW EDB fibronectin domain; EDBPD; angiogenesis; gene therapy; transplant;
 implant; receptor molecule interaction.

OS Unidentified.

PN WO200220563-A2.

PD 14-MAR-2002.

PF 30-AUG-2001; 2001WO-EP010016.

PR 07-SEP-2000; 2000DE-01045803.

PR 02-MAY-2001; 2001DE-01023133.

PA (SCHD) SCHERING AG.

PA (REDL/) REDLITZ A.

PA (KOPF/) KOPFITZ M.

PA (EGNE/) EGNER U.

PA (BAHR/) BAHR I.

PA (MENR/) MENRAD A.

PI Menrad A;

DR WPI; 2002-479458/51.

PT New proteins binding specifically to the EDB-fibronectin domain, are
 cell adhesion and proliferation mediators useful e.g. in screening tests.
 PS Claim 18; Page 41-42; 66pp; German.

XX The present invention relates to a new protein which binds specifically
 to the EDB fibronectin domain (EDBPD), is specifically expressed or
 activated in endothelial cells, stromal cells of a tumour and tumour
 cells, and has an apparent molecular weight of 120-130 kDa for the light
 chain and 150-160 kDa for the heavy chain. The protein can be used to
 screen compounds which bind to EDBPD or its receptor, for coating the
 surfaces to which endothelial cells bind, in cell cultures, in
 combination with transplants or in combination with implants
 (specifically lung implants, artificial heart pacemakers or valves,
 vascular implants, endoprostheses, screws, bars, plates, wires, nails,
 rods, artificial joints, breast implants, artificial cranial plates,
 false teeth, tooth fillings or tooth bridges, as it improves the
 integration of transplants or implants in the body. The protein is also
 useful in clarifying EDB-specific adhesion mechanisms and receptor
 molecule interactions involved in angiogenesis. The present sequence is a
 protein of the invention

XX
 SQ Sequence 91 AA;

Query Match 100.0%; Score 462; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.8e-44;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPOLTDLSFVDITDSSIGLRWTPNLSSTIIGYRITVAAGEGPIPEDFVDSVGYYTV 60
 DB 1 EVPQITDLSFVDITDSSIGLRWTPNLSSTIIGYRITVAAGEGPIPEDFVDSVGYYTV 60
 QY 61 TGLEPGIDYDISVITTLINGESAPPTLTQQT 91
 DB 61 TGLEPGIDYDISVITTLINGESAPPTLTQQT 91

RESULT 3

ABP74705
 ID ABP74705 standard; protein; 91 AA.

AC ABP74705;

DT 03-FEB-2003 (first entry)

DE Human ED-B domain of fibronectin SEQ ID NO:589.

KW Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
 T cell.

OS Homo sapiens.

PN WO200281646-A2.

PD 17-OCT-2002.

PF 04-APR-2002; 2002WO-US011101.

PR 06-APR-2001; 2001US-0282211P.

PR 07-NOV-2001; 2001US-0337017P.

PR 07-MAR-2002; 2002US-0363210P.

PA (CTL-) CTL IMMUNOTHERAPIES CORP.

PI Simard JTL, Diamond DC, Liu L, Xie Z;

DR WPI; 2003-067518/06.

PT Novel epitopes useful as vaccines, comprises peptides or nucleic acid
 encoding the peptides, that are useful epitopes of target-associated
 antigens.

PS Claim 1; Page 26; 352pp; English.

XX The present invention describes an isolated epitope (I) and an epitope
 cluster. Also described is a vaccine or immunotherapeutic composition
 (VC) comprising (I). (I) has cytostatic activity; VC is useful for
 treating an animal, by administering to an animal the vaccine or
 immunotherapeutic composition. VC is also useful for evaluating
 immunogenicity of a vaccine or immunotherapeutic composition, by
 administering VC to an HLA-transgenic animal and evaluating
 immunogenicity based on a characteristic of the animal, or by in vitro
 primary stimulation of a T cell and evaluating immunogenicity. (I) is
 useful for determining specific T cell frequency, by contacting T cells
 with a MHC-peptide complex, and further comprises ELISPOT analysis,
 limiting dilution analysis, flow cytometry, in situ hybridisation and/or
 polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
 ABP74713 represent sequences used in the exemplification of the present
 invention

XX Sequence 91 AA;

Query Match 100.0%; Score 462; DB 6; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.8e-44;

Matches 91: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPOLTLDSFVDITDSSIGLRWTPLNSSITIGRITVVAAGGIPFDFVDSVGYTV 60
DB 1 EVPOLTLDSFVDITDSSIGLRWTPLNSSITIGRITVVAAGGIPFDFVDSVGYTV 60

QY 61 TGLEPGIDYDISVITLLINGSESAPTLTQOT 91
DB 61 TGLEPGIDYDISVITLLINGSESAPTLTQOT 91

RESULT 4
ADCO9564
ID ADCO9564 standard; peptide; 91 AA.
XX
AC ADCO9564;
XX
DT 18-DEC-2003 (first entry)
XX
XX Epitope with high affinity for MHC class I #SEQ ID 569.
DE
XX
XX Epitope; immunological; vaccine;
KW major histocompatibility complex class I, MHC class I; cancer;
KW immunisation.
XX
OS Unidentified.
XX
PN NO2003008537-A2.
XX
PD 30-JAN-2003.
XX
PF 29-MAR-2002; 2002WO-US010189.
XX
PR 06-APR-2001; 2001US-0282211P.
PR 07-NOV-2001; 2001US-0337017P.
PR 07-MAR-2002; 2002US-0363210P.
XX
PA (CTL-) CTL IMMUNOTHERAPIES CORP.
XX
PI Simard JTL, Diamond DC, Liu L, Xie Z;
XX
DR WPI; 2003-248010/24.
XX
PT Epitope having high affinity for major histocompatibility complex class I
PT useful for treating an animal, evaluating immunogenicity of a vaccine or
PT therapeutic composition and for diagnosing a disease.
XX
PS Claim 1; SEQ ID NO 589; 239pp; English.

CC The invention relates to an isolated epitope polypeptide that has high
CC affinity for major histocompatibility complex (MHC) class I, and an
CC epitope cluster comprising the polypeptide. Also disclosed is a vaccine
CC or immunotherapeutic composition containing an epitope of the invention.
CC Compositions of the invention may be used in the treatment of cancer. The
CC method can be combined with a radiation therapy, chemotherapy,
CC biochemotherapy or surgery. The composition is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
CC-peptide complexes of the invention are useful for determining specific T
CC cell frequency. This method is useful for evaluating immunological
CC response, by performing the method prior to and subsequent to an
CC immunisation step. Compositions of the invention are useful for
CC diagnosing a disease. The current sequence represents an epitope of the
CC invention with high affinity for MHC class I.
CC
SQ Sequence 91 AA;

Query Match 100.0%; Score 462; DB 7; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.8e-44;
Matches 91: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPOLTLDSFVDITDSSIGLRWTPLNSSITIGRITVVAAGGIPFDFVDSVGYTV 60
DB 1 EVPOLTLDSFVDITDSSIGLRWTPLNSSITIGRITVVAAGGIPFDFVDSVGYTV 60

QY 61 TGLEPGIDYDISVITLLINGSESAPTLTQOT 91
DB 61 TGLEPGIDYDISVITLLINGSESAPTLTQOT 91

RESULT 5
ABG98133
ID ABG98133 standard; protein; 147 AA.
XX
AC ABG98133;
XX
DT 08-JAN-2003 (first entry)
XX
XX Human fibronectin gene ED-B region.
DE
XX Cell-mediated immunity; cellular immune response; CTL response;
KW tumour neovasculation; anti-angiogenesis.
XX
OS Homo sapiens.
XX
PN WO200259907-A2.
XX
PD 12-SEP-2002.
XX
PF 07-MAR-2002; 2002WO-US007204.
XX
PR 07-MAR-2001; 2001US-0274063P.
XX
PA (CTL-) CTL IMMUNOTHERAPIES CORP.
XX
PI Simard JTL, Diamond DC;
XX
DR WPI; 2002-750433/81.
DR N-PSDB; ABX03678.
XX
XX Evaluating cell-mediated immunity, in particular cytotoxic T lymphocyte
PT responses, by implanting vascular cells, useful for treatment and
PT research models for directly targeting tumor neovasculation.
XX
PS Example 5; Page 29; 73pp; English.

CC The invention describes a method of evaluating cell-mediated immunity
CC comprising implanting vascular cells into an immunodeficient mammal,
CC establishing an immune response in the mammal, and assaying a
CC characteristic to determine cell-mediated immunity in the mammal. The
CC methods and compositions of the present invention are useful for the
CC generation of a cellular immune response, in particular a CTL response,
CC for treatment directly against a tumour neovasculation. They can also be
CC used for making research models targeting tumour neovasculation. The
CC present invention using the anti-angiogenesis approach takes advantage of
CC the need of tumours to recruit a blood supply to support their continued
CC growth. This approach aims to disrupt a tumour's supply of nutrients to
CC cause it to die or at least limit its growth. This is the amino acid
CC sequence of a protein associated with the neo-vasculature preparation
CC for treatment of cancer described in the invention
CC
SQ Sequence 147 AA;

Query Match 100.0%; Score 462; DB 5; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.2e-44;
Matches 91: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPOLTLDSFVDITDSSIGLRWTPLNSSITIGRITVVAAGGIPFDFVDSVGYTV 60
DB 35 EVPOLTLDSFVDITDSSIGLRWTPLNSSITIGRITVVAAGGIPFDFVDSVGYTV 94

QY 61 TGLEPGIDYDISVITLLINGSESAPTLTQOT 91
DB 95 TGLEPGIDYDISVITLLINGSESAPTLTQOT 125

RESULT 6

ABP74706
ID ABP74706 standard; protein; 147 AA.
XX
XX
XX ABP74706;
AC
XX
XX 03-FEB-2003 (first entry)
DT
XX
XX Human ED-B domain of fibronectin SEQ ID NO:590.
DE
XX
XX Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
KM T cell.
KM
XX Homo sapiens.
OS
XX MO200281646-A2.
FN
XX
XX 17-OCT-2002.
PD
XX
XX 04-APR-2002; 2002WO-US011101.
PF
XX
XX 06-APR-2001; 2001US-0282211P.
PR 07-NOV-2001; 2001US-0337011P.
PR 07-MAR-2002; 2002US-0363210P.
XX
XX (CTL1-) CTL IMMUNOTHERAPEUTICS CORP.
PA
XX
XX Simard JUL, Diamond DC, Liu L, Xie Z;
PI
XX WPI; 2003-067518/06.
DR
XX
XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid
PT encoding the peptides, that are useful epitopes of target-associated
PT antigens.
XX
XX
XX Claim 1; Page 26; 352pp; English.
PS
XX
XX The present invention describes an isolated epitope (I) and an epitope
CC cluster. Also described is a vaccine or immunotherapeutic composition
CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
CC treating an animal, by administering to an animal the vaccine or
CC immunotherapeutic composition. VC is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic composition, by
CC administering VC to an HLA-transgenic animal and evaluating
CC immunogenicity based on a characteristic of the animal, or by in vitro
CC immunogenicity stimulation of a T cell and evaluating immunogenicity. (I) is
CC useful for determining specific T cell frequency, by contacting T cells
CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
CC ABP74713 represent sequences used in the exemplification of the present
CC invention
XX
XX
XX Sequence 147 AA;
SQ
XX
XX Query Match 100.0%; Score 462; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.2e-44;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 EVPOLTLSTVDTLSSIGLRMPPLNSSTIGRITVVVAAGGIPFEDFVDSVGYTV 60
Db 35 EVPOLTLSTVDTLSSIGLRMPPLNSSTIGRITVVVAAGGIPFEDFVDSVGYTV 94
XX
XX 61 TGLEPGIDYDISVTLINGESAPITLTOOT 91
Qy 95 TGLEPGIDYDISVTLINGESAPITLTOOT 125
Db
XX
XX RESULT 7
ID ABO01289 standard; protein; 2220 AA.
XX
XX ABO01289;
XX

DT 06-AUG-2003 (first entry)
XX
XX Human protein NOV1b.
DE
XX
XX Human; NOX; cardiomyopathy; atherosclerosis; hypertension;
KM congenital heart defect; prostate cancer; diabetes; metabolic disorder;
KM neoplasm; graft versus host disease; AIDS; bronchial asthma;
KM Crohn's disease; multiple sclerosis; infectious disease; anorexia;
KM cancer-associated cachexia; neurodegenerative disorder;
KM Alzheimer's disease; Parkinson's disease; immune disorder;
KM haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy;
KM SNP; single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
XX
XX Key location/qualifiers
FH Misc-difference 639
FT /note= "May be Phe as the result of a single nucleotide
FT polymorphism"
XX
XX MO200303008-A2.
PN
XX
XX 20-MAR-2003.
PD
XX
XX 09-SEP-2002; 2002WO-US028596.
PF
XX
XX 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318130P.
PR 10-SEP-2001; 2001US-0318430P.
PR 12-SEP-2001; 2001US-0318755P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 26-SEP-2001; 2001US-0324980P.
PR 26-SEP-2001; 2001US-0324980P.
PR 15-FEB-2002; 2002US-0357303P.
PR 28-FEB-2002; 2002US-0360973P.
PR 20-MAR-2002; 2002US-0366131P.
PR 25-MAR-2002; 2002US-0367753P.
PR 02-APR-2002; 2002US-0369479P.
PR 10-MAY-2002; 2002US-0379532P.
PR 17-MAY-2002; 2002US-0381664P.
PR 17-MAY-2002; 2002US-0381672P.
PR 28-MAY-2002; 2002US-0383651P.
PR 29-MAY-2002; 2002US-0384012P.
PR 19-JUN-2002; 2002US-0390155P.
PR 06-SEP-2002; 2002US-00390155.
XX
XX (CUPRA-) CURAGEN CORP.
PA
XX
XX Zhong M, Li L, Gorman J, Spytek KA, Kekuda R, Taupier RJ;
PI Anderson DW, Vernet CM, Catterton E, Miller CE, Shenoy SG;
PI Paturjan M, Pena CE, Tchervet VT, Padigaru M, Guev VY;
PI Malyanar UM, Burgess CF, Gerlach VL, Casman SJ, Rieger DK;
PI Grose WM, Smithson G, Feyman JA, Stirling G, Rothenberg MB;
PI Larochele WJ, Shinkens RA, Crabtree U, Rastelli L, Voss EZ;
PI Boldog FL, Edinger SR, Millet I, Macdougall JR, Ellerman K;
PI Chapoval A;
XX
XX WPI; 2003-313246/30.
DR N-PSDB; ACDC6170.
XX
XX New polypeptides and polynucleotides having properties related to
PT stimulation of biochemical or physiological responses in a cell or
PT tissue, useful for diagnosing or preventing e.g. atherosclerosis,
PT hypertension, prostate cancer.
XX
XX Claim 2; Page 110-111; 849pp; English.
PS
XX
XX The invention relates to an isolated polypeptide comprising one of 127

CC sequences (appearing as AB01288-AB01414) designated as NOVX, a mature
CC form of NOVX, an amino acid sequence which is at least 95% identical to
CC NOVX or an amino acid sequence comprising one or more conservative
CC substitutions in NOVX. Also included are nucleic acids encoding NOVX
CC proteins, determining the presence or amount of NOVX or NOVX DNA in a
CC sample (by introducing the sample to an antibody that binds
CC immunospecifically to the polypeptide), and determining the presence of
CC amount of antibody bound to the polypeptide), determining the levels of
CC or predilection to a disease associated with altered levels of
CC expression of NOVX or NOVX DNA in a first mammalian subject, identifying
CC an agent that binds to NOVX, identifying a potential therapeutic agent
CC for treatment of a pathology related to aberrant expression or aberrant
CC physiological interactions of NOVX, screening for a modulator of activity
CC of or of latency or predilection to a pathology associated with NOVX, a
CC vector comprising NOVX DNA, a cell comprising the vector (used to produce
CC NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides
CC are useful as a marker for cell or tissue type, and in diagnosing and
CC treating pathologies, diseases, conditions or disorders associated with
CC NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, prostate cancer, diabetes, metabolic disorders,
CC neoplasms, graft versus host disease, AIDS, bronchial asthma, Crohn's
CC disease, multiple sclerosis, infectious diseases, anorexia, cancer-
CC associated cachexia, neurodegenerative disorders (e.g. Alzheimer's
CC disease or Parkinson's disease), immune disorders, haemopoietic
CC disorders, dyslipidaemias, and wasting disorders associated with chronic
CC diseases. These may also be used to screen for molecules which inhibit or
CC enhance NOVX activity or function, and for detecting specific cell types.
CC These may also be used in chromosome mapping, gene therapy, tissue
CC typing, and in forensic biology. The present sequence represents a NOVX
CC protein
XX
SQ Sequence 2220 AA:

Query Match 100.0%; Score 462; DB 6; Length 2220;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPOLTDLSFVDITDSSIGLRMTPLNSSTIGRTVVAAGEGPIFEDFVDSVGYTYV 60
DB 1266 EVPOLTDLSFVDITDSSIGLRMTPLNSSTIGRTVVAAGEGPIFEDFVDSVGYTYV 1325
DB 61 TGLEPGIDYDISVITLNGESAPPTLTQQT 91
DB 1326 TGLEPGIDYDISVITLNGESAPPTLTQQT 1356

RESULT 8
AAB50377
ID AAB50377 standard; protein; 246 AA.
XX
AC AAB50377;
XX
DT 12-MAR-2001 (first entry)
XX
DE Human fibronectin.
XX
KM Human; FN; fibronectin; prostate cancer; biallelic marker; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200058509-A2.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-IB000431.
XX
PR 29-MAR-1999; 99US-0126780P.
XX
PA (GBST) GENSET.
XX
PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A;
DR WPI; 2000-594647/56.

DR N-PSDB; AAC89889.
XX
XX Fibronectin polynucleotide and polypeptide sequences, useful for
PT determining the predilection of individuals to cancer, such as prostate
PT cancer.
XX
XX Claim 4; Page 185-190; 208pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC or purified recombinant polynucleotide comprising a contiguous span of at
CC least 12 nucleotides of a fibronectin (FN) gene. The methods and
CC sequences are useful for determining the predilection of individuals to
CC cancer such as prostate cancer and for the prognosis/detection of an
CC eventual treatment response to therapeutic agents acting against prostate
CC cancer. Biallelic markers allow association studies to be performed to
CC identify genes involved in complex traits
XX
SQ Sequence 2446 AA:

Query Match 100.0%; Score 462; DB 3; Length 2446;
Best Local Similarity 100.0%; Pred. No. 1.7e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPOLTDLSFVDITDSSIGLRMTPLNSSTIGRTVVAAGEGPIFEDFVDSVGYTYV 60
DB 1266 EVPOLTDLSFVDITDSSIGLRMTPLNSSTIGRTVVAAGEGPIFEDFVDSVGYTYV 1325
QY 61 TGLEPGIDYDISVITLNGESAPPTLTQQT 91
DB 1326 TGLEPGIDYDISVITLNGESAPPTLTQQT 1356

RESULT 9
AAW9595
ID AAW9595 standard; peptide; 247 AA.
XX
AC AAW9595;
XX
DT 22-JUN-1999 (first entry)
XX
DE Human fibronectin.
XX
KM Human; fibronectin; glycoprotein; extracellular matrix; motif; migration;
KW stimulation; wound healing; periodontal tissue regeneration; metastasis;
KW tumour; invasion; angiogenesis; inflammation; connective tissue function.
XX
OS Homo sapiens.
XX
PN WO9902674-A1.
XX
PD 21-JAN-1999.
XX
PF 01-JUL-1998; 98WO-GB001939.
XX
PR 08-JUL-1997; 97GB-00014276.
XX
PA (UNYU-) UNIV DUNDEE.
XX
PI Schor SL;
XX
DR WPI; 1999-120875/10.
XX
PT New peptides which modulate cell migration have the motif IGD - and are
PT useful to stimulate angiogenesis.
XX
PS Disclosure; Fig 5; 57pp; English.
XX
CC This sequence represents the amino acid sequence of human fibronectin, a
CC widely distributed glycoprotein present in extracellular matrices. The
CC protein contains the motifs IGDs (AAW95953) and IGDQ (AAW9594) which can
CC be used in peptides to stimulate cell migration for wound healing,
CC periodontal tissue regeneration, angiogenesis, inhibition of tumour
CC invasion and metastasis, and in relation to inflammation or connective

CC tissue function
XX Sequence 2477 AA;
SQ

Query Match 100.0%; Score 462; DB 2; Length 2477;
Best Local Similarity 100.0%; Pred. No. 1.8e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPQLTDLSPVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYTV 60
DB 1266 EVPQLTDLSPVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYTV 1325

QY 61 TGLEPGIDYDISVTTLINGESAPTTLTQOT 91
DB 1326 TGLEPGIDYDISVTTLINGESAPTTLTQOT 1356

RESULT 10
ADE63323
ID ADE63323 standard; protein; 2477 AA.
XX
AC ADE63323;
XX
XX 29-JAN-2004 (first entry)
XX
DE Rat Protein CAA9281, SEQ ID NO 9260.
XX
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX
PN WC0003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002MO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
PI Woolf C, D'Urso D, Befort K, Costigan M;
XX
XX WPI, 2003-268312/26.
DR GENBANK; CAA9281.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating

CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2477 AA;

Query Match 100.0%; Score 462; DB 7; Length 2477;
Best Local Similarity 100.0%; Pred. No. 1.8e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPQLTDLSPVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYTV 60
DB 1265 EVPQLTDLSPVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYTV 1324

QY 61 TGLEPGIDYDISVTTLINGESAPTTLTQOT 91
DB 1325 TGLEPGIDYDISVTTLINGESAPTTLTQOT 1355

RESULT 11
AAR25405
ID AAR25405 standard; protein; 91 AA.
XX
AC AAR25405;
XX
XX 18-JAN-1993 (first entry)
XX
DE ED-B.
XX
KM Fibronectin; antibody; cancer.
XX
OS Homo sapiens.
XX
PN JP04169195-A.
XX
PD 17-JUN-1992.
XX
PF 31-OCT-1990; 90JP-00295820.
XX
PR 31-OCT-1990; 90JP-00295820.
XX
XX
PA (HOLI/) HOLIN G.
XX (GAKU/) GAKUEN F.
XX (SACA) OTSUKA PHARM CO LTD.
XX
DR WPI, 1992-253398/31.
XX
XX
PT Monoclonal antibody to fragment ED-B of fibronectin - for determining
PT fibronectin in cancerous tissue.
XX
XX
PS Claim 1; Page 1; 17pp; Japanese.

CC The sequence given is ED-B which is isolated from fibronectin. This
CC peptide was used in the production of an anti-ED-B monoclonal antibody.
CC This antibody is reactive against fibronectin, particularly in cancerous
CC tissue. The antibody recognises ED-B specifically and has reaction
CC specificity to cancerous fibronectin. This antibody is useful as a tracer
CC in determination of immunogen and cancerous fibronectin
XX
SQ Sequence 91 AA;

Query Match 99.4%; Score 459; DB 2; Length 91;
Best Local Similarity 98.9%; Pred. No. 6.2e-44;
Matches 90; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVPQLTDLSPVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYTV 60

Db 1 EVPOLTDLSFVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYYTV 60
QY 61 TGLEPGIDYDISVITLLINGESAPPTLLROOT 91
Db 61 TGLEPGIDYDISVITLLINGESAPPTLLROOT 91

RESULT 12
ID AAR60019 standard; protein; 1336 AA.
AC AAR60019;
XX
DT 25-MAR-2003 (revised)
DT 23-FEB-1995 (first entry)
XX
DE Tissue-binding hybrid protein.
XX
KM Tissue binding; tissue sealing; wound healing; vulnery;
KM tissue-binding domain; TSD; crosslinking domain; fibronectin;
KM fibrinogen-alpha; heparin-binding domain; collagen-binding domain;
KM cell-binding domain; hybrid protein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Domain 2..1336
FT /label= tissue-binding_domain
FT Domain 2..926
FT /label= tissue-binding_domain
FT Domain 928..1336
FT /label= tissue-binding_domain
XX
PN MO9416085-A2.
XX
PD 21-JUL-1994.
XX
PF 30-DEC-1993; 93WO-US012687.
XX
PR 30-DEC-1992; 92US-00998271.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Iran1 MH;
XX
DR WPI; 1994-249231/30.
DR N-PSDB; AAQ70007.
XX
XX New hybrid proteins for use in tissue sealing and wound healing -
PT comprising a tissue-binding domain from a protein covalently linked to a
PT crosslinking domain of another protein.
XX
PS Disclosure; Page 63-69; 87pp; English.
XX
CC Hybrid proteins have a tissue-binding domain (TBD) from 1 protein linked
CC to a crosslinking domain from another protein. The TBD comprises: aa 2-
CC 926, 928-1338 and especially 2-1336 of the sequence given in AAR60019;
CC the heparin-binding domain (aa 1812-2171 of AAR60021) of fibronectin; the
CC collagen-binding domain (aa 282-608 of AAR60021) of fibronectin; or the
CC cell-binding domain (aa 1357-1903 or 1532-1631 of AAR60020) of
CC fibronectin. DNA encoding a fibronectin- fibrinogen hybrid is given in
CC AAQ70007, and sequences for fibronectin and fibrinogen-alpha in AAQ70008
CC and AAQ70009, respectively. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1336 AA;

Query Match 98.1%; Score 453; DB 2; Length 1336;
Best Local Similarity 98.9%; Pred. No. 8,4e-42;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EVPOLTDLSFVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYYTV 60
Db 289 EVPOLTDLSFVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYYTV 348

QY 61 TGLEPGIDYDISVITLLINGESAPPTLLROOT 91
Db 349 TGLEPGIDYDISVITLLINGESAPPTLLROOT 379

RESULT 13
ID AAR60021 standard; protein; 2446 AA.
AC AAR60021;
XX
DT 25-MAR-2003 (revised)
DT 23-FEB-1995 (first entry)
XX
DE Fibrinogen-alpha.
XX
KM Tissue binding; tissue sealing; wound healing; vulnery;
KM tissue-binding domain; TSD; crosslinking domain; fibronectin;
KM fibrinogen-alpha; heparin-binding domain; collagen-binding domain;
KM cell-binding domain; hybrid protein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Domain 282..608
FT /label= collagen-binding_domain
FT /note= "acts as tissue-binding domain of hybrid protein"
FT Domain 1812..2171
FT /label= heparin-binding_domain
FT /note= "acts as tissue-binding domain of hybrid protein"
XX
PN MO9416085-A2.
XX
PD 21-JUL-1994.
XX
PF 30-DEC-1993; 93WO-US012687.
XX
PR 30-DEC-1992; 92US-00998271.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Iran1 MH;
XX
DR WPI; 1994-249231/30.
DR N-PSDB; AAQ70009.
XX
XX New hybrid proteins for use in tissue sealing and wound healing -
PT comprising a tissue-binding domain from a protein covalently linked to a
PT crosslinking domain of another protein.
XX
PS Disclosure; Page 37-48; 87pp; English.
XX
CC Hybrid proteins have a tissue-binding domain (TBD) from 1 protein linked
CC to a crosslinking domain from another protein. The TBD comprises: aa 2-
CC 926, 928-1338 and especially 2-1336 of the sequence given in AAR60019;
CC the heparin-binding domain (aa 1812-2171 of AAR60021) of fibronectin; the
CC collagen-binding domain (aa 282-608 of AAR60021) of fibronectin; or the
CC cell-binding domain (aa 1357-1903 or 1532-1631 of AAR60020) of
CC fibronectin. DNA encoding a fibronectin- fibrinogen hybrid is given in
CC AAQ70007, and sequences for fibronectin and fibrinogen-alpha in AAQ70008
CC and AAQ70009, respectively. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2446 AA;

Query Match 98.1%; Score 453; DB 2; Length 2446;
Best Local Similarity 98.9%; Pred. No. 1.8e-41;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EVPOLTDLSFVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYYTV 60
Db 1266 EVPOLTDLSFVDITDSSIGLRMTPLNSSTIIIGRITVVAAGEGIPFEDFVDSVGYYTV 1325

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Page 8

QY 61 TGLEGIDYDYSVITLINGESAPFTLTQQT 91
DB 1326 TGLEGIDYDYSVITLINGESAPFTLTQQT 1356

XX	RESULT 14
XX	ADCO9565
ID	ADCO9565 standard; peptide; 146 AA.
XX	
AC	ADCO9565;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Epitope with high affinity for MHC class I #SEQ ID 590.
XX	
KM	Epitope; immunological; vaccine;
KM	major histocompatibility complex class I; MHC class I; cancer;
XX	immunisation.
XX	
OS	Unidentified.
XX	
FN	WO2003008537-A2.
XX	
PD	30-JAN-2003.
XX	
PF	29-MAR-2002; 2002WO-US010189.
XX	
PR	06-APR-2001; 2001US-028221P.
PR	07-NOV-2001; 2001US-0337017P.
PR	07-MAR-2002; 2002US-0363210P.
XX	
PA	(CTL-) CTL IMMUNOTHERAPIES CORP.
XX	
PI	Simard JTL, Diamond DC, Liu L, Xie Z;
XX	
DR	WPI; 2003-248010/24.
XX	
PT	Epitope having high affinity for major histocompatibility complex class I
XX	useful for treating an animal, evaluating immunogenicity of a vaccine or
XX	therapeutic composition and for diagnosing a disease.
PS	Claim 1; SEQ ID NO 590; 239pp; English.
XX	
CC	The invention relates to an isolated epitope polypeptide that has high
CC	affinity for major histocompatibility complex (MHC) class I, and an
CC	epitope cluster comprising the polypeptide. Also disclosed is a vaccine
CC	or immunotherapeutic composition containing an epitope of the invention.
CC	Compositions of the invention may be used in the treatment of cancer. The
CC	method can be combined with a radiation therapy, chemotherapy,
CC	biochemotherapy or surgery. The composition is also useful for evaluating
CC	immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
CC	-peptide complexes of the invention are useful for determining specific T
CC	cell frequency. This method is useful for evaluating immunological
CC	response, by performing the method prior to and subsequent to an
CC	immunisation step. Compositions of the invention are useful for
CC	diagnosing a disease. The current sequence represents an epitope of the
CC	invention with high affinity for MHC class I.
XX	
XX	Sequence 146 AA;
XQ	

[illegible]

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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 1342398

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA:
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2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep.*
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9: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep.*
12: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
13: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	91	US-09-942-117-4	Sequence 4, Appl1
2	462	100.0	91	US-10-094-699-89	Sequence 89, Appl1
3	462	100.0	91	US-10-117-937-589	Sequence 589, Appl1
4	462	100.0	91	US-10-450-012-5	Sequence 5, Appl1
5	462	100.0	147	US-10-094-699-90	Sequence 90, Appl1
6	462	100.0	147	US-10-117-937-590	Sequence 590, Appl1
7	462	100.0	2220	US-10-236-392-4	Sequence 4, Appl1
8	148.5	32.1	2296	US-10-741-601-363	Sequence 363, Appl1
9	148.5	32.1	2320	US-10-236-392-2	Sequence 2, Appl1
10	148.5	32.1	2320	US-10-279-733-8	Sequence 8, Appl1
11	148.5	32.1	2328	US-10-182-936A-98	Sequence 98, Appl1
12	148.5	32.1	2328	US-10-171-311-64	Sequence 64, Appl1
13	148.5	32.1	2328	US-10-236-031B-70	Sequence 70, Appl1
14	148.5	32.1	2328	US-10-374-979-98	Sequence 98, Appl1
15	148.5	32.1	2355	US-10-144-194A-104	Sequence 104, Appl1

16	148.5	32.1	2355	US-10-360-101-235	Sequence 235, Appl1
17	148.5	32.1	2355	US-10-447-161-3	Sequence 3, Appl1
18	148.5	32.1	2355	US-10-734-564-94	Sequence 94, Appl1
19	148.5	32.1	2355	US-10-741-601-357	Sequence 357, Appl1
20	148.5	32.1	2355	US-10-741-601-366	Sequence 366, Appl1
21	148.5	32.1	2386	US-09-961-403-1	Sequence 1, Appl1
22	148.5	32.1	2386	US-10-741-601-360	Sequence 360, Appl1
23	122.5	26.5	1259	US-10-741-601-365	Sequence 365, Appl1
24	122.5	26.5	1259	US-10-741-601-362	Sequence 362, Appl1
25	122.5	26.5	1315	US-10-741-601-358	Sequence 358, Appl1
26	122.5	26.5	1341	US-10-741-601-355	Sequence 355, Appl1
27	122.5	26.5	1348	US-10-741-601-353	Sequence 353, Appl1
28	121.5	26.3	88	US-09-864-761-36851	Sequence 36851, A
29	120	26.0	270	US-10-240-488-2	Sequence 2, Appl1
30	120	26.0	271	US-09-943-981-1	Sequence 1, Appl1
31	120	26.0	271	US-09-775-964-1	Sequence 1, Appl1
32	120	26.0	457	US-09-775-964-22	Sequence 22, Appl1
33	120	26.0	472	US-09-775-964-21	Sequence 21, Appl1
34	120	26.0	545	US-10-408-765A-349	Sequence 349, Appl1
35	120	26.0	547	US-09-775-964-13	Sequence 13, Appl1
36	120	26.0	549	US-09-775-964-23	Sequence 23, Appl1
37	120	26.0	573	US-09-775-964-30	Sequence 30, Appl1
38	120	26.0	574	US-09-775-964-24	Sequence 24, Appl1
39	120	26.0	693	US-10-741-601-364	Sequence 364, Appl1
40	120	26.0	793	US-10-171-311-62	Sequence 62, Appl1
41	120	26.0	826	US-09-775-964-14	Sequence 14, Appl1
42	120	26.0	847	US-10-741-601-361	Sequence 361, Appl1
43	119.5	25.9	86	US-10-087-684-96	Sequence 96, Appl1
44	119.5	25.9	86	US-10-218-779-96	Sequence 96, Appl1
45	116.5	25.2	599	US-10-279-733-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-09-942-117-4
; Sequence 4, Application US/09942117
; Publication No. US2002019700A1
GENERAL INFORMATION:
APPLICANT: NENRAD, ANDREAS
APPLICANT: REDLITZ, ALEXANDER
APPLICANT: KOPPLITZ, MARCUS
APPLICANT: EGNER, URSULA
APPLICANT: BAHN, INKE
TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
FILE REFERENCE: SCH-1832
CURRENT FILING DATE: 2002-06-24
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: DE 10045803.3
PRIOR FILING DATE: 2000-05-07
PRIOR APPLICATION NUMBER: DE 10123133.4-41
PRIOR FILING DATE: 2001-05-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 91
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-942-117-4

Query Match 100.0%; Score 462; DB 9; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVPOLDLSEFVDITDSISGLRWTPLNSSTIGRTTVAAAGCIPFEDFVSSGYTV 60
Db 1 EVPOLDLSEFVDITDSISGLRWTPLNSSTIGRTTVAAAGCIPFEDFVSSGYTV 60
QY 61 TGLEPGIDYDVSITLINGSAPFTLTQOT 91

Db 61 TGLEPGIDYDISVTTLINGESAPPTLTQOT 91

RESULT 2

US-10-094-699-89
; Sequence 89, Application US/10094699
; Publication No. US20030046714A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: CTILIM.015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-699-89

Query Match 100.0%; Score 462; DB 14; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVPOLDLSFVDITDSSIGLRWTPPLNSSTIIGRITVVAAGEGIPFEDFVDSVGYTV 60

Db 1 EVPOLDLSFVDITDSSIGLRWTPPLNSSTIIGRITVVAAGEGIPFEDFVDSVGYTV 60

Qy 61 TGLEPGIDYDISVTTLINGESAPPTLTQOT 91

Db 61 TGLEPGIDYDISVTTLINGESAPPTLTQOT 91

RESULT 3

US-10-117-937-589
; Sequence 589, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LUT, Leping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTROPE SEQUENCES
; FILE REFERENCE: CTILIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 589
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-589

Query Match 100.0%; Score 462; DB 15; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVPOLDLSFVDITDSSIGLRWTPPLNSSTIIGRITVVAAGEGIPFEDFVDSVGYTV 60

Db 1 EVPOLDLSFVDITDSSIGLRWTPPLNSSTIIGRITVVAAGEGIPFEDFVDSVGYTV 60

Qy 61 TGLEPGIDYDISVTTLINGESAPPTLTQOT 91

Db 61 TGLEPGIDYDISVTTLINGESAPPTLTQOT 91

RESULT 4

US-10-450-012-5
; Sequence 5, Application US/10450012
; Publication No. US20040091973A1
; GENERAL INFORMATION:
; APPLICANT: Giovannoni, Leonardo
; TITLE OF INVENTION: Process for selecting anti-angiogenesis
; TITLE OF INVENTION: antibody fragments, anti-angiogenesis antibody fragments thus
; FILE REFERENCE: 0380-P03209US0
; CURRENT APPLICATION NUMBER: US/10/450,012
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/EP01/14330
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: FI2000A000247
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-450-012-5

Query Match 100.0%; Score 462; DB 16; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVPOLDLSFVDITDSSIGLRWTPPLNSSTIIGRITVVAAGEGIPFEDFVDSVGYTV 60

Db 1 EVPOLDLSFVDITDSSIGLRWTPPLNSSTIIGRITVVAAGEGIPFEDFVDSVGYTV 60

Qy 61 TGLEPGIDYDISVTTLINGESAPPTLTQOT 91

Db 61 TGLEPGIDYDISVTTLINGESAPPTLTQOT 91

RESULT 5

US-10-094-699-90
; Sequence 90, Application US/10094699
; Publication No. US20030046714A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: CTILIM.015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-699-90

Query Match 100.0%; Score 462; DB 14; Length 147;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVPOLDLSFVDITDSSIGLRWTPPLNSSTIIGRITVVAAGEGIPFEDFVDSVGYTV 60


```
QY      61  TGLEPGIDYDISVITTLINGESAPPTLTQOT  91
DB      95  TGLEPGIDYDISVITTLINGESAPPTLTQOT 125

RESULT 6
US-10-117-937-590
; Sequence 590, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhicong
; TITLE OF INVENTION: EPTIOTPE SEQUENCES
; FILE REFERENCE: CTLLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-590

Query Match      100.0%; Score 462; DB 15; Length 147;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  EVPOLTDLSPVDITDSSIGLRWTPUNSGTIGRTTVAAAGGIPFEDFVDSVGYTV  60
DB      35  EVPOLTDLSPVDITDSSIGLRWTPUNSGTIGRTTVAAAGGIPFEDFVDSVGYTV  94

QY      61  TGLEPGIDYDISVITTLINGESAPPTLTQOT  91
DB      95  TGLEPGIDYDISVITTLINGESAPPTLTQOT 125

RESULT 7
US-10-236-392-4
; Sequence 4, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomil, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grose, William M
; APPLICANT: Gusev, Viadimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Larochele, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malysankar, Utiel M
; APPLICANT: Miller, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
```

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; APPLICANT: Paturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 4
; LENGTH: 2220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-4

Query Match      100.0%; Score 462; DB 12; Length 2220;
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  EVPOLTDLSPVDITDSSIGLRWTPUNSGTIGRTTVAAAGGIPFEDFVDSVGYTV  60
DB      126  EVPOLTDLSPVDITDSSIGLRWTPUNSGTIGRTTVAAAGGIPFEDFVDSVGYTV 1325

QY      61  TGLEPGIDYDISVITTLINGESAPPTLTQOT  91
DB      1326  TGLEPGIDYDISVITTLINGESAPPTLTQOT 1356

RESULT 8
US-10-741-601-363
; Sequence 363, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C1001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 363
; LENGTH: 2296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-363
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Page 4

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Query Match      32.1%; Score 148.5; DB 16; Length 2296;
Best Local Similarity 36.5%; Pred. No. 8.3e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

Qy 2 VPQUTDLSFVDITDSSIGLAWTPLNSSTIIGYRITVAA-----GEGPIFEDFVDSV 55
Db 907 VPSPRDLOFVEVTDVKTIMWTP-PESAATGYRDVIVPVLPGHGORLPI-----SRN 959

Qy 56 GYTVTGLEPGIDYDISVITLNGESAPTTLTQOT 91
Db 960 TFAEVTGLSPGVITYYFVFAVSHGRESKPLTAQOTT 995
```

```
RESULT 9
US-10-236-392-2
Sequence 2, Application US/10236392
Publication No. US20040067490A1
GENERAL INFORMATION:
APPLICANT: Anderson, David W
APPLICANT: Boldog, Ferenc L
APPLICANT: Burgess, Catherine, E
APPLICANT: Casman, Stacie J
APPLICANT: Catterton, Elina
APPLICANT: Chapoval, Andrei
APPLICANT: Crabtree, Julie
APPLICANT: Edinger, Shlomit, R
APPLICANT: Ellerman, Karen
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Grose, William M
APPLICANT: Gusev, Vladamir
APPLICANT: Kekuda, Ramesh
APPLICANT: Larochele, William J
APPLICANT: Li, Li
APPLICANT: Macdougall, John R
APPLICANT: Malankar, Uriel M
APPLICANT: Miller, Charles E
APPLICANT: Miller, Isabelle
APPLICANT: Padigaru, Murallidhara
APPLICANT: Patuturajan, Meera
APPLICANT: Pena, Carol A
APPLICANT: Peyman, John A
APPLICANT: Rastelli, Luca
APPLICANT: Reiger, Daniel K
APPLICANT: Rothenberg, Mark E
APPLICANT: Shenoy, Suresh
APPLICANT: Shinkets, Richard A
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442A
CURRENT APPLICATION NUMBER: US/10/236,392
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US60/390,155
PRIOR FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US09/635,949
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US60/318,765
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US60/357,303
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US60/367,753
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US60/369,479
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: US09/659,634
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: US60/318,120
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US60/318,130
PRIOR FILING DATE: 2001-09-07
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 794
SOFTWARE: Custom
SEQ ID NO 2
LENGTH: 2320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-236-392-2

Query Match      32.1%; Score 148.5; DB 12; Length 2320;
Best Local Similarity 36.5%; Pred. No. 8.4e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;
```

```
Qy 2 VPQUTDLSFVDITDSSIGLAWTPLNSSTIIGYRITVAA-----GEGPIFEDFVDSV 55
Db 872 VPSPRDLOFVEVTDVKTIMWTP-PESAATGYRDVIVPVLPGHGORLPI-----SRN 924

Qy 56 GYTVTGLEPGIDYDISVITLNGESAPTTLTQOT 91
Db 925 TFAEVTGLSPGVITYYFVFAVSHGRESKPLTAQOTT 960
```

```
RESULT 10
US-10-279-733-8
Sequence 8, Application US/10279733
Publication No. US20030194400A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Liu, Cheng
APPLICANT: Edington, Thomas, S.
TITLE OF INVENTION: Targeted Thrombosis
FILE REFERENCE: 1361.016W01
CURRENT APPLICATION NUMBER: US/10/279,733
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 60/336331
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 2320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-279-733-8
```

```
Query Match      32.1%; Score 148.5; DB 14; Length 2320;
Best Local Similarity 36.5%; Pred. No. 8.4e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

Qy 2 VPQUTDLSFVDITDSSIGLAWTPLNSSTIIGYRITVAA-----GEGPIFEDFVDSV 55
Db 872 VPSPRDLOFVEVTDVKTIMWTP-PESAATGYRDVIVPVLPGHGORLPI-----SRN 924

Qy 56 GYTVTGLEPGIDYDISVITLNGESAPTTLTQOT 91
Db 925 TFAEVTGLSPGVITYYFVFAVSHGRESKPLTAQOTT 960
```

```
RESULT 11
US-10-182-936A-98
Sequence 98, Application US/10182936A
Publication No. US20040038660A1
GENERAL INFORMATION:
APPLICANT: Allen, Kristina M.
APPLICANT: Antosiewicz, Anthony
APPLICANT: Bhat, Bheem
APPLICANT: Damagnez, Veronique
APPLICANT: Robinson, John
APPLICANT: Yavorsky, Paul
TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions
FILE REFERENCE: 032796-143
CURRENT APPLICATION NUMBER: US/10/182,936A
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: PCT/US02/15982
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; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 2328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-936A-96

Query Match      32.1%; Score 148.5; DB 12; Length 2328;
Best Local Similarity 36.5%; Pred. No. 8.5e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

QY 2 VPOLTLDSFYVDITDSSIGLRMTPLNSSTIIGYRITVAA-----GGGIPDFEDFVDSV 55
DB 880 VPSRDLQFVEVDVKTIMWTP-PESAATGYRVDVIVPNLPGHGGRLP-----SRN 932

QY 56 GYTTVTGLFPGIDYDISVITLINGSAPFTLTQOT 91
DB 933 TFAEVTGLSPGYTYFFKVFVAVSHGRSKPLTAQOTT 968

RESULT 12
US-10-171-311-64
; Sequence 64, Application US/10171311
; Publication No. US2003087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Snubhangt
; APPLICANT: Glatc, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersth, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MFI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 2328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-64

Query Match      32.1%; Score 148.5; DB 14; Length 2328;
Best Local Similarity 36.5%; Pred. No. 8.5e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

QY 2 VPOLTLDSFYVDITDSSIGLRMTPLNSSTIIGYRITVAA-----GGGIPDFEDFVDSV 55
DB 880 VPSRDLQFVEVDVKTIMWTP-PESAATGYRVDVIVPNLPGHGGRLP-----SRN 932

QY 56 GYTTVTGLFPGIDYDISVITLINGSAPFTLTQOT 91
DB 933 TFAEVTGLSPGYTYFFKVFVAVSHGRSKPLTAQOTT 968
```

```

RESULT 13
US-10-236-031B-70
; Sequence 70, Application US/10236031B
; Publication No. US20030219760A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, Gavin J.
; APPLICANT: Jensen, Roderick V.
; APPLICANT: Gullans, Steven R.
; APPLICANT: Bueno, Raphael
; TITLE OF INVENTION: Diagnostic and Prognostic Tests
; FILE REFERENCE: B00801/70265 (JRV/JAV)
; CURRENT APPLICATION NUMBER: US/10/236,031B
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/317,399
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/407,431
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 2328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-031B-70

Query Match      32.1%; Score 148.5; DB 15; Length 2328;
Best Local Similarity 36.5%; Pred. No. 8.5e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

QY 2 VPOLTLDSFYVDITDSSIGLRMTPLNSSTIIGYRITVAA-----GGGIPDFEDFVDSV 55
DB 880 VPSRDLQFVEVDVKTIMWTP-PESAATGYRVDVIVPNLPGHGGRLP-----SRN 932

QY 56 GYTTVTGLFPGIDYDISVITLINGSAPFTLTQOT 91
DB 933 TFAEVTGLSPGYTYFFKVFVAVSHGRSKPLTAQOTT 968

RESULT 14
US-10-374-979-98
; Sequence 98, Application US/10374979
; Publication No. US20030219793A1
; GENERAL INFORMATION:
; APPLICANT: John P. Carulli et al.
; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
; FILE REFERENCE: 032796-021
; CURRENT APPLICATION NUMBER: US/10/374,979
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 09/544,398
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/543,771
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 98
; LENGTH: 2328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-979-98

Query Match      32.1%; Score 148.5; DB 15; Length 2328;
Best Local Similarity 36.5%; Pred. No. 8.5e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

QY 2 VPOLTLDSFYVDITDSSIGLRMTPLNSSTIIGYRITVAA-----GGGIPDFEDFVDSV 55
DB 880 VPSRDLQFVEVDVKTIMWTP-PESAATGYRVDVIVPNLPGHGGRLP-----SRN 932
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QY 56 GYVTVGLSPGIDYDISVITLNGESAPPTLTQOT 91
DB 933 TPAEVTGLSPGVYVYFKVFAVSHGRESKPLTAQOTT 968

RESULT 15

US-10-144-194A-104
; Sequence 104, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 104
; LENGTH: 2355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-194A-104

Query Match 32.1%; Score 148.5; DB 15; Length 2355;
Best Local Similarity 36.5%; Pred. No. 8.6e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

QY 2 VPQUTDISFVDIDSSIGLAWTPLNLSSTIGVRIYVAA-----GEGIPFEDFVDSV 55
DB 907 VPSFRDQFVEVDVKTIMWTP-PESAVTGYRVVDVIVNLPGEHGQRLPI-----SRN 959
QY 56 GYVTVGLSPGIDYDISVITLNGESAPPTLTQOT 91
DB 960 TPAEVTGLSPGVYVYFKVFAVSHGRESKPLTAQOTT 995

Search completed: September 21, 2004, 06:30:31
Job time : 602.537 secs

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:47:40 ; Search time 52.1912 Seconds
(without alignments)
90.015 Million cell updates/sec

Title: US-10-676-049-4

Perfect score: 462
Sequence: 1 EVPOLDLSFVDITDSSIGL.....SVITLNGESAPTLTTOQT 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_Aa:*

- 1: /cgm2_6/prodata/2/iaa/5A_COMB.pep:*
- 2: /cgm2_6/prodata/2/iaa/5B_COMB.pep:*
- 3: /cgm2_6/prodata/2/iaa/5A_COMB.pep:*
- 4: /cgm2_6/prodata/2/iaa/5B_COMB.pep:*
- 5: /cgm2_6/prodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgm2_6/prodata/2/iaa/Backlist1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	453	98.1	1336	2	US-08-551-356-6
2	453	98.1	1336	5	PCT-US93-12687-6
3	453	98.1	2446	2	US-08-551-356-2
4	453	98.1	2446	5	PCT-US93-12687-2
5	148.5	32.1	269	2	US-08-727-311-3
6	148.5	32.1	2231	1	US-08-153-799-16
7	148.5	32.1	2324	1	US-08-283-857-1
8	148.5	32.1	2324	5	PCT-US95-09819-1
9	148.5	32.1	2327	6	545158-1
10	148.5	32.1	2356	2	US-09-016-366A-12
11	120	26.0	271	3	US-08-536-891A-1
12	120	26.0	271	3	US-08-536-891A-1
13	120	26.0	271	4	US-09-366-009-14
14	120	26.0	271	4	US-09-366-009-1
15	120	26.0	271	4	US-08-809-156B-1
16	120	26.0	271	4	US-09-043-981-1
17	120	26.0	295	2	US-08-836-854-4
18	120	26.0	367	2	US-08-836-854-18
19	120	26.0	457	4	US-08-836-854-16
20	120	26.0	457	4	US-09-366-009-22
21	120	26.0	472	4	US-08-809-156B-22
22	120	26.0	472	4	US-09-366-009-21
23	120	26.0	547	4	US-08-809-156B-21
24	120	26.0	547	4	US-09-366-009-13
25	120	26.0	547	4	US-08-809-156B-13
26	120	26.0	549	2	US-08-836-854-11
27	120	26.0	549	4	US-09-366-009-23
			549	4	US-08-809-156B-23

28	120	26.0	573	4	US-09-366-009-30	Sequence 30, Appl
29	120	26.0	573	4	US-08-809-156B-30	Sequence 30, Appl
30	120	26.0	574	2	US-08-836-854-21	Sequence 21, Appl
31	120	26.0	574	3	US-09-463-296-1	Sequence 1, Appl
32	120	26.0	574	4	US-09-366-009-24	Sequence 24, Appl
33	120	26.0	574	4	US-08-809-156B-24	Sequence 24, Appl
34	120	26.0	826	4	US-09-366-009-14	Sequence 14, Appl
35	120	26.0	826	4	US-08-809-156B-14	Sequence 14, Appl
36	116.5	25.2	491	1	US-07-804-224-2	Sequence 2, Appl
37	116.5	25.2	491	2	PCT-US92-10511-2	Sequence 2, Appl
38	111.5	24.1	94	2	US-08-717-169-8	Sequence 8, Appl
39	111.5	24.1	94	4	US-09-638-202A-110	Sequence 110, App
40	111.5	24.1	94	4	US-09-228-901A-8	Sequence 8, Appl
41	111.5	24.1	94	4	US-09-096-749A-110	Sequence 110, App
42	111.5	24.1	96	4	US-09-638-202A-112	Sequence 112, App
43	111.5	24.1	96	4	US-09-096-749A-112	Sequence 112, App
44	111.5	24.1	175	1	US-08-078-683A-34	Sequence 34, Appl
45	111.5	24.1	175	4	US-08-471-970A-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-551-356-6
Sequence 6, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Iran, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,356
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
FILING DATE:
APPLICATION NUMBER: US/07/998,271
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holly, Julie A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-356-6
Query Match 98.1%; Score 453; DB 2; Length 1336;
Best Local Similarity 98.9%; Pred. No. 1.7e-44;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 EVPOLDLSFVDITDSSIGLRTPLNSTIGYRTVAAGGIPFEDVDSVGYTV 60
|||||

Tue Sep 21 07:04:11 2004

us-10-676-049-4.open.rai

Page 2

Db 289 EVPOLDLSPVDITDSSIGLRMTPLNSSTIIIGYRITVVAAGEGIPFEDFVSSVGYTV 348
QY 61 TGLEPGIDYDISVITTLINGESAPTLLTOOT 91
Db 349 TGLEPGIDYDISVITTLINGESAPTLLTOOT 379

RESULT 2
PCT-US93-12687-6
Sequence 6, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Irani, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-6

Query Match 98.1%; Score 453; DB 5; Length 1336;
Best Local Similarity 98.9%; Pred. No. 1.7e-44;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EVPOLDLSPVDITDSSIGLRMTPLNSSTIIIGYRITVVAAGEGIPFEDFVSSVGYTV 60
Db 289 EVPOLDLSPVDITDSSIGLRMTPLNSSTIIIGYRITVVAAGEGIPFEDFVSSVGYTV 348
QY 61 TGLEPGIDYDISVITTLINGESAPTLLTOOT 91
Db 349 TGLEPGIDYDISVITTLINGESAPTLLTOOT 379

RESULT 3
US-08-551-356-2
Sequence 2, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Irani, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.

STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,356
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
FILING DATE:
APPLICATION NUMBER: US/07/998,271
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holly, Julie A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-356-2

Query Match 98.1%; Score 453; DB 2; Length 2446;
Best Local Similarity 98.9%; Pred. No. 3.7e-44;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EVPOLDLSPVDITDSSIGLRMTPLNSSTIIIGYRITVVAAGEGIPFEDFVSSVGYTV 60
Db 1266 EVPOLDLSPVDITDSSIGLRMTPLNSSTIIIGYRITVVAAGEGIPFEDFVSSVGYTV 1325
QY 61 TGLEPGIDYDISVITTLINGESAPTLLTOOT 91
Db 1326 TGLEPGIDYDISVITTLINGESAPTLLTOOT 1356

RESULT 4
PCT-US93-12687-2
Sequence 2, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Irani, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION: 322
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-2

Query Match
Best Local Similarity 98.1%; Score 453; DB 5; Length 2446;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVPLTDLISFVDITDSSIGLRMTPLNSSTIIIGRTITVAAGGCIPIFFEDFVDSVGYTV 60
Db 1266 EVPLTDLISFVDITDSSIGLRMTPLNSSTIIIGRTITVAAGGCIPIFFEDFVDSVGYTV 1325

QY 61 TGLPEGIDYDISVITLINGSASAPTLTQOT 91
Db 1326 TGLPEGIDYDISVITLINGSASAPTLTQOT 1356

RESULT 5
US-08-727-311-3
Sequence 3, Application US/08727311.
Patent No. 5928876
GENERAL INFORMATION:
APPLICANT: Masanobu OBARA et al.
TITLE OF INVENTION: PEPTIDE AND COLLAGEN CONTRACTION INHIBITOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendroch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,311
FILING DATE: October 8, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:

US-08-727-311-3
Query Match
Best Local Similarity 32.1%; Score 148.5; DB 2; Length 269;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

QY 2 VPOLTLISFVDITDSSIGLRMTPLNSSTIIIGRTITVAAGGCIPIFFEDFVDSV 55
Db 4 VPSEFRLQFVEVDVDTKTIKMTLP-PSASVTVGRVDVTPVNLPSBHGRLPI-----SRN 56

QY 56 GYTVTGLPEGIDYDISVITLINGSASAPTLTQOT 91
Db 57 TFAVTLGSLPGVITYFFKVFVAVSHGRSKPLTAQCTT 92

RESULT 6
US-08-153-799-16
Sequence 16, Application US/08153799
Patent No. 5765883
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8903916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 665 2400
TELEFAX: (908) 771 6159
TELEX: 219484
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Protein
LOCATION: 1..2231
OTHER INFORMATION: /note="Human fibronectin"

Tue Sep 21 07:04:11 2004

us-10-676-049-4.open.ra1

Page 4

US-08-153-799-16

Query Match 32.1%; Score 148.5; DB 1; Length 2324;
Best Local Similarity 36.5%; Pred. No. 2.3e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

QY 2 VPOLTDLSFVDITDSSIGLAWTPLNSSTIIGRTIVAA-----GEGIPFEDFVDSV 55
DB 876 VPSRDLQFVEVDVKTIMTP-PESAATGIRVDVLPVNLPGHGRLPI-----SRN 928
OY 56 GYVTVGLBPGIDYDISVITLINGSBAPTLLTOOT 91
DB 929 TFAEVTGLSPGVITYYFKVFAVSHGRESKPLTAQOTT 964

RESULT 7
US-08-283-857-1

Sequence 1, Application US/08283857
Patent No. 5792742
GENERAL INFORMATION:
APPLICANT: GOLD, Leslie I.
APPLICANT: ROSTAGNO, Agueda A.
APPLICANT: BARON, Martin
APPLICANT: CAMPBELL, Iain D.
APPLICANT: WILLIAMS, Michael, J.
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,857
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/714,134
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOLD=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2324 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-283-857-1

Query Match 32.1%; Score 148.5; DB 1; Length 2324;
Best Local Similarity 36.5%; Pred. No. 2.4e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

QY 2 VPOLTDLSFVDITDSSIGLAWTPLNSSTIIGRTIVAA-----GEGIPFEDFVDSV 55
DB 876 VPSRDLQFVEVDVKTIMTP-PESAATGIRVDVLPVNLPGHGRLPI-----SRN 928

DB 929 TFAEVTGLSPGVITYYFKVFAVSHGRESKPLTAQOTT 964

RESULT 8
PCT-US95-09819-1

Sequence 1, Application PC/TUS9509819
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09819
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,857
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOLD=1A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2324 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-09819-1

Query Match 32.1%; Score 148.5; DB 5; Length 2324;
Best Local Similarity 36.5%; Pred. No. 2.4e-08;
Matches 35; Conservative 13; Mismatches 35; Indels 13; Gaps 3;

QY 2 VPOLTDLSFVDITDSSIGLAWTPLNSSTIIGRTIVAA-----GEGIPFEDFVDSV 55
DB 876 VPSRDLQFVEVDVKTIMTP-PESAATGIRVDVLPVNLPGHGRLPI-----SRN 928
OY 56 GYVTVGLBPGIDYDISVITLINGSBAPTLLTOOT 91
DB 929 TFAEVTGLSPGVITYYFKVFAVSHGRESKPLTAQOTT 964

RESULT 9
5455158-1

Patent No. 5455158
APPLICANT: VOGEL, TIKVA, LEVANON, AVIGDOR, WEBBER, MOSHE M.;
GUY, RACHEL, PANET, AMOS
TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND
USERS AND METHODS OF PRODUCING SAME
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/58,241
FILING DATE: 04-MAY-1993
PRIOR APPLICATION DATA:


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; APPLICATION NUMBER: 345,952
; FILING DATE: 28-APR-1989
; APPLICATION NUMBER: 291,951
; FILING DATE: 29-DEC-1988
; SEQ ID NO:1
; LENGTH: 2327
5455158-1

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Query Match	32.1%;	Score 148.5;	DB 6;	Length 2327;
Best Local Similarity	36.5%;	Pred. No. 2.4e-08;		
Matches	35;	Conservative	13;	Mismatches 35;
				Indels 13;

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QY      2 VPQLTDLSPFDITDSSIGLRKMTPLNSTIIGRITVAA-----GEQIPIDFEDVDSV 55
      |||::||:|::|||:|::|||:|::|||
Db      879 VPSPRDLQFEVETDVKVTIMTP-PSAAVTGVVDVLPVNLPGEHGRLPI-----SRN 931

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QY 56 GYVVTGLEGPIDDISVITLLINGESAPETLTQOT 91
: ||||| : : |||||
Db 932 TFAETGLSPGVITYFKVAVSHGRESKPTLAQQT 967

RESULT 10
US-09-016-366A-12
; Sequence 12, Application US/09016366A

GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu

TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:

STREET: 600
CITY: Boston
STATE: MA

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; ZIP: 02210-2211  
; COMPUTER READABLE  
; MEDIUM TYPE: Di
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; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
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FILING DATE: January 30, 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:

FILING DATE: 05-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.

REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500

TELEX: INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

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;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;

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US-09-016-366A-12

Query Match 32.1%; Score 148.5; DB 2; Length 2386

2 VPQTDLSFVDITDSSIGLRMTPLNSSTIGRITVAA-----GEGIPFEDFVDSV 55

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Db      907 VPSPRLQVEVETDVKNTIMTP-PESAVTGRVDIVPNLPGHQRLP-----SRN 955
QY      56 GYTVTGLERGLDYDISVITLNGESAPTLTQQT 91
          : ||||| : : : : :
Db      960 TFAEVTGLSPGVTYEKFVAVSHGSEKPLTAQQT 995

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RESULT 11
US-08-536-891A-1

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; Patent No. 6033907
;
; GENERAL INFORMATION:
; APPLICANT: David A. Williams
; INVENTOR: David A. Williams
; TITLE: Mediated DNA Transfer

```

```
;; NUMBER OF SEQUENCES: 2
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Thomas Q. Henry
;; CMT: Park One Tower Suite 3700 111 Monument Circle
```

;
;
;
CITY: Indianap
STATE: Indiana
COUNTRY: USA
RTD 46304

```

; ;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
;
; COMPUTER: COMPAQ
; OPERATING SYSTEM: MSDOS

```

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; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/536,891A
; FILING DATE: 26 October 1995

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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03817
; FILING DATE: March 27 1995

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; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/218,355
 ; FILING DATE: March 25, 1994
 ; REMOVAL/ACQUISITION INFORMATION:

NAME: Thomas Q. Henry
REGISTRATION NUMBER: 28,309
REFERENCE/DOCKET NUMBER: 7037-52/IU-33-CIP-2
REPRODUCTION INFORMATION:

TELEPHONE: (317) 634-3456
TELEFAX: (317) 637-7561
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 271 amino acids
TYPE: amino acid
TOPOLOGY: linear
NOTED TYPE: acetoin ferredoxin

US-08-536-891A-1

Query Match 26.0%; Score 22.0%;

Matches	27;	Conservative	16;	Mismatches	35;	Indels	2;	Gaps	2	
QY	12	DITDSIGLRWTP	PLNSSTII	IGRIIVVA	AGEGIP	PIFEDEFVDS	VSGYYT	VTNGL	EPGGLDYDI	71

Db 104 DATETTTTISR-TKETITGQVDANPANGQPI-QRTIKSDVRSYHITGLQPSIDYKX 16
QY 72 SVITTLNGESAPTTLTQQT 91

Db 162 YLYTINDNARSSPVVIDAST 181

US-08-933-100B-14
; Sequence 14, Application US/08933100E
; Patent No. 6274704
CURRENT INFORMATION:

APPLICANT: FUKAI, FUMIO
APPLICANT: KATAYAMA, TAKASHI
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDE AND CANCER

TITLE OF INVENTION: METASTASIS INHIBITOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,100B
FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PERRY, GLENN
REGISTRATION NUMBER: 28458
REFERENCE/DOCKET NUMBER: 7896/242094
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 271
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: sequence of a part (1600-1870) of Heparin binding site
US-08-933-100B-14

Query Match 26.0%; Score 120; DB 3; Length 271;
Best Local Similarity 33.8%; Pred. No. 3.1e-06;
Matches 27; Conservative 16; Mismatches 35; Indels 2; Gaps 2;

QY 12 DITDSIGLWTPNLSSTIGRTVVAAGEGIPEDFVDSVGYVTWGLEPGIDYDI 71
DB 104 DATETITITISMR-TKETITIGFQVDVAPANGQPTI-QRTIKPVRSYITIGLOPGTDYKI 161

QY 72 SVITLINGSAPTTLTQQT 91
DB 162 VLYTLNDNARSSPVVIDAST 181

RESULT 13
US-09-366-009-1
Sequence 1, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Yeno, Takashi
Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikumoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-AUG-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051647/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-366-009-1

Query Match 26.0%; Score 120; DB 4; Length 271;
Best Local Similarity 33.8%; Pred. No. 3.1e-06;
Matches 27; Conservative 16; Mismatches 35; Indels 2; Gaps 2;

QY 12 DITDSIGLWTPNLSSTIGRTVVAAGEGIPEDFVDSVGYVTWGLEPGIDYDI 71
DB 104 DATETITITISMR-TKETITIGFQVDVAPANGQPTI-QRTIKPVRSYITIGLOPGTDYKI 161

QY 72 SVITLINGSAPTTLTQQT 91
DB 162 VLYTLNDNARSSPVVIDAST 181

RESULT 14
US-08-809-156B-1
Sequence 1, Application US/08809156B
Patent No. 6472204
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Yeno, Takashi
Koyama, No. 6472204uto
Hashino, Kimikazu
Kato, Ikumoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977,6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-809-156B-1

Query Match 26.0%; Score 120; DB 4; Length 271;
Best Local Similarity 33.8%; Pred. No. 3.1e-06;
Matches 27; Conservative 16; Mismatches 35; Indels 2; Gaps 2;

QY 12 DITDSIGLWTPNLSSTIGYRTVVAAGEGIPFEDFVDSVGYVTGTEPGIDYDI 71
DB 104 DATETTTISMR-TKETITIGFQVDVAVPANGQTFI-QRTIKPDRSYTTTGLOPGTDYKI 161
QY 72 SVITLLINGESAPFTLTQQT 91
DB 162 YLYTINDNARSSPVVIDAST 181

RESULT 15
US-09-043-981-1
Sequence 1, Application US/09043981
Patent No. 6670177
GENERAL INFORMATION:
APPLICANT: Williams, David A.
TITLE OF INVENTION: METHODS FOR ENHANCED VIRUS MEDIATED DNA TRANSFER USING
FILE REFERENCE: 7037-297
CURRENT APPLICATION NUMBER: US/09/043,981
CURRENT FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: US96/15712
EARLIER FILING DATE: 1996-09-30
EARLIER APPLICATION NUMBER: 08/536,891
EARLIER FILING DATE: 1995-09-29
EARLIER APPLICATION NUMBER: 60/024,169
EARLIER FILING DATE: 1996-08-19
NUMBER OF SEQ. ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ. ID NO. 1
LENGTH: 271
TYPE: PRT
ORGANISM: Homo sapiens
US-09-043-981-1

Query Match 26.0%; Score 120; DB 4; Length 271;
Best Local Similarity 33.8%; Pred. No. 3.1e-06;
Matches 27; Conservative 16; Mismatches 35; Indels 2; Gaps 2;
QY 12 DITDSIGLWTPNLSSTIGYRTVVAAGEGIPFEDFVDSVGYVTGTEPGIDYDI 71
DB 104 DATETTTISMR-TKETITIGFQVDVAVPANGQTFI-QRTIKPDRSYTTTGLOPGTDYKI 161
QY 72 SVITLLINGESAPFTLTQQT 91

DB 162 YLYTINDNARSSPVVIDAST 181

Search completed: September 21, 2004, 06:15:27
Job time : 52.1912 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2004, 06:15:34; Search time 13.6667 Seconds
(without alignments)
56.663 Million cell updates/sec

Title: US-10-676-049-2
Perfect score: 85
Sequence: 1 GYWTYGLPGIDYD 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 146418

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	40	47.1	15 4 US-09-526-879-2	Sequence 2, Appl
2	40	47.1	15 4 US-09-526-879-4	Sequence 4, Appl
3	40	47.1	15 4 US-09-526-879-5	Sequence 5, Appl
4	40	47.1	15 4 US-09-526-879-6	Sequence 6, Appl
5	40	47.1	15 4 US-09-526-879-7	Sequence 7, Appl
6	40	47.1	15 4 US-09-526-879-8	Sequence 8, Appl
7	40	47.1	15 4 US-09-526-879-9	Sequence 9, Appl
8	33	38.8	2 US-08-340-283-158	Sequence 158, App
9	33	38.8	15 4 US-09-526-879-3	Sequence 3, Appl
10	33	38.8	15 4 US-09-526-879-12	Sequence 12, Appl
11	33	38.8	15 4 US-09-526-879-13	Sequence 13, Appl
12	32	37.6	15 3 US-09-248-588-90	Sequence 90, Appl
13	30	35.3	15 3 US-09-049-577-3	Sequence 3, Appl
14	30	35.3	15 3 US-09-390-598-3	Sequence 3, Appl
15	30	35.3	15 3 US-09-328-553-3	Sequence 3, Appl
16	28	32.9	15 1 US-08-290-448A-89	Sequence 89, Appl
17	28	32.9	15 1 US-08-220-448A-89	Sequence 89, Appl
18	28	32.9	15 1 US-08-175-069A-89	Sequence 89, Appl
19	28	32.9	15 2 US-08-480-190-185	Sequence 185, App
20	28	32.9	15 2 US-08-488-379-185	Sequence 185, App
21	28	32.9	15 4 US-08-461-939B-89	Sequence 89, Appl
22	28	32.9	15 4 US-08-464-000-89	Sequence 185, App
23	28	32.9	15 4 US-08-475-392A-185	Sequence 185, App
24	28	32.9	15 5 PCT-US93-07545-185	Sequence 185, App
25	27	31.8	15 5 US-09-530-139-74	Sequence 74, Appl
26	27	31.8	14 1 US-07-690-983D-30	Sequence 30, Appl
27	27	31.8	14 4 US-08-891-525-3	Sequence 3, Appl

28	27	31.8	15 1 US-08-625-691-4	Sequence 4, Appl
29	27	31.8	15 2 US-08-659-984A-9	Sequence 9, Appl
30	27	31.8	15 3 US-08-915-189-12	Sequence 12, Appl
31	27	31.8	15 3 US-08-972-760-12	Sequence 12, Appl
32	27	31.8	15 3 US-09-089-645A-12	Sequence 12, Appl
33	27	31.8	15 3 US-08-660-531-9	Sequence 9, Appl
34	27	31.8	15 4 US-09-503-998-12	Sequence 12, Appl
35	27	31.8	15 4 US-09-373-694-12	Sequence 12, Appl
36	27	31.8	15 4 US-09-939-481-12	Sequence 1, Appl
37	27	31.8	9 2 US-08-368-834-1	Sequence 1, Appl
38	26	30.6	10 1 US-08-447-154-1	Sequence 1, Appl
39	26	30.6	10 1 US-08-164-935-6	Sequence 6, Appl
40	26	30.6	10 2 US-08-724-548-27	Sequence 27, Appl
41	26	30.6	10 2 US-08-724-548-28	Sequence 28, Appl
42	26	30.6	10 2 US-08-724-548-29	Sequence 29, Appl
43	26	30.6	10 2 US-08-724-548-30	Sequence 30, Appl
44	26	30.6	10 2 US-08-724-548-31	Sequence 31, Appl
45	26	30.6	10 3 US-07-978-674B-27	Sequence 27, Appl

ALIGNMENTS

```
RESULT 1
US-09-526-879-2
; Sequence 2, Application US/09526879
; Patent No. 6451971
; GENERAL INFORMATION:
; APPLICANT: AKIYAMA, KATSUHIKO
; APPLICANT: GOTO, TAKESHI
; APPLICANT: FUKAI, FUMIO
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
; FILE REFERENCE: 007898-0257795
; CURRENT APPLICATION NUMBER: US/09/526, 879
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: JP 070127/1999
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Physiologically active peptide
US-09-526-879-2

Query Match          47.1% Score 40; DB 4; Length 15;
Best Local Similarity 75.0% Pred. No. 2.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 GLEPGIDY 14
      |||:|:|
Db      1 GLEPGVDY 8

RESULT 2
US-09-526-879-4
; Sequence 4, Application US/09526879
; Patent No. 6451971
; GENERAL INFORMATION:
; APPLICANT: AKIYAMA, KATSUHIKO
; APPLICANT: GOTO, TAKESHI
; APPLICANT: FUKAI, FUMIO
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
; FILE REFERENCE: 007898-0257795
; CURRENT APPLICATION NUMBER: US/09/526, 879
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: JP 070127/1999
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 4
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-4
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Query Match
Best Local Similarity 47.1%; Score 40; DB 4; Length 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 7 GLEPGIDY 14
||:|:|
Db 1 GLKPGVDY 8
```

```
RESULT 3
US-09-526-879-5
Sequence 5, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
APPLICANT: FUKAI, FUMIO
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007898-0257795
CURRENT APPLICATION NUMBER: US/09/526,879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-5
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```
Query Match
Best Local Similarity 47.1%; Score 40; DB 4; Length 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 7 GLEPGIDY 14
||:|:|
Db 1 GLKPGVDY 8
```

```
RESULT 4
US-09-526-879-6
Sequence 6, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
APPLICANT: FUKAI, FUMIO
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007898-0257795
CURRENT APPLICATION NUMBER: US/09/526,879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-6
```

```
Query Match
Best Local Similarity 47.1%; Score 40; DB 4; Length 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 GLEPGIDY 14
||:|:|
Db 1 GLKPGVDY 8
```

```
RESULT 5
US-09-526-879-7
Sequence 7, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
APPLICANT: FUKAI, FUMIO
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007898-0257795
CURRENT APPLICATION NUMBER: US/09/526,879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-7
```

```
Query Match
Best Local Similarity 47.1%; Score 40; DB 4; Length 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 7 GLEPGIDY 14
||:|:|
Db 1 GLKPGVDY 8
```

```
RESULT 6
US-09-526-879-8
Sequence 8, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
APPLICANT: FUKAI, FUMIO
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007898-0257795
CURRENT APPLICATION NUMBER: US/09/526,879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-8
```

```
Query Match
Best Local Similarity 47.1%; Score 40; DB 4; Length 15;
```

Best Local Similarity 75.0%; Pred. No. 2.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GLEPGIDY 14
||:||||
Db 1 GLKPGVDY 8

RESULT 7
US-09-526-879-9
; Sequence 9, Application US/09526879
; Patent No. 6451971
; GENERAL INFORMATION:
; APPLICANT: AKIYAMA, KATSUHIKO
; APPLICANT: GOTO, TAKESHI
; APPLICANT: FUKAI, FUMIO
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
; FILE REFERENCE: 007898-0257795
; CURRENT APPLICATION NUMBER: US/09/526,879
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: JP 070127/1999
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Physiologically active peptide
US-09-526-879-9

Query Match 47.1%; Score 40; DB 4; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GLEPGIDY 14
||:||||
Db 1 GLKPGVDY 8

RESULT 8
US-08-340-283-158
; Sequence 158, Application US/08340283
; Patent No. 5861318
; GENERAL INFORMATION:
; APPLICANT: Elhammer, Ake P.
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
; TITLE OF INVENTION: N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 205
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
; ADDRESS: (1920-32-1)
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,283
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootten, Thomas A.
; REGISTRATION NUMBER: 35,004
; REFERENCE/DOCKET NUMBER: 4828
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (616) 365-7914
TELEFAX: (616) 385-6897
TELEX: 224401
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-340-283-158

Query Match 38.8%; Score 33; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VTGSEPGI 12
||:||||
Db 2 VTGSEPGI 9

RESULT 9
US-09-526-879-3
; Sequence 3, Application US/09526879
; Patent No. 6451971
; GENERAL INFORMATION:
; APPLICANT: AKIYAMA, KATSUHIKO
; APPLICANT: GOTO, TAKESHI
; APPLICANT: FUKAI, FUMIO
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
; FILE REFERENCE: 007898-0257795
; CURRENT APPLICATION NUMBER: US/09/526,879
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: JP 070127/1999
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Physiologically active peptide
US-09-526-879-3

Query Match 38.8%; Score 33; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GLEPGID 13
||:||||
Db 1 GLKPGVD 7

RESULT 10
US-09-526-879-12
; Sequence 12, Application US/09526879
; Patent No. 6451971
; GENERAL INFORMATION:
; APPLICANT: AKIYAMA, KATSUHIKO
; APPLICANT: GOTO, TAKESHI
; APPLICANT: FUKAI, FUMIO
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
; FILE REFERENCE: 007898-0257795
; CURRENT APPLICATION NUMBER: US/09/526,879
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: JP 070127/1999
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: Tyr or Ala
NAME/KEY: MOD_RES
LOCATION: (12)
OTHER INFORMATION: Val or Ala
NAME/KEY: MOD_RES
LOCATION: (13)
OTHER INFORMATION: Tyr or Ala
NAME/KEY: MOD_RES
LOCATION: (15)
OTHER INFORMATION: Val or Ala
US-09-526-879-12

Query Match
Best Local Similarity 38.8%; Score 33; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 GLEPGID 13
||:||||
Db 1 GLKRGVD 7

RESULT 11
US-09-526-879-13
Sequence 13, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
APPLICANT: FUKAI, FUMIO
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007898-0257795
CURRENT APPLICATION NUMBER: US/09/526,879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: Tyr or Ala
NAME/KEY: MOD_RES
LOCATION: (12)
OTHER INFORMATION: Val or Ala
NAME/KEY: MOD_RES
LOCATION: (13)
OTHER INFORMATION: Tyr or Ala
US-09-526-879-13

Query Match
Best Local Similarity 38.8%; Score 33; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 GLEPGID 13
||:||||
Db 1 GLKRGVD 7

RESULT 12
US-09-248-588-90
Sequence 90, Application US/09248588
Patent No. 6231864
GENERAL INFORMATION:
APPLICANT: Birkebeck, Ashley J.
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
FILE REFERENCE: SYN-101 4564/69529
CURRENT APPLICATION NUMBER: US/09/248,588
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: 60/074537
EARLIER FILING DATE: 1998-02-12
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 90
LENGTH: 15
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-248-588-90

Query Match
Best Local Similarity 37.6%; Score 32; DB 3; Length 15;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGLRGI 12
:|||||
Db 5 SGLRGI 11

RESULT 13
US-09-049-577-3
Sequence 3, Application US/09049577
Patent No. 5968604
GENERAL INFORMATION:
APPLICANT: Feng, Teng-Yung
APPLICANT: Lin, Hao-Jen
TITLE OF INVENTION: AMPHIPATHIC PROTEIN-1
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,577
FILING DATE: 27-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. Rocky
REGISTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 08919/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-049-577-3

Query Match 35.3%; Score 30; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YVTGLEPG 11
| | | | |
| | | | |
Db 3 YKVTLLDPG 11

RESULT 14
US-09-390-598-3
; Sequence 3, Application US/09390598
; Patent No. 6297360
; GENERAL INFORMATION:
; APPLICANT: Feng, Teng-yung
; APPLICANT: Lin, Hao-Jan
; TITLE OF INVENTION: AMPHIPATHIC PROTEIN-1
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/390,598
; FILING DATE: 27-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 08919/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-390-598-3

Query Match 35.3%; Score 30; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YVTGLEPG 11
| | | | |
| | | | |
Db 3 YKVTLLDPG 11

RESULT 15
US-09-328-553-3
; Sequence 3, Application US/09328553
; Patent No. 6566588
; GENERAL INFORMATION:
; APPLICANT: Feng, Teng-Yung
; APPLICANT: Lin, Hao-Jan
; TITLE OF INVENTION: AMPHIPATHIC PROTEIN-1
; FILE REFERENCE: 08919-025001
; CURRENT APPLICATION NUMBER: US/09/328,553
; CURRENT FILING DATE: 1999-06-09

; PRIOR APPLICATION NUMBER: US 09/049,577
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Goseypium hirsutum
US-09-328-553-3

Query Match 35.3%; Score 30; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YVTGLEPG 11
| | | | |
| | | | |
Db 3 YKVTLLDPG 11

Search completed: September 21, 2004, 06:42:05
Job time: 14.6667 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 06:37:00 ; Search time 18.6667 Seconds
(without alignments)
77.297 Million cell updates/sec

Title: US-10-676-049-3
Perfect score: 77
Sequence: 1 TGLEPGIDYDISVIT 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2522

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	33.8	14	2 S07768	soluble hydrogenas
2	25	32.5	10	1 RHAQ1	gonadolibertin I -
3	25	32.5	13	2 PH1599	Ig H chain V-D-J r
4	23	29.9	10	1 RHFGG	gonadolibertin - pi
5	23	29.9	10	1 RHSHG	gonadolibertin - sh
6	22	28.6	9	2 S70345	antre oxidase (cop
7	22	28.6	11	2 G61497	seed protein ws-23
8	22	28.6	14	2 A61002	photosystem ii oxy
9	22	28.6	15	2 B26501	lipoprotein lipase
10	21	27.3	10	2 S62880	polygalacturonase
11	21	27.3	10	2 PH1592	Ig H chain V-D-J r
12	21	27.3	11	2 S19775	wound-induced prot
13	21	27.3	11	2 PH1583	Ig H chain V-D-J r
14	21	27.3	11	2 S18385	NADP-cytochrome P4
15	21	27.3	15	2 PA0071	superoxide dismuta
16	21	27.3	15	2 S62609	glutathione-disulf
17	20	26.0	9	2 JQ0814	MHC class I histoc
18	20	26.0	11	2 A40795	glycoprotein H-a -
19	20	26.0	11	2 PH0929	T-cell receptor be
20	20	26.0	13	2 PM0176	acidic ribosomal p
21	20	26.0	13	2 S26440	ig kappa chain J s
22	20	26.0	15	2 S61284	phosphoprotein, 80
23	20	26.0	15	2 S67975	apolipoprotein, Cb2
24	19	24.7	9	2 E41978	callikain-like 5 -
25	19	24.7	10	2 S62308	polyferredoxin - M
26	19	24.7	11	2 PH1600	Ig H chain V-D-J r
27	19	24.7	12	2 S26547	T-cell receptor be
28	19	24.7	12	2 S36899	ribosomal protein
29	19	24.7	14	2 S74128	superoxide dismuta

30	19	24.7	14	2 C39170	acyl-lacetyl-carrier
31	19	24.7	15	2 S21202	glucan 1,4-alpha-g
32	19	24.7	15	2 T09463	ribosomal protein
33	19	24.7	15	2 PA0088	protein QP200051 -
34	19	24.7	15	2 A36279	chemottractant pr
35	19	24.7	15	2 B56046	urinary tract ston
36	19	24.7	15	2 A53085	lipid transfer pro
37	19	24.7	15	2 I78838	flit3 ligand isoform
38	19	24.7	15	2 PH1582	Ig H chain V-D-J r
39	19	24.7	15	2 PM0052	pyruvate kinase (E
40	19	24.7	15	4 I38032	hypothetical MW1/T
41	18	23.4	10	2 B33143	pneumadin - human
42	18	23.4	10	2 A33143	pneumadin - rat
43	18	23.4	11	2 S69349	neuropeptide Fpmi
44	18	23.4	12	2 S26546	T-cell receptor be
45	18	23.4	12	2 S26544	T-cell receptor be

ALIGNMENTS

RESULT 1
S07768 soluble hydrogenase (EC 1.12.-.-) large chain - Anabaena cylindrica (fragment)
C/Species: Anabaena cylindrica
C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 21-Mar-1996
C/Accession: S07768
R/Ewart, G.D.; Reed, K.C.; Smith, G.D.
Eur. J. Biochem. 187, 215-223, 1990
A/Title: Soluble hydrogenase of Anabaena cylindrica. Cloning and sequencing of a potent
A/Accession: S07768
A/Molecule type: protein
A/Residues: 1-14 <EWA>
C/Keywords: oxidoreductase

Query Match 33.8% Score 26; DB 2; Length 14;
Best Local Similarity 57.1% Pred. No. 3.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 2
RHAQ1 gonadolibertin I - American alligator
N/Alternate names: gonadotropin-releasing hormone I
C/Species: Alligator mississippiensis (American alligator)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
C/Accession: A60066
R/Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson
Regul. Pept. 33, 105-116, 1991
A/Title: Primary structure of two forms of gonadotropin-releasing hormone from brains o
A/Reference number: A60066; MUID:91352338; PMID:1882082
A/Accession: A60066
A/Molecule type: protein
A/Residues: 1-10 <LOV>
C/Superfamily: gonadolibertin
C/Keywords: amidated carboxyl end, hormone, hypothalamus, pyroglutamic acid
F.1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F.10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 33.5% Score 25; DB 1; Length 10;
Best Local Similarity 80.0% Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGLEPG 6
DB 6 GLEPG 10

RESULT 3

PH1599
 Ig H chain V-D-J region (wild-type clone 307) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1599
 J:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A/Reference number: PH1580; PMID:93301609; PMID:8315387
 A/Accession: PH1599
 A/Molecule type: DNA
 A/Residues: 1-13 <LEV>
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 32.5%; Score 25; DB 2; Length 13;
 Best Local Similarity 42.9%; Pred. No. 4.5e+02;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 9 YDISVIT 15
 |||
 1 YETIVIT 7

RESULT 4

RHPG
 gonadoliberin - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997
 C/Accession: A01411
 R/Baba, Y.; Matsuo, H.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 44, 459-463, 1971
 A/Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of the
 A/Reference number: A90172; PMID:72114303; PMID:4946067
 A/Accession: A01411
 A/Molecule type: protein
 A/Residues: 1-10 <BAB>
 R/Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 45, 822-827, 1971
 A/Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase method
 A/Reference number: A90176; PMID:72065376; PMID:4942726
 A/Contents: annotation; synthesis
 A/Note: the synthetic and natural hormones have the same physicochemical and biological
 R/Baba, Y.; Arimura, A.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 45, 483-487, 1971
 A/Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.
 A/Reference number: A90175; PMID:72117544; PMID:4946275
 A/Contents: annotation
 A/Note: TRP-3 appears to be essential for biological activity
 C/Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and fo
 C/Superfamily: gonadoliberin
 C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F./Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F./Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.9%; Score 23; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 7.3e-02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GLRPG 6
 |||
 Db 6 GLRPG 10

RESULT 5

RHSHG
 gonadoliberin - sheep
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Mar-1997
 C/Accession: A93780; A01411
 R/Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Monahan, M.; Rivler, J.; Fellows, R.; Bl
 Proc. Natl. Acad. Sci. U.S.A. 69, 278-282, 1972

A/Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing factor
 A/Reference number: A93780; PMID:72094314; PMID:4550508
 A/Accession: A93780
 A/Molecule type: protein
 A/Residues: 1-10 <BUR>
 A/Note: the natural and synthetic hormones have the same biological activity
 C/Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and fo
 C/Superfamily: gonadoliberin
 C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F./Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F./Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.9%; Score 23; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 7.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GLRPG 6
 |||
 Db 6 GLRPG 10

RESULT 6

S70345
 amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragments)
 C/Species: Aspergillus niger
 C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
 C/Accession: S70345
 R/Frederick, I.; Pec, P.; Lubova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.
 Biochim. Biophys. Acta 1295, 59-72, 1996
 A/Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the
 A/Reference number: S70344; PMID:96283794; PMID:8679675
 A/Accession: S70345
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 15,6-9 <FR>
 C/Keywords: oxidoreductase

Query Match 28.6%; Score 22; DB 2; Length 9;
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 LEPGIDY 9
 |||
 Db 3 IEPNEX 9

RESULT 7

seed protein ws-23 - winged bean (fragment)
 C/Species: Psophocarpus tetragonolobus (winged bean)
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
 C/Accession: G61497
 J. Hixano, H.
 J. Protein Chem. 8, 115-130, 1989
 A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dim
 A/Reference number: A61491; PMID:89351606; PMID:2765119
 A/Accession: G61497
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-11 <HIR>
 C/Keywords: glycoprotein; seed

Query Match 28.6%; Score 22; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LEPG 6
 |||
 Db 8 LEPG 11

RESULT 8

A61002

photosystem II oxygen-evolving complex protein 1 - common tobacco (fragment)
 N:Alternate names: thylakoid membrane protein
 C:Species: Nicotiana tabacum (common tobacco)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C:Accession: A61002
 R:Bauw, G.; Rasmussen, H.H.; Van Den Bultke, M.; Van Damme, J.; Puyse, M.; Gesser, B.; C
 Electrophoresis 11, 528-536, 1990
 A>Title: Two-dimensional gel electrophoresis, protein electrophoresis and microsequencing
 A:Reference number: A61002; PMID:91031404; PMID:1699755
 A:Accession: A61002
 A:Molecule type: protein
 A:Residues: 1-14 <BAU>
 C:Keywords: chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 28.6%; Score 22; DB 2; Length 14;
 Best Local Similarity 33.3%; Pred. No. 1.6e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GEGDGYD 10
 DB 2 GVPPXITFD 10

RESULT 9
 B26501
 Lipoprotein lipase (EC 3.1.1.34) - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 28-Apr-1993
 C:Accession: B26501
 R:Bengtsson-Oliveria, G.; Oliveria, T.; Jernvall, H.
 Eur. J. Biochem. 161, 281-288, 1986
 A>Title: Lipoprotein lipases from cow, guinea-pig and man. Structural characterization a
 A:Reference number: A91178; PMID:87054027; PMID:3536511
 A:Accession: B26501
 A:Molecule type: protein
 A:Residues: 1-15 <BEN>
 C:Keywords: carboxylic ester hydrolase

Query Match 28.6%; Score 22; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GIDYD 10
 DB 4 GKDYD 8

RESULT 10
 S62880
 polylacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
 C:Species: Aspergillus sp.
 C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S62880
 R:Serrallona, E.; Dzurva, M.; Markovic, O.; Joernvall, H.
 FEBS Lett. 382, 164-166, 1996
 A>Title: An essential tyrosine residue of Aspergillus polylacturonase.
 A:Reference number: S62880; PMID:96196586; PMID:8612742
 A:Accession: S62880
 A:Molecule type: protein
 A:Residues: 1-10 <STR>
 C:Keywords: glycosidase; hydrolase
 F:4/Active site: Tyr #status predicted

Query Match 27.3%; Score 21; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGLEP 5
 DB 5 TGRKP 9

RESULT 11

PH1592
 Ig H chain V-D-J region (wild-type clone 143) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1592
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
 A:Reference number: PH1580; PMID:93301609; PMID:8315387
 A:Accession: PH1592
 A:Molecule type: DNA
 A:Residues: 1-10 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 27.3%; Score 21; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGIDY 9
 DB 6 PANDY 10

RESULT 12
 S19775
 wound-induced protein - tomato (fragment)
 C:Species: Lycopersicon esculentum (tomato)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
 C:Accession: S19775
 R:Parsons, B.L.
 submitted to the EMBL Data Library, May 1991
 A:Reference number: S19773
 A:Accession: S19775
 A:Molecule type: mRNA
 A:Residues: 1-11 <PAR>
 A:Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 27.3%; Score 21; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GIDY 9
 DB 7 GIDY 10

RESULT 13
 PH1583
 Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1583
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
 A:Reference number: PH1580; PMID:93301609; PMID:8315387
 A:Accession: PH1583
 A:Molecule type: DNA
 A:Residues: 1-11 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 27.3%; Score 21; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LEPIDY 9
 DB 5 LGPPMDY 11

RESULT 14

Tue Sep 21 07:04:08 2004

us-10-676-049-3.closed.rpr

Page 4

S18385
NADP-cytochrome P450 reductase-related protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 07-Feb-1997
C:Accession: S18385
R:Nadler, S.G.; Strobel, H.W.
Arch. Biochem. Biophys. 290, 277-284, 1991
A:Title: Identification and characterization of an NADPH-cytochrome P450 reductase deriv
A:Reference number: S18385; PMID:92027739; PMID:1929397
A:Accession: S18385
A:Molecule type: protein
A:Residues: 1-11 <NAD>
C:Keywords: NADP

Query Match 27.3%; Score 21; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 DYDI 11
|||:
Db 8 DYDL 11

RESULT 15

PA0071
superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - fungus (Fusarium sporotrichioides) (Fragment
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0071
R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JRPD, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0071
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Keywords: metalloprotein; oxidoreductase

Query Match 27.3%; Score 21; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGIDYDISVI 14
|:|:
Db 5 PDLPYDYGAL 14

Search completed: September 21, 2004, 06:46:07
Job time : 19.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2004, 06:14:13; Search time 10.6667 Seconds
(without alignments)
73.224 Million cell updates/sec

Title: US-10-676-049-3

Perfect score: 77

Sequence: 1 TGLBFGIDYDISVIT 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 801

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	33.8	14	1	DHSL_ANACY
2	25	32.5	10	1	GONI_ALUMI
3	23	29.9	10	1	GONI_CLOPA
4	22	28.6	12	1	V25K_WSSV
5	22	28.6	13	1	F1BB_RABIT
6	22	28.6	15	1	SODM_STRGR
7	21	27.3	10	1	UHAI_HUMAN
8	20	26.0	10	1	PAPI_PARMA
9	20	26.0	13	1	OPS3_DROVI
10	20	26.0	13	1	SODM_CANFA
11	20	26.0	13	1	YPE2_LACTC
12	19	24.7	8	1	UF06_MOUSE
13	19	24.7	10	1	VEG6_BACSU
14	19	24.7	10	1	UN12_CLOPA
15	19	24.7	13	1	GLGS_SPTOL
16	19	24.7	15	1	UC16_MAIZE
17	18	23.4	10	1	PNEU_HUMAN
18	18	23.4	10	1	PNEU_RAT
19	18	23.4	12	1	POED_MERTM
20	18	23.4	13	1	POED_HYDAT
21	18	23.4	14	1	COCO_LIMPO
22	18	23.4	14	1	IF2G_RAT
23	18	23.4	15	1	UN04_CLOPA
24	18	23.4	15	1	COXI_THOUB
25	18	23.4	15	1	PH2_BERAM
26	18	23.4	9	1	UPAF_HUMAN
27	17	22.1	10	1	PARF_LOCOM
28	17	22.1	13	1	MPI_MITOC
29	17	22.1	13	1	UN10_CLOPA
30	17	22.1	15	1	AVP2_CAVPO
31	17	22.1	15	1	DIDH_PSESP
32	17	22.1	15	1	MALT_BACTO
33	17	22.1	15	1	

34	17	22.1	15	1	UC29_MAIZE	P80635 zea mays (m
35	17	22.1	15	1	UP02_METAN	P83439 metarhizium
36	16	20.8	8	1	ALIS_CALVO	P41641 calliphora
37	16	20.8	10	1	ESL_LACCA	P81758 laccobacill
38	16	20.8	10	1	HTF_TABXT	P14586 tabanus atr
39	16	20.8	11	1	BPPB_AGRHA	P01021 agkistrodon
40	16	20.8	11	1	BPP AGKHP	P04562 agkistrodon
41	16	20.8	12	1	TAT0_TREME	P01371 tremella me
42	16	20.8	12	1	TM2A_METMA	P80652 methanosarc
43	16	20.8	13	1	CHEP_PAPID	P42718 parapolylbia
44	16	20.8	13	1	CRIC_BOVIN	P28489 bos taurus
45	16	20.8	15	1	48KD_BACCE	P80173 bacillus ce

ALIGNMENTS

RESULT 1	DHSL_ANACY	STANDARD;	PRT;	14 AA.
AC	P17874;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Soluble hydrogenase 50 kDa subunit (EC 1.12.--) (Fragment).			
OS	Anabaena cylindrica.			
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.			
OX	NCBI_TaxID=1165;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=90126821; PubMed=2129525;			
RA	Ewart G.D., Reed K.C., Smith G.D.;			
RT	"Soluble hydrogenase of Anabaena cylindrica. Cloning and sequencing			
RT	of a potential gene encoding the tritium exchange subunit."			
RL	Eur. J. Biochem. 187:215-223(1990).			
CC	-1- FUNCTION: SOLUBLE HYDROGENASE CATALYZES BOTH PRODUCTION AND			
CC	CONSUMPTION OF HYDROGEN FROM SUITABLE ARTIFICIAL ELECTRON DONORS			
CC	OR ACCEPTORS. THIS SUBUNIT (50 kDa) IS REQUIRED FOR HYDROGEN			
CC	PRODUCTION WITH REDUCED METHYL-VIOLOGEN.			
CC	-1- SUBUNIT: Heterodimer of a large and a small subunit.			
DR	PIR: S07768; S07768.			
KM	Oxidoreductase.			
FT	NON_TER			
SQ	SEQUENCE 14 AA; 1551 MW; 9254DARF141CFR2A CRC64;			
QY	8 DYDLSVI 14			
DB	5 DYDLVIT 11			
QY	8 DYDLSVI 14			
DB	5 DYDLVIT 11			
RESULT 2	GONI_ALUMI	STANDARD;	PRT;	10 AA.
AC	P37041; P20407;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Gonadolibetin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)			
DE	(Lutibetin I)			
OS	Alligator mississippiensis (American alligator).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Archosauria; Crocodylidae; Alligatorinae; Alligator.			
OX	NCBI_TaxID=8496;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Brain;			
RX	MEDLINE=91552338; PubMed=1882082;			
RA	Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,			

RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure of two forms of gonadotropin-releasing hormone
 from brains of the American alligator (Alligator mississippiensis).",
 RL Regul. Pept. 33:105-116(1991).
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the GnRH family.
 DR PIR: A60066; RHA01.
 DR InterPro: IPR002012; GnRH.
 DR Pfam: PF00446; GnRH; 1.
 DR PROSITE: PS00473; GnRH; 1.
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 AMIDATION.
 FT MOD_RES 10 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 32.5%; Score 25; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 2,4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GLEPG 6
 |||||
 Db 6 GLEPG 10

RESULT 3

GON1_CLUPA STANDARD; PRT; 10 AA.
 AC P81749;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH)
 DE (Luliberin I).
 GN GnRH.
 OS Clupea pallasi (Pacific herring).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
 OC Clupea.
 OX NCBI_Taxid=30724;
 RN [1]
 RP SEQUENCE AND FUNCTION.
 RC TISSUE=Brain, and pituitary;
 RX MEDLINE=20114351; PubMed=10650929;
 RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
 RA Chang J.P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure and function of three gonadotropin-releasing
 hormones, including a novel form, from an ancient teleost, herring.";
 RL Endocrinology 141:505-512(2000).
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the GnRH family.
 DR InterPro: IPR002012; GnRH.
 DR Pfam: PF00446; GnRH; 1.
 DR PROSITE: PS00473; GnRH; 1.
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 AMIDATION.
 FT MOD_RES 10 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1105 MW; 264B20B72871F5A3 CRC64;

Query Match 29.9%; Score 23; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GLEPG 6
 |||||
 Db 6 GLEPG 10

RESULT 4
 V25K_MSSV STANDARD; PRT; 12 AA.
 ID V25K_MSSV
 AC P82004;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 25 kDa structural polypeptide (Fragment).
 OS White spot syndrome virus (WSSV).
 OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
 OX NCBI_Taxid=92652;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=South Carolina;
 RX MEDLINE=20214217; PubMed=10752552;
 RA Wang Q., Poulos B.T., Lightner D.V.;
 RT "Protein analysis of geographic isolates of shrimp white spot syndrome
 virus.";
 RL Arch. Virol. 145:263-274(2000).
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
 CC NON_TER 12
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1283 MW; C5409AD9BCEB731A9 CRC64;

Query Match 28.6%; Score 22; DB 1; Length 12;
 Best Local Similarity 33.3%; Pred. No. 9e+02;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 IDYDISVT 15
 : : : : :
 Db 3 LSFILSVT 11

RESULT 5

FIBB_RABIT STANDARD; PRT; 13 AA.
 AC F14478;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen beta chain [contains: fibrinopeptide B] (Fragment).
 GN FGB.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Gron Dahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 polymerize into fibrin and acting as a cofactor in platelet
 aggregation.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 which cleaves fibrinopeptides A and B from alpha and beta chains,
 and thus exposes the N-terminal polymerization sites responsible
 for the formation of the soft clot.
 DR InterPro: IPR002181; Fibrinogen C.
 DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma; Sulfation.
 FT MOD_RES 1 SULFATION.
 FT MOD_RES 4 FIBRINOPEPTIDE B.
 FT MOD_RES 13 FIBRINOPEPTIDE B.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CBA1A CRC64;

Query Match 28.6%; Score 22; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 9,8e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 DYDISVT 14
 |||||
 Db 3 DYDDEVLT 9

RESULT 6

SODM_STRGR STANDARD; PRT; 15 AA.

ID SODM_STRGR

AC P80733;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).

GN SOD2.

OS Streptomyces griseus.

OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;

OC Streptomycetaceae; Streptomyces.

OC NCBI_TaxId=1911;

OX [1]

RP SEQUENCE.

RP STRAIN=KCTC 9006; PubMed=8900409;

RX MEDLINE=97056064; PubMed=8900409;

RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Han Y.C., Kang S.-O.;

RT "Unique isozymes of superoxide dismutase in Streptomyces griseus"; Arch. Biochem. Biophys. 334:341-348 (1996).

RL -1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.

CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

CC -1- COFACTOR: Binds 1 iron or zinc ion per subunit (By similarity).

CC -1- SUBUNIT: Tetramer.

CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.

DR InterPro: IPR001189; SODismutase.

DR Pfam: PF00061; sode, 1.

DR PROSITE: PS00068; SOD_MN, PARTIAL.

KW Oxidoreductase; Metal-binding; Iron; Zinc.

FT NON TER 15 15

SQ SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;

Query Match 28.6%; Score 22; DB 1; Length 15;

Best Local Similarity 66.7%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 EPGIDY 9

Db 7 EPPYDY 12

RESULT 7

UHA3_HUMAN STANDARD; PRT; 10 AA.

ID UHA3_HUMAN

AC P40930;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

OX [1]

RP SEQUENCE.

RP TISSUE=Heart;

RX MEDLINE=95203287; PubMed=7895732;

RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;

RT "The human myocardial two-dimensional gel protein database: update 1994"; J. Electrophoresis 15:1453-1465 (1994).

RL Electrophoresis 15:1453-1465 (1994).

CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.8, its MW is: 47.3 kDa.

FT NON TER 10 10

SQ SEQUENCE 10 AA; 1049 MW; 6B8CDEA1A041876B CRC64;

Query Match 27.3%; Score 21; DB 1; Length 10;

Best Local Similarity 57.1%; Pred. No. 1.1e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LEPGIDY 9

Db 2 VEPTTY 8

RESULT 8

PAP1_PAPMA STANDARD; PRT; 10 AA.

ID PAP1_PAPMA

AC P81863;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Pardaxin I (PX1) (Fragment).

OS Pardachinus marmoratus (Red sea moses sole).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuroctiformes;

OC Soleiidae; Soleidae; Pardachinus.

OX NCBI_TaxId=31087;

OX [1]

RP SEQUENCE.

RP TISSUE=Skin secretion;

RX MEDLINE=87057369; PubMed=3782138;

RA Lazarovici P., Primor N., Loew L.M.;

RT "Purification and pore-forming activity of two hydrophobic polypeptides from the secretion of the Red sea moses sole (Pardachinus marmoratus)"; J. Biol. Chem. 261:16704-16713 (1986).

RL -1- FUNCTION: Exhibits unusual shark repellent and surfactant properties. Forms voltage-dependent, ion-permeable channels in membranes. At high concentration causes cell membrane lysis. Shown to be 5-10 times more toxic, cytolytic and active in membrane pore formation than pardaxin II.

CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the pardaxin family.

KW Toxin.

FT NON TER 10 10

SQ SEQUENCE 10 AA; 1063 MW; D399C36760572DD9 CRC64;

Query Match 26.0%; Score 20; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 1.6e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LEPGID 8

Db 5 LIPGIE 10

RESULT 9

OPS3_DROVI STANDARD; PRT; 12 AA.

ID OPS3_DROVI

AC P17645;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Opsin Rh3 (Inner R7 photoreceptor cells opsin) (Fragment).

OS Drosophila virilis (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxId=7244;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90249748; PubMed=2140105;

RA Fortini M.E., Rubin G.M.;

RT "Analysis of cis-acting requirements of the Rh3 and Rh4 genes reveals a bipartite organization to rhodopsin promoters in Drosophila melanogaster"; J. Genes Dev. 4:444-463 (1990).

RL -1- FUNCTION: Visual pigments are the light-absorbing molecules that mediate vision. They consist of an apoprotein, opsin, covalently linked to cis-retinal.

```

CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC -1- MISCELLANEOUS: Each Drosophila eye is composed of 800 facets or
CC CC ommatidia. Each ommatidium contains 8 photoreceptor cells (R1-R8),
CC CC the R1 to R6 cells are outer cells, while R7 and R8 are inner
CC CC cells.
CC CC -1- MISCELLANEOUS: Opsin Rh3 is sensitive to UV light.
CC CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC CC Opsin subfamily.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: X51350; CA35742.1; -.
CC CC FlyBase: FBgn0013091; DvIR.Rh3.
CC CC InterPro: IPR000276; GPCR_Rhodopsin.
CC CC DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; PARTIAL.
CC CC PROSITE: PS00238; OPSIN; PARTIAL.
CC CC KMW Photoreceptor; Retinal protein; Transmembrane; Phosphorylation;
CC CC Glycoprotein; G-protein coupled receptor; Vision.
CC CC FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (PROBABLE).
CC CC FT NON_TER 12 12
CC CC SQ SEQUENCE 12 AA; 1253 MW; 04024F3495865B0 CRC64;

Query Match 26.0%; Score 20; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 7 IDYDISYI 14
   |::|||
Db 1 MDENISGI 8

RESULT 10
ID SODM CANFA STANDARD; PRT; 13 AA.
AC PS4712;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
GN SOD2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC HSC-2DPAGE; PS4712; DOG.
CC InterPro: IPR001189; SODismutase.
CC Pfam: PR00081; sodfe; 1.
CC PROSITE: PS00088; SOD_MN; PARTIAL.
CC Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
CC NON_TER 13 13

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SQ SEQUENCE 13 AA; 1476 MW; 9C9651DE8BE0672A CRC64;
Query Match 26.0%; Score 20; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 5 PEIDYD 10
   |::|||
Db 5 PDLPYD 10

RESULT 11
ID YPB2_LACLC STANDARD; PRT; 13 AA.
AC P42021;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PPV 5' region (ORF2) (Fragment).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OC NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245610; PubMed=8186586;
RA Mierau I., Handrikman A.J., Vetterop O., Tan P.S.T., Leenhouts K.L.,
RA Konings W.N., Venema G., Kok J.;
RT "Tripeptidase gene (pepT) of Lactococcus lactis: molecular cloning
RT and nucleotide sequencing of pepT and construction of a chromosomal
RT deletion mutant."
RL J. Bacteriol. 176:2854-2861(1994).
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: L27596; AAA20625.1; -.
CC CC KMW Hypothetical protein.
CC CC FT NON_TER 1
CC CC SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;

Query Match 26.0%; Score 20; DB 1; Length 13;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TGLEPGI 7
   |::|||
Db 2 TAREPFI 8

RESULT 12
ID UF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Micher L.V., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."

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RL Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.2, its MW is: 50 kDa.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 817 MW; A35DB878676B05B1 CRC64;

Query Match 24.7%; Score 19; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 EPGIDY 9
 DB 3 EPGGAY 8

RESULT 13

FARS CALVO STANDARD; PRT; 9 AA.
 ID FARS CALVO
 AC P41860;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRamide 5.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OC NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Dive H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rahfeld J.F., Thorpe A., and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 DR PIR; E41578; E41978.
 KW Neuropeptide; Amidation.
 FT MOD_RSS 9
 SQ SEQUENCE 9 AA; 1068 MW; 39D10699CAB6D667 CRC64;

Query Match 24.7%; Score 19; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGIDY 9
 DB 2 PGDGF 6

RESULT 14

VEG6_BACSU STANDARD; PRT; 10 AA.
 ID VEG6_BACSU
 AC P80659;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vegetative protein 6 (VEG6) (Fragment).
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=168 / ISS5;
 RX MEDLINE=97237728; PubMed=9084183;
 RA Schmidt R., Bernhardt J., Antelmann H., Voelker U., Mach H.,
 RA Voelker A., Hecker M.;
 RT "Identification of vegetative proteins for a two-dimensional protein
 index of Bacillus subtilis.";

RL Microbiology 143:991-998(1997).
 CC -1- CAUTION: Could not be found in the genome of B.subtilis 168.
 CC protein is: 10, its MW is: 10 kDa.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 973 MW; 8793A6B2C8772861 CRC64;

Query Match 24.7%; Score 19; DB 1; Length 10;
 Best Local Similarity 62.5%; Pred. No. 2.3e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 TGLEPGID 8
 DB 3 TGL--GVD 8

RESULT 15

UN12_CLOPA STANDARD; PRT; 13 AA.
 ID UN12_CLOPA
 AC P81353;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 12 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=M5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.8, ITS MW IS: 42.7 kDa.
 FT VARIANT 4
 FT NON TER 5
 FT VARIANT 5
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1465 MW; 70AA9E98455D405B CRC64;

Query Match 24.7%; Score 19; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LEFGI 7
 DB 7 INPGI 11

Search completed: September 21, 2004, 06:41:18
 Job time : 11.6667 secs

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OM protein - protein search, using sw model

Run on: September 21, 2004, 06:30:41; Search time 58.3333 Seconds
(without alignments)
81.133 Million cell updates/sec

Title: US-10-676-049-3

Perfect score: 77
Sequence: 1 TGLEPGIDYDISVIT 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3954

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL.25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	32.5	15	3 Q9UR90	Q9UR90 saccharomyc
2	23	29.9	14	2 Q44172	Q44172 synchococc
3	23	29.9	15	4 Q9UC00	Q9UC00 homo sapien
4	22	28.6	11	11 P97755	P97755 rattus norv
5	22	28.6	12	10 P82334	P82334 pisum sativ
6	22	28.6	13	8 Q8WEJ8	Q8WEJ8 gnetum gnet
7	22	28.6	13	8 Q8SHT3	Q8SHT3 gnetum nodi
8	22	28.6	14	10 P82340	P82340 pisum sativ
9	21	27.3	11	5 P82208	P82208 bombyx mori
10	21	27.3	11	10 Q04131	Q04131 lycopersico
11	21	27.3	15	5 Q9TWE1	Q9TWE1 plasmodium
12	20	26.0	6	5 P83569	P83569 sepia offic
13	20	26.0	9	7 Q31415	Q31415 gallus gall
14	20	26.0	10	11 Q9QVE8	Q9QVE8 mus sp. pro
15	20	26.0	11	6 Q9TRX0	Q9TRX0 sus scrofa
16	20	26.0	11	7 Q19718	Q19718 homo sapien

17	20	26.0	14	3 Q8J1G3	Q8J1G3 ashbya goss
18	20	26.0	15	4 Q9UCB9	Q9UCB9 homo sapien
19	20	26.0	15	11 Q9QV25	Q9QV25 rattus sp.
20	19	24.7	9	5 Q96417	Q96417 drosophila
21	19	24.7	11	2 P96319	P96319 desulfovibr
22	19	24.7	11	6 Q8H1W4	Q8H1W4 felis silve
23	19	24.7	13	6 Q865C9	Q865C9 sus scrofa
24	19	24.7	14	4 Q9P2A2	Q9P2A2 homo sapien
25	19	24.7	15	2 Q9R5L9	Q9R5L9 bacillus st
26	19	24.7	15	4 Q9UCD5	Q9UCD5 homo sapien
27	19	24.7	15	6 Q9TRR5	Q9TRR5 cycotolagus
28	19	24.7	15	8 Q9TR79	Q9TR79 pyralisella
29	18	23.4	10	6 Q9TR48	Q9TR48 bos taurus
30	18	23.4	10	11 Q9QVE9	Q9QVE9 mus sp. pro
31	18	23.4	11	12 Q8QGN9	Q8QGN9 tomato leaf
32	18	23.4	12	4 Q16452	Q16452 homo sapien
33	18	23.4	13	5 Q9TRR4	Q9TRR4 rattus seir
34	18	23.4	13	8 Q8WEK0	Q8WEK0 cycas clirci
35	18	23.4	14	1 Q9TMM2	Q9TMM2 pyrococcus
36	18	23.4	14	10 Q941T6	Q941T6 itagaria nu
37	18	23.4	14	10 Q9S8X6	Q9S8X6 glycine max
38	18	23.4	15	2 Q46456	Q46456 clostridium
39	18	23.4	15	4 Q9UC90	Q9UC90 homo sapien
40	18	23.4	15	5 P82211	P82211 bombyx mori
41	18	23.4	15	6 Q9TRN5	Q9TRN5 sus scrofa
42	17.5	22.7	15	2 P83071	P83071 bacillus ce
43	17.5	22.7	15	4 Q9UC04	Q9UC04 homo sapien
44	17	22.1	8	6 Q8WNS1	Q8WNS1 bos taurus
45	17	22.1	9	4 Q96T78	Q96T78 homo sapien

ALIGNMENTS

RESULT 1
Q9UR90 PRELIMINARY; PRT; 15 AA.
ID Q9UR90;
AC Q9UR90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Cyclophilin A (Fragment).
DS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
CX NCBI_TaxID=4932;
RN (1)
RP
RX MEDLINE=93278320; PubMed=1304384;
RA Zydeowsky L.D., Ho S.I., Baker C.H., McIntyre K., Walsh C.T.;
RT "Overexpression, purification, and characterization of yeast
RT cyclophilins A and B".
RL Protein Sci. 1:961-969(1992).
SQ SEQUENCE 15 AA; 1648 MW; 9FD36BDC370A405 CRC64;

Query Match 32.5%; Score 25; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 IDYDISVIT 15
|||
Db 7 IDQDDVEIT 15
RESULT 2
ID Q44172 PRELIMINARY; PRT; 14 AA.
AC Q44172;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Cpca protein (Fragment).
GN CPCA.

OS *Synechococcus* sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.
CX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR6009;
RA de Lorimer R., Guglielmi G., Bryant D.A., Stevens S.E.;
RT "Structure and mutation of a gene encoding a Mr 33000 phycocyanin-
associated linker polypeptide."
RL Arch. Microbiol. 153:541-549(1990).
DR EMBL: X81868; CA57456.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1601 MW; 98D40C7EP60CDAA5A CRC64;

Query Match 29.3%; Score 23; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 4.1e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 IDYDISVIT 15
DB 6 IDYAINALS 14

RESULT 3

OSUCCO
ID Q9UCCO PRELIMINARY; PRT; 15 AA.
AC Q9UCCO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Insulin-like growth factor receptor alpha subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94079865; PubMed=825768;
RA Kasuya U., Paz I.B., Maddux B.A., Goldfine I.D., Hefta S.A.,
RA Fujita-Yamaguchi Y.;
RT "Characterization of human placental insulin-like growth factor-
RT I/insulin hybrid receptors by protein microsequencing and
RT purification."
RL Biochemistry 32:13531-13536(1993).
SQ SEQUENCE 15 AA; 1721 MW; 98BC15D6D81784B CRC64;

Query Match 29.9%; Score 23; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 PGID 8
DB 5 PGID 8

RESULT 4

OSUCCO
ID P97755 PRELIMINARY; PRT; 11 AA.
AC P97755;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Secretogranin II (SGII) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
SQ SEQUENCE=66343805; PubMed=8756552;

RL Endocrinology 137:3815-3822(1996).
DR EMBL: AF107301; -; NOT_ANNOTATED_CDS.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1298 MW; 3E4E8DA446C1B5A7 CRC64;

Query Match 28.6%; Score 22; DB 11; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 LEFGIDY 9
DB 2 LEFSTOY 8

RESULT 5

OSUCCO
ID P82334 PRELIMINARY; PRT; 12 AA.
AC P82334;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ferredoxin (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
CX NCBI_TaxID=3886;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RX STRAIN=cv. DE GRACE; TISSUE=LEAF;
RA MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins."
RL Plant Cell 12:319-341(2000).
CC -1- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER
CC ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.
CC -1- CORACOR: BINDS A 2FE-2S CLUSTER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST STROMAL SIDE OF THE THYLAKOID
CC MEMBRANE.
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.1, ITS MW IS: 27.9 KDA.
CC -1- SIMILARITY: BELONGS TO THE 2FE2S PLANT-TYPE FERREDOXIN FAMILY.
DR GO: GO:0009579; C:chloroplast; IEA.
DR GO: GO:0009579; C:chloroplast; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR PROSITE: PS00197; 2FE2S FERREDOXIN; PARTIAL.
KW Chloroplast; Thylakoid; Electron transport; Iron-sulfur.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1376 MW; 16933A25A572330 CRC64;

Query Match 28.6%; Score 22; DB 10; Length 12;
Best Local Similarity 57.1%; Pred. No. 5.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 9 YDISVIT 15
DB 3 YNKTUIT 9

RESULT 6

OSUCCO
ID Q8WEJ8 PRELIMINARY; PRT; 13 AA.
AC Q8WEJ8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase (Fragment).
SQ SEQUENCE=66343805; PubMed=8756552;

OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Gnepophyta; Gnepopsida; Gnetales; Gnetales; Gnetales;
 OC NCBI_Taxid=3389;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21555473; PubMed=11697913;
 RA Gagerli F., Sperisen C., Buchler U., Brunner I., Brodbeck S.,
 RA Palmer J.D., Qu Y.L.;
 RT "The evolutionary split of pinaceae from other conifers: evidence from
 an intron loss and a multigene phylogeny."
 RL Mol. Phylogenet. Evol. 21:167-175(2001).
 DR EMBL; AF227467; AAL8911.1;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1 1
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1437 MW; DB0F6BCAF94945A2 CRC64;
 QY Query Match 28.6%; Score 22; DB 8; Length 13;
 Best Local Similarity 28.6%; Pred. No. 5.6e+03;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Db 2 VSTVSVI 8

RESULT 7
 085HT3 PRELIMINARY; PRT; 13 AA.
 ID 085HT3;
 AC 085HT3;
 DT 01-JUN-2003 (TRENBLREL. 24, Created)
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NADH.
 OS Gnetum nodiflorum.
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Gnepophyta; Gnepopsida; Gnetales; Gnetales; Gnetales;
 OC NCBI_Taxid=45078;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mon H., Renner S.S.;
 RT "Horizontal gene transfer from flowering plants to Gnetum."
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY231297; AAP32080.1;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1 1
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1437 MW; DB0F6BCAF94945A2 CRC64;
 QY Query Match 28.6%; Score 22; DB 8; Length 13;
 Best Local Similarity 28.6%; Pred. No. 5.6e+03;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Db 2 VSTVSVI 8

RESULT 8
 P82340 PRELIMINARY; PRT; 14 AA.
 ID P82340;
 AC P82340;
 DT 01-JUN-2000 (TRENBLREL. 14, Created)
 DT 01-JUN-2000 (TRENBLREL. 14, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Unknown protein from 2D-page of thylakoid lumen (SPOT204) (Fragment).
 OS Pisum sativum (Garden pea)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_Taxid=3888;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
 RX MEDLINE=20181728; PubMed=10715320;
 RA Pelletier U.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 targeting analysis of lumenal and peripheral thylakoid proteins."
 RL Plant Cell 12:319-341(2000).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
 CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 DR GO; GO:0009597; C:chloroplast; IEA.
 DR GO; GO:0009579; C:thylakoid; IEA.
 KW Chloroplast; Thylakoid.
 FT NON TER 14 14
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1505 MW; 2EABFAF980F3D7D7 CRC64;
 QY Query Match 28.6%; Score 22; DB 10; Length 14;
 Best Local Similarity 37.5%; Pred. No. 6.1e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Db 3 SGFQPVVD 10

RESULT 9
 P82208 PRELIMINARY; PRT; 9 AA.
 ID P82208;
 AC P82208;
 DT 01-OCT-2001 (TRENBLREL. 18, Created)
 DT 01-OCT-2001 (TRENBLREL. 18, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 GN Bombyx mori (Silk moth).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OC NCBI_Taxid=7051;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=XINXANG X KEMING; TISSUE=Body wall, and Fat body;
 RX MEDLINE=21177481; PubMed=11280994;
 RA Zhong B.X.;
 RT "Protein database for several tissues derived from five instar of
 silkworm."
 RL I Chuan Hsueh Pao 28:217-224(2001).
 FT NON TER 9 9
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1009 MW; 377C3AB45B042D7 CRC64;
 QY Query Match 27.3%; Score 21; DB 5; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 2 PVISYD 7

RESULT 10
 Q04131 PRELIMINARY; PRT; 11 AA.
 ID Q04131;
 AC Q04131;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Wound induced protein (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Solanales; Solanaceae; Solanum.
OK NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pk-red; Tissue=Pericarp;
RX MEDLINE=9135536; PubMed=1715787;
RA Parsons B.L., Martoo A.K.;
RT "Wound regulated accumulation of specific transcripts in tomato fruit:
interactions with fruit development, ethylene and light.";
RL Plant Mol. Biol. 17:453-464(1991).
DR EMBL/ X59884; CAA42539.1; -
DR PIR/ S19775; S19775.
FT NON TER
SQ SEQUENCE 11 AA; 1278 MW; 92CB25782873325 CRC64;

Query Match 27.3%; Score 21; DB 10; Length 11;
Best Local Similarity 75.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GIDY 9
Db 7 GLDY 10

RESULT 11

09TWE1 PRELIMINARY; PRT; 15 AA.
AC O9TWE1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Glutathione disulfide reductase (EC 1.6.4.2) (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE.
RX MEDLINE=96202957; PubMed=8631352;
RA Krauth-Stegel R.L., Muller J.G., Lottspeich F., Schluter R.H.;
RT "Glutathione reductase and glutamate dehydrogenase of Plasmodium
falciparum, the causative agent of tropical malaria.";
RL Eur. J. Biochem. 235:345-350(1996).
DR PIR/ S62609; S62609.
SQ SEQUENCE 15 AA; 1409 MW; 2CB94C0B4DA247F6 CRC64;

Query Match 27.3%; Score 21; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 9.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 9 YDISVT 14
Db 2 YDLIVI 7

RESULT 12

P83569 PRELIMINARY; PRT; 6 AA.
AC P83569;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Sperm attracting peptide SepSaP.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND
RP AMIDATION.
RX TISSUE=ESG;
RX PubMed=12207899;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;

RT attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).
CC -!- FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE
CC COLLISION
CC -!- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE OVARIAN FOLLICLES FIRING
CC VITELLOGENESIS. ACCUMULATES IN THE OOCYTES BEFORE BEING SECRETED
CC DURING FERTILIZATION. EXPRESSION CONTINUES IN THE EMBEDDED OOCYTE.
CC ACCUMULATES IN THE EGG CAPSULE AFTER FERTILIZATION.
CC -!- MASS SPECTROMETRY: MW=596.6; METHOD=MALDI.
KM Amidation.
FT MOD RES
SQ SEQUENCE 6 AA; 597 MW; 72C8676AA0470000 CRC64;

Query Match 26.0%; Score 20; DB 5; Length 6;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 3 LEPTG 7
Db 2 IDPGV 6

RESULT 13

031415 PRELIMINARY; PRT; 9 AA.
AC 031415;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE MHC class I antigen (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kanki T., Kuwasawa N., Sekiya Y., Ichikawa Y.;
RT "Responsive expression of a MHC class I epitope and genes following
Marek's disease virus infection.";
RL Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL/ D90399; BA14395.1; -
DR PIR/ JQ0914; JQ0914.
FT NON TER
SQ SEQUENCE 9 AA; 859 MW; BA55A76455B861B5 CRC64;

Query Match 26.0%; Score 20; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TGLEPGI 7
Db 3 TGSNPSI 9

RESULT 14

09QVE8 PRELIMINARY; PRT; 10 AA.
AC 09QVE8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMP2/16 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinge A., Debarle M., Sautiere P., Chevallier P.;
RT "Molecular characterization of six intermediate proteins in the

RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1224 MW; D4050B040B11EAB6 CRC64;

Query Match 26.0%; Score 20; DB 11; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGIDYD 10
|||:
1 PGQDHE 6

RESULT 15

Q9TRX0 PRELIMINARY; PRT; 11 AA.
AC Q9TRX0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lanosterol 14 alpha-demethylase, cytochrome P-45014DM (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=91316123; PubMed=1859829;
RA Sono H., Sonoda Y., Sato Y.;
RT "Purification and characterization of cytochrome P-45014DM (lanosterol
14 alpha-demethylase) from pig liver microsomes.";
RL Biochim. Biophys. Acta 1078:388-394(1991).
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1084 MW; 8A7A5CB2AA72861 CRC64;

Query Match 26.0%; Score 20; DB 6; Length 11;
Best Local Similarity 57.1%; Pred. No. 1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GLEPGID 8
|||:
Db 1 GLLTGLD 7

Search completed: September 21, 2004, 06:45:09
Job time : 59.333 secs

Blank

OM protein - protein search, using sw model

Run on: September 21, 2004, 05:57:18 ; Search time 72.3333 Seconds

(without alignment)

Title: US-10-676-049-3

Perfect score: 77

Sequence: 1 TGLEPCIDYDISVIT 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 156107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 447529

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: Genesegp180s:.*
2: Genesegp190s:.*
3: Genesegp2000s:.*
4: Genesegp2001s:.*
5: Genesegp2002s:.*
6: Genesegp2003as:.*
7: Genesegp2003bs:.*
8: Genesegp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	15	AAO17877	AAO17877 EDB_fibro
2	64	83.1	15	AAO4093	AAO4093 AntiLentiv
3	64	83.1	15	AAO8821	AAO8821 EDB-anti
4	56	72.7	15	AAO17876	AAO17876 EDB_fibro
5	48	62.3	15	AAO19571	AAO19571 Fibrinoge
6	48	62.3	15	AAO19567	AAO19567 Fibrinoge
7	48	62.3	15	AAO19570	AAO19570 Fibrinoge
8	48	62.3	15	AAO19575	AAO19575 Fibrinoge
9	47	61.0	15	AAO19573	AAO19573 Fibrinoge
10	44	57.1	15	AAO19569	AAO19569 Fibrinoge
11	43	55.8	15	AAO19574	AAO19574 Fibrinoge
12	39	50.6	15	AAO48854	AAO48854 Peptide I
13	39	50.6	15	AAO19568	AAO19568 Peptide I
14	36	46.8	15	AAO19566	AAO19566 Peptide h
15	34	44.2	11	ABR75726	ABR75726 Liver tes
16	32	41.6	15	AAO29719	AAO29719 Mycobacte
17	31	40.3	10	ABP16861	ABP16861 HIV B07 s
18	31	40.3	10	ABP19000	ABP19000 HIV B62 s
19	31	40.3	11	AAO88267	AAO88267 Hsp-65 pe
20	29	37.7	9	AAO07133	AAO07133 Synthetic
21	29	37.7	11	AAO00499	AAO00499 Hepatitis
22	29	37.7	14	AAO57578	AAO57578 Moraxella
23	29	37.7	14	AAO55094	AAO55094 M. catarr
24	29	37.7	14	AAO97011	AAO97011 Human pep
25	29	37.7	15	AAO81622	AAO81622 Heat choc

26	29	37.7	15	2	AAO99629
27	29	37.7	15	5	AAO49397
28	29	37.7	15	5	ABP46771
29	28	36.4	9	4	AAO24947
30	28	36.4	10	2	AAO37239
31	28	36.4	10	4	AAO24617
32	28	36.4	10	4	AAO24815
33	28	36.4	11	4	ABP15906
34	28	36.4	12	3	AAO93166
35	28	36.4	12	3	AAO32225
36	27.5	35.7	10	3	AAO27511
37	27.5	35.7	10	3	AAO27510
38	27.5	35.7	10	6	ABU52442
39	27.5	35.7	10	6	ABU52443
40	27	35.1	7	4	ABO84977
41	27	35.1	9	4	ABO98539
42	27	35.1	9	4	ABO98546
43	27	35.1	10	2	AAO40221
44	27	35.1	10	4	AAO86098
45	27	35.1	12	2	AAO21261

ALIGNMENTS

RESULT 1
AAO17877
ID AAO17877 standard; peptide: 15 AA.
XX
AC AAO17877;
XX
DT 20-AUG-2002 (first entry)
XX
DE EDB_fibronectin domain binding peptide #3.
XX
KM EDB_fibronectin domain; EDBFD; angiogenesis; gene therapy; transplant;
XX
KW Implant; receptor molecule interaction.
XX
OS Unidentified.
XX
PN WO200220563-A2.
XX
PD 14-MAR-2002.
XX
PF 30-AUG-2001; 2001WO-EP010016.
XX
PR 07-SEP-2000; 2000DE-01045803.
XX
PR 02-MAY-2001; 2001DE-01023133.
XX
PA (SCHD) SCHERING AG.
XX
PA (REDL) REDLITZ A.
XX
PA (KOPF) KOPF M.
XX
PA (EGNE) EGNER U.
XX
PA (BAHR) BAHR I.
XX
PA (MENR) MENRAD A.
XX
PI Menrad A;
XX
DR WPI; 2002-479458/51.
XX
PT New proteins binding specifically to the ED-b fibronectin domain, are
XX
PT cell adhesion and proliferation mediators useful e.g. in screening tests.
XX
PS Claim 2; Page 41; 66pp; German.
XX
CC The present invention relates to a new protein which binds specifically
XX
CC to the EDB_fibronectin domain (EDBFD), is specifically expressed or
XX
CC activated in endothelial cells, stromal cells of a tumour and tumour
XX
CC cells, and has an apparent molecular weight of 120-130 kDa for the light
XX
CC chain and 150-160 kDa for the heavy chain. The protein can be used to
XX
CC screen compounds which bind to EDBFD or its receptor, for coating
XX
CC surfaces to which endothelial cells bind, in cell cultures, in
XX
CC combination with transplants or in combination with implants

CC (specifically lung implants, artificial heart pacemakers or valves,
 CC vascular implants, endoprostheses, screws, bars, plates, wires, nails,
 CC rods, artificial joints, breast implants, artificial cranial plates,
 CC false teeth, tooth fillings or tooth bridges, as it improves the
 CC integration of transplants or implants in the body. The protein is also
 CC useful in clarifying EDB-specific adhesion mechanisms and receptor
 CC molecule interactions involved in angiogenesis. The present sequence is a
 CC protein of the invention
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISYT 15
 Db 1 TGLEPGIDYDISYT 15

RESULT 2

AA04093
 ID AA04093 standard; protein; 15 AA.

AC AA04093;

DT 25-MAR-2003 (revised)
 DT 10-SEP-1990 (first entry)

XX Antigenic determinant of anti-ED-B antibody.

DE ED-B; fibronectin; cancer; oncogenesis.

XX Synthetic.

XX JF02076598-A.

PD 15-MAR-1990.

XX 14-SEP-1988; 88JP-00230458.

PR 14-SEP-1988; 88JP-00230458.

PA (FUJITA GAKUEN G H.

PA (SAGA) OTSUKA PHARM CO LTD.

DR WPI; 1990-128252/17.

PT Anti ED-B antibody - has antigen determinant having 1 of 3 specific

PS sequences of 16, 16 or 14 aminoacid(s).

PS Claim 1; Page 623; 15PP; Japanese.

CC The peptide is the antigenic determinant of ED-B, the region of
 CC cartonomatous fibronectin (CFN), with no cross reactivity with cellular
 CC FN, plasmin FN etc. Antibodies raised against the peptide are useful in
 CC screening for CFN and thus cancer, and in immuno-purification of of ED-B
 CC or CFN. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 15 AA;

Query Match 83.1%; Score 64; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDIS 12
 Db 4 TGLEPGIDYDIS 15

RESULT 3

AA08821
 ID AA08821 standard; peptide; 15 AA.

XX AAE08821;
 AC
 XX 19-NOV-2001 (first entry)
 DT
 XX ED-B antigenic determinant #2.
 DE
 XX ED-B domain; cytotoxic; antigenic determinant; coagulant; fibronectin;
 XX tumor; ocular disorder; psoriasis; vascular proliferation; angiogenesis;
 XX rheumatoid arthritis; blood vessel occlusion; blood coagulation.
 KW
 XX Unidentified.

OS
 XX WO200162800-A1.
 PN
 XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-EP002062.
 PF
 XX 24-FEB-2000; 2000US-00512082.

XX (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.
 XX Neri D, Tatti L, Viti F, Birchler M;
 PI
 XX WPI; 2001-541701/60.

DR
 XX An antibody, with specific affinity for a characteristic epitope of the
 PT ED-B domain of fibronectin for the treatment of diseases characterized by
 PT vascular proliferation.

XX Disclosure; Page 3; 73pp; English.

XX The invention relates to an antibody with specific affinity for a
 CC characteristic epitope of the ED-B domain of fibronectin, where the
 CC antibody has improved affinity to ED-B. The invention also relates to
 CC conjugates comprising antibodies with a suitable photoactive molecule
 CC useful in the detection and/or coagulation of blood vessels. An antibody
 CC with improved affinity to the ED-B domain is useful for diagnosis and
 CC therapy of tumours and diseases characterised by vascular proliferation,
 CC cancer, rheumatoid arthritis, neo-vasculature associated ocular disorders
 CC and psoriasis. Treatment of angiogenesis related pathologies comprises
 CC the injection of conjugates comprising antibody and a molecule capable of
 CC inducing blood coagulation and blood vessel occlusion. The present
 CC sequence is ED-B antigenic determinant related to the invention

XX Sequence 15 AA;

Query Match 83.1%; Score 64; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDIS 12
 Db 4 TGLEPGIDYDIS 15

RESULT 4

AA017876
 ID AA017876 standard; peptide; 15 AA.

AC AA017876;

DT 20-AUG-2002 (first entry)

DE EDB fibronectin domain binding peptide #2.

XX EDB fibronectin domain; EDBD; angiogenesis; gene therapy; transplant;
 KW implant; receptor molecule interaction.
 XX Unidentified.

XX WO200220563-A2.

XX 14-MAR-2002.
 PD 30-AUG-2001; 2001WO-EP010016.
 PF 07-SEP-2000; 2000DE-01045803.
 XX 02-MAY-2001; 2001DE-01023133.
 PR (SCHD) SCHERING AG.
 XX (REDL) REDLITZ A.
 PA (KOPF) KOPFITZ M.
 PA (EGNE) EGNER U.
 PA (BAHR) BAHR I.
 PA (WENR) WENRAD A.
 XX Menrad A;
 PI WPI; 2002-479458/51.
 DR New proteins binding specifically to the ED-b fibronectin domain, are
 XX cell adhesion and proliferation mediators useful e.g. in screening tests.
 PT Claim 2; Page 41; 66pp; German.
 XX
 CC The present invention relates to a new protein which binds specifically
 CC to the ED-b fibronectin domain (EDbPD), is specifically expressed or
 CC activated in endothelial cells, stromal cells of a tumour and tumour
 CC cells, and has an apparent molecular weight of 120-130 kDa for the light
 CC chain, and 150-160 kDa for the heavy chain. The protein can be used to
 CC screen compounds which bind to EDbPD or its receptor, for coating
 CC surfaces to which endothelial cells bind, in cell cultures, in
 CC combination with transplants or in combination with implants
 CC (specifically lung implants, artificial heart pacemakers or valves,
 CC vascular implants, endoprotheses, screws, bars, plates, wires, nails,
 CC rods, artificial joints, breast implants, artificial cranial plates,
 CC false teeth, tooth fillings or tooth bridges, as it improves the
 CC integration of transplants or implants in the body. The protein is also
 CC useful in clarifying EDB-specific adhesion mechanisms and receptor
 CC molecule interactions involved in angiogenesis. The present sequence is a
 CC protein of the invention
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 72.7%; Score 56; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0079;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGLRPGIDYD 10
 DB 6 TGLRPGIDYD 15
 XX
 RESULT 5
 ID AAB19571 standard; peptide; 15 AA.
 AC AAB19571;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Fibrinogen-derived peptide with anti-cell adhesion activity.
 XX
 KW Cell adhesion; inhibitor; antimetastatic; metastasis; cancer; antitumour;
 KW antiinflammatory; antithrombotic; antiaesthetic; antiallergic;
 KW antithrombotic; antifibrotic; immunostimulant; vulnerary; therapy;
 KW fibronectin; human; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX EP1036798-A1.
 PN
 PA
 XX
 XX 20-SEP-2000.

XX 16-MAR-2000; 2000EP-00105572.
 PF 16-MAR-1999; 99JP-00070127.
 XX
 PR (HISM) HISAMITSU PHARM CO LTD.
 XX
 PA Akiyama K, Goto T, Fukai F, Ueki M;
 PI WPI; 2000-588967/56.
 DR
 XX
 XX Novel peptides having cell adhesion inhibiting properties are useful for
 PT treating cancer metastasis, inflammation and fibrosis.
 CC Claim 3; Page 8; 25pp; English.
 XX
 CC The present sequence represents a peptide derived from amino acid
 CC residues 1567-1581 of human fibronectin, but having the residue
 CC equivalent to Val-1581 substituted by alanine. Native and Ala-substituted
 CC fibrinogen-derived peptides of the invention (see AAB19566-71) are
 CC physiologically active, possessing cell adhesion inhibitory activity
 CC against human chronic myelocytic leukaemia K562 cells, human histiocytic
 CC lymphoma U937 cells and the Ramos cell line derived from human Burkitt's
 CC lymphoma, but not against human melanoma A375SM or fibrosarcoma HT1080
 CC cells. The peptides are used as antimetastatic agents that inhibit
 CC metastasis of cancers based on cell adhesion. They are also useful for
 CC investigating and treating diseases in which adhesion between cells or
 CC between cells and extracellular matrices are implicated, such as cancer,
 CC rheumatism, asthma, allergy, thrombosis, organ transplant rejection,
 CC wound healing such as fibrosis, inflammation, immuno-inflammatory
 CC conditions including enteritis such as ulcerative colitis, and autoimmune
 CC diseases. The peptides are prepared by chemical synthesis and are
 CC modified with biotin
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 62.3%; Score 48; DB 3; Length 15;
 Best Local Similarity 66.7%; Pred. No. 0.2;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GLRPGIDYDISV 13
 DB 1 GLRPGVDYITV 12
 XX
 RESULT 6
 ID AAB19567 standard; peptide; 15 AA.
 AC AAB19567;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Fibrinogen-derived peptide with anti-cell adhesion activity.
 XX
 KW Cell adhesion; inhibitor; antimetastatic; metastasis; cancer; antitumour;
 KW antiinflammatory; antithrombotic; antiaesthetic; antiallergic;
 KW antithrombotic; antifibrotic; immunostimulant; vulnerary; therapy;
 KW fibronectin; human.
 XX
 OS Homo sapiens.
 XX
 PN EP1036798-A1.
 XX
 PD 20-SEP-2000.
 PF 16-MAR-2000; 2000EP-00105572.
 XX
 XX 16-MAR-1999; 99JP-00070127.
 XX (HISM) HISAMITSU PHARM CO LTD.
 PA
 XX
 XX Akiyama K, Goto T, Fukai F, Ueki M;

XX WPI; 2000-588967/56.
XX
XX Novel peptides having cell adhesion inhibiting properties are useful for
PT treating cancer metastasis, inflammation and fibrosis.
PS
PS Claim 2; Page 8; 25pp; English.

CC The present sequence represents a peptide corresponding to amino acid
CC residues 1567-1581 of human fibronectin. The peptide is physiologically
CC active, possessing cell adhesion inhibitory activity against human
CC chronic myelocytic leukaemia K562 cells, human histiocytic lymphoma U937
CC cells and the Ramos cell line derived from human Burkitt's lymphoma, but
CC not against human melanoma A375SM or fibrosarcoma HT1080 cells. The
CC peptide, and its claimed alanine-substituted derivatives (see AAB19568-
71), are used as antimetastatic agents that inhibit metastasis of cancers
CC based on cell adhesion. They are also useful for investigating and
CC treating diseases in which adhesion between cells or between cells and
CC extracellular matrices are implicated, such as cancer, rheumatism,
CC asthma, allergy, thrombosis, organ transplant rejection, wound healing
CC such as fibrosis, inflammation, immuno-inflammatory conditions including
CC enteritis such as ulcerative colitis, and autoimmune diseases. The
CC peptides are prepared by chemical synthesis and are modified with biotin

XX
SQ Sequence 15 AA;

Query Match 62.3%; Score 48; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.2;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 GLEPGIDYDISV 13
||:||||:|
Db 1 GLKPGVDYITTV 12

RESULT 7
AAB19570
ID AAB19570 standard; peptide; 15 AA.
XX
XX AAB19570;

AC 22-JAN-2001 (first entry)
XX
XX

DE Fibrinogen-derived peptide with anti-cell adhesion activity.
XX

KW Cell adhesion; inhibitor; antimetastatic; metastasis; cancer; antitumour;
KW antiinflammatory; antirheumatic; antiaesthetic; antiallergic;
KW antithrombotic; antifibrotic; immunostimulant; vulnery; therapy;
KW fibronectin; human; mutant; mutein.
XX

OS Homo sapiens.
OS Synthetic.
XX

PN EPI036798-A1.
XX

PD 20-SEP-2000.
XX

PF 16-MAR-2000; 2000EP-00105572.
XX

PR 16-MAR-1999; 99JP-00070127.
XX

PA (HISM) HISAMITSU PHARM CO LTD.
XX

PI Akiyama K, Goto T, Fukai F, Ueki M;
XX

DR WPI; 2000-588967/56.
XX

PT Novel peptides having cell adhesion inhibiting properties are useful for
PT treating cancer metastasis, inflammation and fibrosis.
XX

PS Claim 3; Page 8; 25pp; English.
XX

CC The present sequence represents a peptide derived from amino acid

CC residues 1567-1581 of human fibronectin, but having the residue
CC equivalent to Tyr-1579 substituted by alanine. Native and Ala-substituted
CC fibrinogen-derived peptides of the invention (see AAB19566-71) are
CC physiologically active, possessing cell adhesion inhibitory activity
CC against human chronic myelocytic leukaemia K562 cells, human histiocytic
CC lymphoma U937 cells and the Ramos cell line derived from human Burkitt's
CC lymphoma, but not against human melanoma A375SM or fibrosarcoma HT1080
CC cells. The peptides are used as antimetastatic agents that inhibit
CC metastasis of cancers based on cell adhesion. They are also useful for
CC investigating and treating diseases in which adhesion between cells or
CC between cells and extracellular matrices are implicated, such as cancer,
CC rheumatism, asthma, allergy, thrombosis, organ transplant rejection,
CC wound healing such as fibrosis, inflammation, immuno-inflammatory
CC conditions including enteritis such as ulcerative colitis, and autoimmune
CC diseases. The peptides are prepared by chemical synthesis and are
CC modified with biotin

XX
SQ Sequence 15 AA;

Query Match 62.3%; Score 48; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.2;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 GLEPGIDYDISV 13
||:||||:|
Db 1 GLKPGVDYITTV 12

RESULT 8
AAB19575
ID AAB19575 standard; peptide; 15 AA.
XX
XX AAB19575;

AC 22-JAN-2001 (first entry)
XX
XX

DE Fibrinogen-derived peptide.
XX

KW Fibrinogen; cell adhesion; inhibitor; human; mutant; mutein.
XX

OS Homo sapiens.
OS Synthetic.
XX

PN EPI036798-A1.
XX

PD 20-SEP-2000.
XX

PF 16-MAR-2000; 2000EP-00105572.
XX

PR 16-MAR-1999; 99JP-00070127.
XX

PA (HISM) HISAMITSU PHARM CO LTD.
XX

PI Akiyama K, Goto T, Fukai F, Ueki M;
XX

DR WPI; 2000-588967/56.
XX

PT Novel peptides having cell adhesion inhibiting properties are useful for
PT treating cancer metastasis, inflammation and fibrosis.
XX

PS Example 4; Page 8; 25pp; English.
XX

CC The present sequence represents a peptide derived from amino acid
CC residues 1567-1581 of human fibronectin, but having the residue
CC equivalent to Thr-1577 substituted by alanine. Unlike other, claimed
CC fibrinogen-derived peptides of the invention (see AAB19566-71), the
CC present does not have cell adhesion inhibitory activity. The claimed
CC peptides are useful as antimetastatic agents

XX
SQ Sequence 15 AA;

Query Match 62.3%; Score 48; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.2;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 GLEPGIDYDISV 13
DB 1 GLKPGVDYITIV 12

RESULT 9

AAB19573
ID AAB19573 standard; peptide; 15 AA.

AC AAB19573;

DT 22-JAN-2001 (first entry)

DE Fibrinogen-derived peptide.

KM Fibrinogen; cell adhesion; inhibitor; human; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

PN EPI036798-A1.

PD 20-SEP-2000.

PF 16-MAR-2000; 2000EP-00105572.

PR 16-MAR-1999; 99JP-00070127.

PA (HISM) HISAMITSU PHARM CO LTD.

PI Akiyama K, Goto T, Fukai F, Ueki M;

DR WPI; 2000-588967/56.

PT Novel peptides having cell adhesion inhibiting properties are useful for

PS Example 4; Page 8; 25pp; English.

XX The present sequence represents a peptide derived from amino acid

CC residues 1567-1581 of human fibronectin, but having the residue

CC equivalent to Thr-1575 substituted by alanine. Unlike other, claimed

CC fibrinogen-derived peptides of the invention (see AAB19566-71), the

CC present does not have cell adhesion inhibitory activity. The claimed

CC peptides are useful as antimetastatic agents

SQ Sequence 15 AA;

Query Match 61.0%; Score 47; DB 3; Length 15;

Best Local Similarity 66.7%; Pred. No. 0.29; 1; Indels 0; Gaps 0;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GLEPGIDYDISV 13

DB 1 GLKPGVDYITIV 12

RESULT 10

AAB19569
ID AAB19569 standard; peptide; 15 AA.

AC AAB19569;

DT 22-JAN-2001 (first entry)

DE Fibrinogen-derived peptide with anti-cell adhesion activity.

KM Cell adhesion; inhibitor; antimetastatic; metastasis; cancer; antitumour;

KM antiinflammatory; antirheumatic; antiallergic; antiallergic;

KM antithrombotic; antifibrotic; immunostimulant; volnetary; therapy;

XX Homo sapiens.

OS Synthetic.

PN EPI036798-A1.

PD 20-SEP-2000.

PF 16-MAR-2000; 2000EP-00105572.

PR 16-MAR-1999; 99JP-00070127.

PA (HISM) HISAMITSU PHARM CO LTD.

PI Akiyama K, Goto T, Fukai F, Ueki M;

DR WPI; 2000-588967/56.

PT Novel peptides having cell adhesion inhibiting properties are useful for

PS Claim 3; Page 8; 25pp; English.

XX The present sequence represents a peptide derived from amino acid

CC residues 1567-1581 of human fibronectin, but having the residue

CC equivalent to Val-1578 substituted by alanine. Native and Ala-substituted

CC fibrinogen-derived peptides of the invention (see AAB19566-71) are

CC physiologically active, possessing cell adhesion inhibitory activity

CC against human chronic myelocytic leukaemia K562 cells, human histiocytic

CC lymphoma U937 cells and the Ramos cell line derived from human Burkitt's

CC cells. The peptides are used as antimetastatic agents that inhibit

CC metastasis of cancers based on cell adhesion. They are also useful for

CC investigating and treating diseases in which adhesion between cells or

CC between cells and extracellular matrices are implicated, such as cancer,

CC rheumatism, asthma, allergy, thrombosis, organ transplant rejection,

CC wound healing such as fibrosis, inflammation, immuno-inflammatory

CC conditions including enteritis such as ulcerative colitis, and autoimmune

CC modified with biotin

SQ Sequence 15 AA;

Query Match 57.1%; Score 44; DB 3; Length 15;

Best Local Similarity 63.6%; Pred. No. 0.97; 1; Indels 0; Gaps 0;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GLEPGIDYDIS 12

DB 1 GLKPGVDYITIT 11

RESULT 11

AAB19574
ID AAB19574 standard; peptide; 15 AA.

AC AAB19574;

DT 22-JAN-2001 (first entry)

DE Fibrinogen-derived peptide.

KM Fibrinogen; cell adhesion; inhibitor; human; mutant; mutein.

PR 16-MAR-1999; 99JP-00070127.
 XX (HISM) HISAMITSU PHARM CO LTD.
 XX
 XX Akiyama K, Goto T, Fukai F, Ueki M;
 XX WPI; 2000-588967/56.
 XX
 PT Novel peptides having cell adhesion inhibiting properties are useful for
 PT treating cancer metastasis, inflammation and fibrosis.
 XX
 PS Example 4; Page 8; 25pp; English.
 XX
 CC The present sequence represents a peptide derived from amino acid
 CC residues 1567-1581 of human fibronectin, but having the residue
 CC equivalent to Ile-1576 substituted by alanine. Unlike other, claimed
 CC fibrinogen-derived peptides of the invention (see ABA19566-71), the
 CC present does not have cell adhesion inhibitory activity. The claimed
 CC peptides are useful as antimetastatic agents
 CC
 SQ Sequence 15 AA;
 Query Match 55.8%; Score 43; DB 3; Length 15;
 Best Local Similarity 58.3%; Pred. No. 1.5;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGLEPGIDYDISV 13
 Db 1 TGLRPGVGYVTV 12
 RESULT 12
 AAM48854
 ID AAM48854 standard; peptide; 15 AA.
 XX
 AC AAM48854;
 XX
 DT 11-SEP-1998 (first entry)
 XX
 DE Peptide II having affinity for fibronectin.
 XX
 KM Fibronectin; gelatin; trypsin; phosphatidylethanolamine;
 KM baby hamster kidney cell; metastatic; tumour.
 XX
 OS Bos sp.
 XX
 PN WO9817242-A1.
 XX
 PD 30-APR-1998.
 XX
 PF 23-OCT-1997; 97WO-US018853.
 XX
 PR 24-OCT-1996; 96US-0029509P.
 XX
 PA (UNIT) UNIV ILLINOIS FOUND.
 XX
 PI Groves MJ, Gao X;
 XX
 DR WPI; 1998-261156/23.
 XX
 PT New peptide(s) which bind to fibronectin - are obtained by digesting
 PT gelatin with a protease, used for inhibiting binding of cells or delivery
 PT of bioactive agents, particularly for treating tumours.
 XX
 PS Claim 4; Page 45; 55pp; English.
 XX
 CC The present sequence represents a peptide derived from the tryptic
 CC digestion of bovine skin gelatin. The invention provides a method for the
 CC identification of unique fibronectin-targeting peptides, such as the
 CC present one, derived from tryptic digestion of purified gelatin. Peptide
 CC II linked to phosphatidylethanolamine through its N-terminus was shown to
 CC retain the fibronectin affinity and to inhibit the spreading of baby
 CC hamster kidney cells, which is a well recognized in vitro model of

CC metastatic tumour spreading activity. Therefore, peptide II is claimed to
 CC be useful for inhibiting binding of cells to fibronectin, e.g. for
 CC treating tumours or metastases. They are also claimed to be useful for
 CC delivering a bioactive agent to a fibronectin-enriched surface such as on
 CC tumour cells
 CC
 SQ Sequence 15 AA;
 Query Match 50.6%; Score 39; DB 2; Length 15;
 Best Local Similarity 46.7%; Pred. No. 7.2;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TGLEPGIDYDISVT 15
 Db 1 TGLPVGVGYYVTVLT 15
 RESULT 13
 AAB19568
 ID AAB19568 standard; peptide; 15 AA.
 XX
 AC AAB19568;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Fibrinogen-derived peptide with anti-cell adhesion activity.
 XX
 KM Cell adhesion; inhibitor; antimetastatic; metastasis; cancer; antitumour;
 KM antiinflammatory; antirheumatic; antiaesthetic; antiallergic;
 KM antithrombotic; antifibrotic; immunostimulant; vulnerary; therapy;
 KM fibronectin; human; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN EP1036798-A1.
 XX
 PD 20-SEP-2000.
 XX
 PF 16-MAR-2000; 2000EP-00105572.
 XX
 PR 16-MAR-1999; 99JP-00070127.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Akiyama K, Goto T, Fukai F, Ueki M;
 XX
 DR WPI; 2000-588967/56.
 XX
 PT Novel peptides having cell adhesion inhibiting properties are useful for
 PT treating cancer metastasis, inflammation and fibrosis.
 XX
 PS Claim 3; Page 8; 25pp; English.
 XX
 CC The present sequence represents a peptide derived from amino acid
 CC residues 1567-1581 of human fibronectin, but having the residue
 CC equivalent to Tyr-1574 substituted by alanine. Native and Ala-substituted
 CC fibrinogen peptides of the invention (see AAB19566-71) are
 CC physiologically active, possessing cell adhesion inhibitory activity
 CC against human chronic myelocytic leukemia K562 cells, human histiocytic
 CC lymphoma U937 cells and the Ramos cell line derived from human Burkitt's
 CC lymphoma, but not against human melanoma A375SM or fibrosarcoma HT1080
 CC cells. The present Ala-substituted peptide has a stronger cell adhesion
 CC inhibitory activity than its non-substituted equivalent. The peptides are
 CC used as antimetastatic agents that inhibit metastasis of cancers based on
 CC cell adhesion. They are also useful for investigating and treating
 CC diseases in which adhesion between cells or between cells and
 CC extracellular matrices are implicated, such as cancer, rheumatism,
 CC asthma, allergy, thrombosis, organ transplant rejection, wound healing
 CC such as fibrosis, inflammation, immuno-inflammatory conditions including
 CC enteritis such as ulcerative colitis, and autoimmune diseases. The
 CC peptides are prepared by chemical synthesis and are modified with biotin

Tue Sep 21 07:04:07 2004

us-10-676-049-3.closed.rag

Page 8

Sequence 11 AA;

Query Match 44.2%; Score 34; DB 6; Length 11;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 4 EPGIDY 9
Db 3 EPGVDY 8.

Search completed: September 21, 2004, 06:40:43
Job time : 74.333 secs

OM protein - protein search, using sw model

Run on: September 21, 2004, 06:42:10 : Search time 70.6667 Seconds
(without alignments)
68.165 Million cell updates/sec

Title: US-10-676-049-3
Perfect score: 77
Sequence: 1 TGLEPGIDYDISVIT 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1342398 seqs, 32113274 residues

Total number of hits satisfying chosen parameters: 221706

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	15	9	US-09-942-117-3 Sequence 3, Appl1
2	64	83.1	15	10	US-09-300-425B-23 Sequence 23, Appl1
3	64	83.1	15	14	US-10-321-558-2 Sequence 2, Appl1
4	56	72.7	15	9	US-09-942-117-2 Sequence 2, Appl1
5	50	64.9	15	9	US-09-942-117-19 Sequence 19, Appl1
6	39	50.6	15	16	US-10-720-025-56 Sequence 56, Appl1
7	34	44.2	11	15	US-10-285-394-5 Sequence 5, Appl1
8	29	37.7	15	10	US-09-880-748-2782 Sequence 2782, Ap
9	29	37.7	15	12	US-10-293-418-2782 Sequence 2782, Ap
10	28	36.4	9	9	US-09-780-053-440 Sequence 440, App
11	28	36.4	10	9	US-09-780-053-110 Sequence 110, App
12	28	36.4	10	9	US-09-780-053-308 Sequence 308, App
13	28	36.4	10	16	US-10-766-283-4 Sequence 4, Appl1
14	28	36.4	12	14	US-10-071-962-17 Sequence 17, Appl1
15	27.5	35.7	10	14	US-10-228-806-51 Sequence 50, Appl1

15	27.5	35.7	10	14	US-10-228-806-51	Sequence 51, Appl1
16	27.5	35.7	10	15	US-10-100-303A-37	Sequence 37, Appl1
17	27.5	35.7	10	15	US-10-100-303A-38	Sequence 38, Appl1
18	27.5	35.7	9	16	US-10-600-187-42	Sequence 49, Appl1
19	27	35.1	9	16	US-10-600-187-56	Sequence 56, Appl1
20	27	35.1	10	14	US-10-113-732-5	Sequence 583, App
21	27	35.1	13	16	US-10-468-370-583	Sequence 583, App
22	27	35.1	13	16	US-10-468-370-584	Sequence 584, App
23	27	35.1	14	8	US-08-891-525-3	Sequence 3, Appl1
24	27	35.1	14	14	US-10-198-590-3	Sequence 63, Appl1
25	27	35.1	14	14	US-10-091-300-63	Sequence 74, Appl1
26	27	35.1	14	15	US-10-279-633-74	Sequence 2164, Ap
27	27	35.1	15	9	US-09-942-117-18	Sequence 2164, Ap
28	27	35.1	15	10	US-09-880-748-2164	Sequence 221, App
29	27	35.1	15	8	US-08-344-824-221	Sequence 148, App
30	27	35.1	10	14	US-10-133-210-148	Sequence 165, App
31	26	33.8	10	14	US-10-353-929-165	Sequence 276, App
32	26	33.8	12	10	US-09-965-738-276	Sequence 12, Appl1
33	26	33.8	12	16	US-10-654-623-12	Sequence 9, Appl1
34	26	33.8	13	9	US-09-813-333-9	Sequence 9, Appl1
35	26	33.8	13	12	US-10-239-103-9	Sequence 1, Appl1
36	26	33.8	13	16	US-10-044-703-9	Sequence 45, Appl1
37	26	33.8	14	16	US-10-361-275-1	Sequence 60, Appl1
38	26	33.8	15	12	US-10-128-510-20	Sequence 20, Appl1
39	26	33.8	15	13	US-10-193-142-20	Sequence 20, Appl1
40	26	33.8	15	14	US-10-134-493-20	Sequence 20, Appl1
41	26	33.8	15	14	US-10-061-216-20	Sequence 20, Appl1
42	26	33.8	15	14		
43	26	33.8	15	14		
44	26	33.8	15	14		
45	26	33.8	15	14		

ALIGNMENTS

RESULT 1
US-09-942-117-3
; Sequence 3, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BARR, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942,117
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-942-117-3
Query Match 100.0%; Score 77; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. NO. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDISVIT 15
DB 1 TGLEPGIDYDISVIT 15

RESULT 2

US-09-300-425B-23
; Sequence 23, Application US/09300425B
; Publication No. US20030045681A1
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TARTI, Lorenzo
; APPLICANT: VITTI, Francesca
; APPLICANT: BIRCHER, Manfred
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONTUGATES
; TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
; FILE REFERENCE: SCH-1733P1
; CURRENT APPLICATION NUMBER: US/09/300,425B
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/075,338
; PRIOR FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide formula
US-09-300-425B-23

Query Match

Best Local Similarity 83.1%; Score 64; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDIS 12
|||||

Db 4 TGLEPGIDYDIS 15

RESULT 3

US-10-321-558-2
; Sequence 2, Application US/10321558
; Publication No. US2003017663A1
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TARTI, LORENZO
; APPLICANT: VITTI, FRANCISCA
; APPLICANT: BIRCHER, MANFRED
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY
; FILE REFERENCE: NOTAR-1 C1
; CURRENT APPLICATION NUMBER: US/10/321,558
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 09/512,082
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 09/300,425
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/075,338
; PRIOR FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-321-558-2

Query Match

Best Local Similarity 83.1%; Score 64; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYDIS 12
|||||

Db 4 TGLEPGIDYDIS 15

RESULT 4
US-09-942-117-2
; Sequence 2, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAHR, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942,117
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-2

Query Match
Best Local Similarity 72.7%; Score 56; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGIDYD 10
|||||

Db 6 TGLEPGIDYD 15

RESULT 5

US-09-942-117-19
; Sequence 19, Application US/09942117
; Publication No. US20020197700A1
; GENERAL INFORMATION:
; APPLICANT: MENRAD, ANDREAS
; APPLICANT: REDLITZ, ALEXANDER
; APPLICANT: KOPPLITZ, MARCUS
; APPLICANT: EGNER, URSULA
; APPLICANT: BAHR, INKE
; TITLE OF INVENTION: RECEPTOR OF THE EDB-FIBRONECTIN DOMAINS
; FILE REFERENCE: SCH-1832
; CURRENT APPLICATION NUMBER: US/09/942,117
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: DE 10045803.3
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: DE 10123133.4-41
; PRIOR FILING DATE: 2001-05-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-942-117-19

Query Match

Best Local Similarity 64.9%; Score 50; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GIDYDISVT 15
|||||
Db 1 GIDYDISVT 10

RESULT 6
US-10-720-025-56

; Sequence 56, Application US/10720025
; Publication No. US20040171545A1
; GENERAL INFORMATION:
; APPLICANT: REPRESENTATIVE: Greenlee, Winner and Sullivan, P.C.
; APPLICANT: Emory University
; APPLICANT: Chaikof, Elliot L.
; APPLICANT: Nagapudi, Karthik
; APPLICANT: Brinkman, William T.
; APPLICANT: Conticello, Vincent P.
; APPLICANT: McMillan, Robert A.
; APPLICANT: Wright, Elizabeth R.
; APPLICANT: Payne, Sonja C.
; TITLE OF INVENTION: PLASTIC AND ELASTIC PROTEIN COPOLYMERS
; FILE REFERENCE: 133-02 US
; CURRENT APPLICATION NUMBER: US/10/720,025
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/428,438
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: CA 2,417,634
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: JP 2003-98691
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: AU 2003236491
; PRIOR FILING DATE: 2003-08-27
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic construct.
US-10-720-025-56

Query Match 50.6%; Score 39; DB 16; Length 15;
Best Local Similarity 46.7%; Pred. No. 9.5;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TGLEPGIDYDISVT 15
||| | | | | | | | | | | | | | | |
Db 1 TGLPVGIVGVYVYVLT 15

RESULT 7
US-10-285-394-5

; Sequence 5, Application US/10285394
; Publication No. US20030228583A1
; GENERAL INFORMATION:
; APPLICANT: AMACHER, DAVID E.
; APPLICANT: PASULO, LISA M.
; APPLICANT: HERATH, HERATH MUDIVANSELAGE ATHULA CHANDRASIRI
; APPLICANT: HOLT, GORDON DUANE
; APPLICANT: STIGER, THOMAS R.
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
; FILE REFERENCE: POA-003-01
; CURRENT APPLICATION NUMBER: US/10/285,394
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,964
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-394-5

Query Match 44.2%; Score 34; DB 15; Length 11;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EPQIDY 9
||| | | | | | | | | | |
Db 3 EPQVDY 8

RESULT 8
US-09-880-748-2782

; Sequence 2782, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2782
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2782

Query Match 37.7%; Score 29; DB 10; Length 15;
Best Local Similarity 55.6%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGLEPGIDY 9
||| | | | | | | | | | |
Db 7 TGYQGVDY 15

RESULT 9
US-10-293-418-2782

; Sequence 2782, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16

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/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2782
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-293-418-2782
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Query Match          37.7%; Score 29; DB 12; Length 15;
Best Local Similarity 55.6%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 GLEPGIDY 9
    |||
Db 7 TGYVQGVDF 15
```

```
RESULT 10
US-09-780-053-440
/ Sequence 440, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Chailita-Eid
/ APPLICANT: Mary Farris
/ APPLICANT: Eliana Levin
/ APPLICANT: Steve Chappell Mitchell
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 440
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-440
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```
Query Match          36.4%; Score 28; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 GLEPGIDY 9
    |||
Db 2 GLAPSVDF 9
```

```
RESULT 11
US-09-780-053-110
/ Sequence 110, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Chailita-Eid
/ APPLICANT: Mary Farris
/ APPLICANT: Eliana Levin
/ APPLICANT: Steve Chappell Mitchell
/ APPLICANT: Aya Jakobovits
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
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```
/ SEQ ID NO 110
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-110
```

```
Query Match          36.4%; Score 28; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 GLEPGIDY 9
    |||
Db 1 GLAPSVDF 8
```

```
RESULT 12
US-09-780-053-308
/ Sequence 308, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Chailita-Eid
/ APPLICANT: Mary Farris
/ APPLICANT: Eliana Levin
/ APPLICANT: Steve Chappell Mitchell
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 308
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-308
```

```
Query Match          36.4%; Score 28; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 GLEPGIDY 9
    |||
Db 1 GLAPSVDF 8
```

```
RESULT 13
US-10-766-283-4
/ Sequence 4, Application US/10766283
/ Publication No. US20040126827A1
/ GENERAL INFORMATION:
/ APPLICANT: Singh, Bal Ram
/ TITLE OF INVENTION: NOVEL PROTEINS WITHIN THE TYPE E
/ BOTULINUM NEUROTOXIN COMPLEX
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows 95
/ SOFTWARE: FastSeq for Windows Version 2.0b
```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/766,283
; FILING DATE: 27-Jan-2004
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/546,136
; FILING DATE: 10-APR-2000
; APPLICATION NUMBER: US 08/889,354
; FILING DATE: 08-JUL-1997
; APPLICATION NUMBER: US 60/021,348
; FILING DATE: 08-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 08387/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-766-283-4

Query Match          36.4%; Score 28; DB 16; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TGLEPGIDYD 10
        | : | | |
Db      1 TNLKPYLTD 10

RESULT 14
US-10-071-962-17
; Sequence 17, Application US/10071962
; Publication No. US20030170237A1
; GENERAL INFORMATION:
; APPLICANT: Baifu Ni
; APPLICANT: Bill N.C. Sun
; APPLICANT: Cedilly R.Y. Sun
; TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and
; FILE OF INVENTION: Screening Method Therefor
; FILE REFERENCE: 98-3
; CURRENT APPLICATION NUMBER: US/10/071,962
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/303,155A
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,575
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: mouse
US-10-071-962-17

Query Match          36.4%; Score 28; DB 14; Length 12;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GLEPGIDY 9
        | : | | |
Db      5 GGHGFDY 12

RESULT 15
US-10-228-806-50
; Sequence 50, Application US/10228806
```

```

; Publication No. US20030049237A1
; GENERAL INFORMATION:
; APPLICANT: Bannou, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions
; FILE OF INVENTION: to Allergy
; FILE REFERENCE: 2002834-0043
; CURRENT APPLICATION NUMBER: US/10/228,806
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arachis hypogaea
US-10-228-806-50

Query Match          35.7%; Score 27.5; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      2 GLEPGIDYD 10
        | : | | |
Db      3 GRPG-DYD 10

Search completed: September 21, 2004, 07:03:18
Job time : 70.6667 secs
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OM protein - protein search, using sw model

Run on: September 21, 2004, 06:15:34; Search time 13.6667 Seconds

(without alignments)
56.663 Million cell updates/sec

Title: US-10-676-049-3

Perfect score: 77

Sequence: 1 TGLEPGIDYDISVIR 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 146418

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- Issued Patents AA:*
- 1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
 - 2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
 - 3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
 - 4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
 - 5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
 - 6: /cgn2_6/prodata/2/1aa/backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	62.3	15	4	US-09-526-879-2
2	48	62.3	15	4	US-09-526-879-6
3	48	62.3	15	4	US-09-526-879-8
4	48	62.3	15	4	US-09-526-879-9
5	47	61.0	15	4	US-09-526-879-4
6	44	57.1	15	4	US-09-526-879-7
7	43	55.8	15	4	US-09-526-879-5
8	39	50.6	15	4	US-09-526-879-3
9	35	46.8	15	4	US-09-526-879-12
10	35	46.8	15	4	US-09-526-879-13
11	32	41.6	15	3	US-09-248-588-90
12	29	37.7	9	2	US-08-340-283-158
13	28	36.4	10	2	US-08-724-548-28
14	28	36.4	10	2	US-08-724-548-29
15	28	36.4	10	2	US-08-724-548-30
16	28	36.4	10	2	US-08-724-548-31
17	28	36.4	10	3	US-07-978-674B-28
18	28	36.4	10	3	US-07-978-674B-29
19	28	36.4	10	3	US-07-978-674B-30
20	28	36.4	10	3	US-07-978-674B-31
21	27	35.1	9	4	US-09-644-600-49
22	27	35.1	9	4	US-09-644-600-56
23	27	35.1	9	4	US-09-654-600A-49
24	27	35.1	9	4	US-09-654-600A-56
25	27	35.1	14	1	US-07-690-983D-30
26	27	35.1	14	1	US-08-212-433A-8
27	27	35.1	14	2	US-08-978-404B-28

28	27	35.1	14	3	US-08-716-256-8	Sequence 8, Appl1
29	27	35.1	14	4	US-08-891-525-3	Sequence 3, Appl1
30	27	35.1	14	5	PCT-US95-0323-8	Sequence 8, Appl1
31	27	35.1	15	3	US-08-822-322-3	Sequence 3, Appl1
32	27	35.1	15	3	US-09-466-109-3	Sequence 3, Appl1
33	26	33.8	9	2	US-08-368-834-1	Sequence 1, Appl1
34	26	33.8	9	2	US-08-447-154-1	Sequence 1, Appl1
35	26	33.8	10	2	US-08-724-548-27	Sequence 27, Appl1
36	26	33.8	10	3	US-07-978-674B-27	Sequence 27, Appl1
37	26	33.8	12	2	US-08-368-834-18	Sequence 18, Appl1
38	26	33.8	12	2	US-08-447-154-17	Sequence 17, Appl1
39	26	33.8	13	4	US-08-716-249-13	Sequence 13, Appl1
40	26	33.8	14	2	US-08-271-667B-3	Sequence 3, Appl1
41	26	33.8	14	3	US-08-765-889C-16	Sequence 16, Appl1
42	26	33.8	14	5	PCT-US95-07855-16	Sequence 16, Appl1
43	26	33.8	15	2	US-08-480-190-185	Sequence 185, App
44	26	33.8	15	2	US-08-368-834-7	Sequence 7, Appl1
45	26	33.8	15	2	US-08-468-379-185	Sequence 185, App

ALIGNMENTS

RESULT 1
US-09-526-879-2
Sequence 2, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
APPLICANT: FUKAI, FUMIO
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007896-0257795
CURRENT APPLICATION NUMBER: US/09/526, 879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-2

Query Match 62.3%; Score 48; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.066; 1; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 GLEPGIDYDISV 13
DB 1 GLEPGDYTVIR 12
RESULT 2
US-09-526-879-6
Sequence 6, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
APPLICANT: FUKAI, FUMIO
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007896-0257795
CURRENT APPLICATION NUMBER: US/09/526, 879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-6

Query Match 62.3%; Score 48; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.066;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GLEPGIDYDISV 13
||:|:|:|:|:|:
Db 1 GLKPGVDYITIV 12

RESULT 3
US-09-526-879-8
Sequence 8, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007898-0257795
CURRENT APPLICATION NUMBER: US/09/526, 879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-8

Query Match 62.3%; Score 48; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.066;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GLEPGIDYDISV 13
||:|:|:|:|:|:
Db 1 GLKPGVDYITIV 12

RESULT 4
US-09-526-879-9
Sequence 9, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007898-0257795
CURRENT APPLICATION NUMBER: US/09/526, 879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-9

Query Match 62.3%; Score 48; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.066;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GLEPGIDYDISV 13
||:|:~|:|:|:|:
Db 1 GLKPGVDYITIV 12

RESULT 5
US-09-526-879-4
Sequence 4, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007898-0257795
CURRENT APPLICATION NUMBER: US/09/526, 879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-4

Query Match 61.0%; Score 47; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 0.098;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GLEPGIDYDISV 13
||:|:|:|:|:|:
Db 1 GLKPGVDYITIV 12

RESULT 6
US-09-526-879-7
Sequence 7, Application US/09526879
Patent No. 6451971
GENERAL INFORMATION:
APPLICANT: AKIYAMA, KATSUHIKO
APPLICANT: GOTO, TAKESHI
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
FILE REFERENCE: 007898-0257795
CURRENT APPLICATION NUMBER: US/09/526, 879
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: JP 070127/1999
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Physiologically active peptide
US-09-526-879-7

Best Local Similarity 63.6%; Pred. No. 0.31;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GLEPGIDYDIS 12
||:|||||:
Db 1 GLKPGVDYTV 11

RESULT 7
US-09-526-879-5
; Sequence 5, Application US/09526879
; Patent No. 6451971
; GENERAL INFORMATION:
; APPLICANT: AKIYAMA, KATSUHIKO
; APPLICANT: GOTO, TAKESHI
; APPLICANT: FUKAI, FUMIO
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
; FILE REFERENCE: 007898-0257795
; CURRENT APPLICATION NUMBER: US/09/526, 879
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: JP 070127/1999
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Physiologically active peptide
US-09-526-879-5

Query Match 55.8%; Score 43; DB 4; Length 15;
Best Local Similarity 58.3%; Pred. No. 0.46;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GLEPGIDYDISV 13
||:|||||:
Db 1 GLKPGVDYTV 12

RESULT 8
US-09-526-879-3
; Sequence 3, Application US/09526879
; Patent No. 6451971
; GENERAL INFORMATION:
; APPLICANT: AKIYAMA, KATSUHIKO
; APPLICANT: GOTO, TAKESHI
; APPLICANT: FUKAI, FUMIO
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
; FILE REFERENCE: 007898-0257795
; CURRENT APPLICATION NUMBER: US/09/526, 879
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: JP 070127/1999
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Physiologically active peptide
US-09-526-879-3

Query Match 50.6%; Score 39; DB 4; Length 15;
Best Local Similarity 56.3%; Pred. No. 2.2;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GLEPGIDYDISV 13
||:|||||:
Db 1 GLKPGVDYTV 11

Db 1 GLKPGVDYTV 12

RESULT 9
US-09-526-879-12
; Sequence 12, Application US/09526879
; Patent No. 6451971
; GENERAL INFORMATION:
; APPLICANT: AKIYAMA, KATSUHIKO
; APPLICANT: GOTO, TAKESHI
; APPLICANT: FUKAI, FUMIO
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
; FILE REFERENCE: 007898-0257795
; CURRENT APPLICATION NUMBER: US/09/526, 879
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: JP 070127/1999
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Physiologically active peptide
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Tyr or Ala
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Val or Ala
; NAME/KEY: MOD_RES
; LOCATION: (13)
; OTHER INFORMATION: Tyr or Ala
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: Val or Ala
US-09-526-879-12

Query Match 46.8%; Score 36; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 7.1;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GLEPGIDYDIS 12
||:|||||:
Db 1 GLKPGVDYTV 11

RESULT 10
US-09-526-879-13
; Sequence 13, Application US/09526879
; Patent No. 6451971
; GENERAL INFORMATION:
; APPLICANT: AKIYAMA, KATSUHIKO
; APPLICANT: GOTO, TAKESHI
; APPLICANT: FUKAI, FUMIO
; TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE PEPTIDES
; FILE REFERENCE: 007898-0257795
; CURRENT APPLICATION NUMBER: US/09/526, 879
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: JP 070127/1999
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Physiologically active peptide
; NAME/KEY: MOD_RES

LOCATION: (8)
OTHER INFORMATION: Tyr or Ala
NAME/KEY: MOD RES
LOCATION: (12)
OTHER INFORMATION: Val or Ala
NAME/KEY: MOD_RES
LOCATION: (13)
OTHER INFORMATION: Tyr or Ala
US-09-526-879-13

Query Match 46.8%; Score 36; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 7.1;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GLEPGIDYDIS 12
|||:|:|:
DB 1 GLEPGVDXTIT 11

RESULT 11
US-09-248-588-90
Sequence 90, Application US/09248588
Patent No. 6231864
GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
FILE REFERENCE: SYN-101 4564/69529
CURRENT APPLICATION NUMBER: US/09/248,588
EARLIER FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: 60/074537
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 90
LENGTH: 15
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-248-588-90

Query Match 41.6%; Score 32; DB 3; Length 15;
Best Local Similarity 71.4%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGLEPGI 7
|||:|:|:
DB 5 SGLEPGV 11

RESULT 12
US-08-340-283-158
Sequence 158, Application US/08340283
Patent No. 5863318
GENERAL INFORMATION:
APPLICANT: Elhammer, Ake P.
TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
TITLE OF INVENTION: N-ACETYLGLACOSAMINYLTRANSFERASE ACTIVITY
NUMBER OF SEQUENCES: 205
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
ADDRESS: (1920-32-1)
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Wootten, Thomas A.
REGISTRATION NUMBER: 35,004
REFERENCE/DOCKET NUMBER: 4828
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 385-7914
TELEFAX: (616) 385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-340-283-158

Query Match 37.7%; Score 29; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1;

QY 1 TGLEPGI 7
|||:|:|:
DB 3 TGSEPGI 9

RESULT 13
US-08-724-548-28
Sequence 28, Application US/08724548
Patent No. 5830637
GENERAL INFORMATION:
APPLICANT: Guler, Ronald
TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF
TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joseph T. Bisele
ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,
ADDRESSEE: Levy, Bisele and Richard
STREET: 711 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10017-4059
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" DISKETTE
COMPUTER: IBM-XT COMPATIBLE
OPERATING SYSTEM: DOS 3.3
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,548
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 07/978,674
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE: 03/22/93
NAME: BISELE, JOSEPH T.
REGISTRATION NUMBER: 25,331
REFERENCE/DOCKET NUMBER: 2727-68 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 687-6000

TELEX: (212) 426767
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: Peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE: Internal fragment
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
US-08-724-548-28

Query Match 36.4%; Score 28; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CY 5 PGIDYDI 11
DB 4 PGDXDL 10

RESULT 14
US-08-724-548-29
Sequence 29, Application US/08724548
Patent No. 5830637
GENERAL INFORMATION:
APPLICANT: Frank, Ronald
APPLICANT: Guler, Sinan
TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF
TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE
TITLE OF INVENTION: PROCESS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joseph T. Eisele
ADDRESSEE: Kane, Daisimer, Sullivan, Kurucz,
ADDRESSEE: Levy, Eisele and Richard
STREET: 711 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10017-4059
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" DISKETTE
COMPUTER: IBM-XT COMPATIBLE
OPERATING SYSTEM: DOS 3.3:
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,548
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/978,674
FILING DATE: 03/22/93
ATTORNEY/AGENT INFORMATION:
NAME: EISELE, JOSEPH T.
REGISTRATION NUMBER: 25,331
REFERENCE/DOCKET NUMBER: 2727-68 PCT
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 687-6000
TELEFAX: (212) 682-3485
TELEX: (212) 426767
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: Peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE: Internal fragment
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
US-08-724-548-29

Query Match 36.4%; Score 28; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CY 5 PGIDYDI 11
DB 3 PGDXDL 9

RESULT 15
US-08-724-548-30
Sequence 30, Application US/08724548
Patent No. 5830637
GENERAL INFORMATION:
APPLICANT: Frank, Ronald
APPLICANT: Guler, Sinan
TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF
TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE
TITLE OF INVENTION: PROCESS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joseph T. Eisele
ADDRESSEE: Kane, Daisimer, Sullivan, Kurucz,
ADDRESSEE: Levy, Eisele and Richard
STREET: 711 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10017-4059
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" DISKETTE
COMPUTER: IBM-XT COMPATIBLE
OPERATING SYSTEM: DOS 3.3:
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,548
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/978,674
FILING DATE: 03/22/93
ATTORNEY/AGENT INFORMATION:
NAME: EISELE, JOSEPH T.
REGISTRATION NUMBER: 25,331

Tue Sep 21 07:04:07 2004

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Page 6

REFERENCE/DOCKET NUMBER: 2727-68 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 687-6000
TELEFAX: (212) 682-3485
TELEX: (212) 426767
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: Peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE: internal fragment
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
US-08-724-548-30

Query Match 36.4%; Score 28; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CY 5 PGIDYDI 11
||:|:
Db 2 PGDXDL 8

Search completed: September 21, 2004, 06:42:06
Job time : 14.6667 secs